## A NEW FRAMEWORK FOR UNDERSTANDING MATERNAL CONTINUITY ACROSS GENERATIONS

Every human life begins with a mother. From the first connection in the womb to the distant past of our species, an unbroken chain of maternal relationships links each individual to generations of women who came before.

In this book, the author revisits his earlier Theory of Matriarchism and reconstructs it in the light of modern science. Maternal Continuity Theory (MCT) offers a comprehensive interdisciplinary framework that connects gestational biology, genealogy, mitochondrial genetics, population science, evolution, and theological reflection.

### INSIDE THIS BOOK

- The three dimensions of maternal continuity: gestational, genealogical, and maternal genetic
- Serial maternal links and the distinction between transmission and relatedness
- Mitochondrial DNA inheritance and the reality of heteroplasmy
- Human evolution, ancient DNA, and population-level inference
- Genealogical modelling with real-world examples
- Assisted reproduction, mitochondrial replacement, and boundary conditions
- Qur'anic perspectives on creation, gestation, and human kinship
- Testable propositions, limitations, and future empirical research

### ABOUT THE AUTHORS

Prof. Dr Kazi Abdul Mannan is interdisciplinary areas including human origins, genealogy, reproductive biology, and comparative theology. His earlier work, *A Theory of Matriarchism: The Universal Origins of Humanity*, initated a long-standing inquiry into maternal ancestry and human continuity. In this book, he revisits that theory, addresses its limitations, and presents Maternal *Continuity Theory* (MCT) as a modern, testable, and scientifically informed framework.

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*From* MATRIARCHISM *to* MATERNAL CONTINUITY

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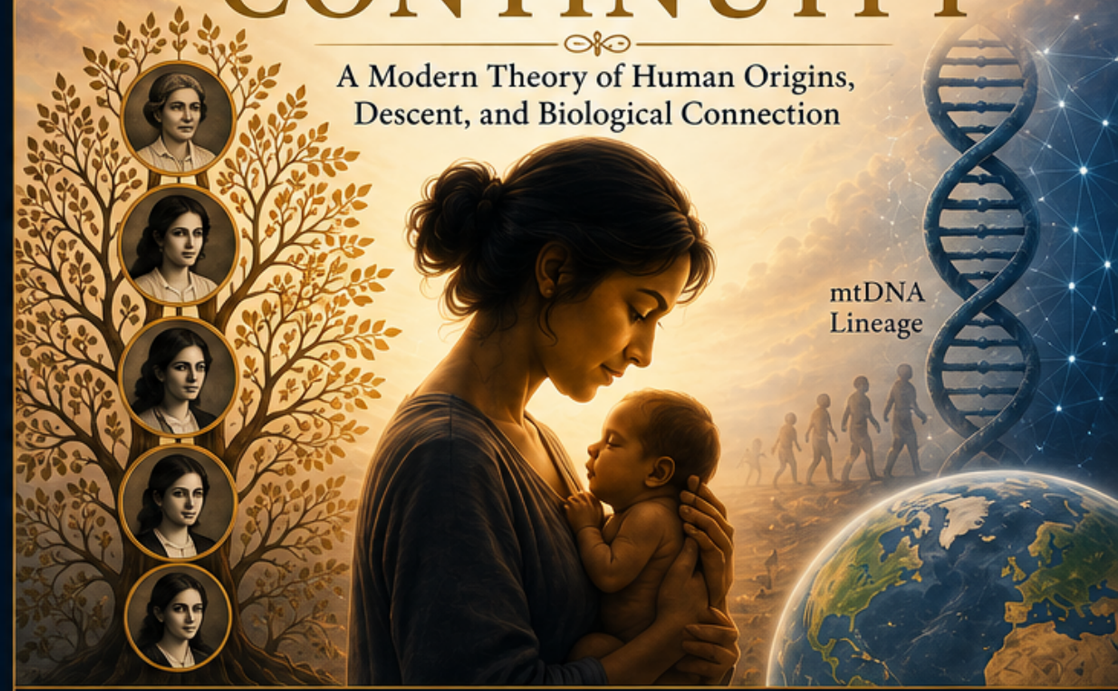
# *From* MATRIARCHISM *to* MATERNAL CONTINUITY

A Modern Theory of Human Origins, Descent, and Biological Connection




GESTATIONAL CONTINUITY | GENEALOGICAL CONTINUITY | MATERNAL GENETIC CONTINUITY | SCIENTIFIC EVIDENCE | QUR'ANIC PERSPECTIVE

Integrating Reproductive Biology, Genetics, Genealogy, Evolution, and Comparative Theology


Prof. Dr Kazi Abdul Mannan

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# [i]From Matriarchism to Maternal Continuity

*A Modern Theory of Human Origins, Descent, and Biological Connection*

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## Abstract

Maternal inheritance has been extensively investigated in reproductive biology, genetics, genealogy, and population science, yet these domains are rarely integrated within a single theoretical framework. This study develops **Maternal Continuity Theory (MCT)** as an interdisciplinary model for examining human intergenerational continuity across three analytically distinct but potentially convergent dimensions: **gestational continuity, genealogical continuity, and maternal genetic continuity**. The theory originates from the observable maternal-fetal relationship established during gestation and extends this relationship conceptually through serial mother-offspring links across generations. Unlike earlier formulations that risked conflating anatomical, genealogical, and genetic evidence, the revised MCT distinguishes each evidentiary domain and defines explicit boundaries between direct observation, documentary reconstruction, molecular corroboration, and population-level inference. The framework incorporates reproductive physiology, multigenerational pedigree modelling, predominantly maternal mitochondrial DNA transmission, evolutionary biology, and population genetics. An illustrative multigenerational family from Bangladesh is reanalysed to demonstrate how female-line gestational pathways, broader genealogical descent, and mitochondrial transmission may overlap while remaining biologically distinct. Eight theoretical propositions are advanced, including the Serial Maternal-Link Principle, Domain Independence Principle, Transmission-Relatedness Distinction, Maternal Continuity Convergence Principle, and Deep-Time Inference Boundary. MCT is positioned as complementary to, rather than competing with, evolutionary theory and biparental genetic ancestry. It does not equate mitochondrial coalescence with a unique first human female and does not treat theological interpretations as biomedical evidence. The theory generates a testable research programme based on verified pedigrees, reproductive histories, mtDNA sequencing, and evidence convergence. MCT therefore offers a falsifiable interdisciplinary framework for investigating a persistent maternal dimension of human descent across individual, family, molecular, and population scales.

**Keywords:** Maternal Continuity Theory; gestational continuity; maternal genealogy; mitochondrial DNA; human origins; reproductive biology; population genetics; intergenerational descent

## Preface

Ideas rarely emerge in their final form. A theory may begin with a simple observation, develop through questioning and reflection, and then require substantial reconsideration as new knowledge, evidence, and methods become available. This book represents such an intellectual journey.

My earlier work, **"A Theory of Matriarchism: The Universal Origins of Humanity,"** began with a fundamental question concerning human continuity: if every person who has undergone gestation originates through an embodied relationship with a mother, and that mother herself emerged through an earlier reproductive relationship, how far can this sequence of maternal relationships be traced across generations? The visible umbilical legacy of prenatal life provided the initial point of observation, while family genealogy offered a means of thinking about the recurrence of maternal relationships across successive generations. From this starting point, I attempted to explore a much larger question concerning maternal ancestry and human origins.

Over time, however, I became increasingly aware that the original formulation required both **preservation and reconstruction**. Its central intuition remained important to me, but the scientific interpretation of that intuition needed to be reconsidered in light of contemporary reproductive biology, molecular genetics, mitochondrial inheritance, genealogy, population genetics, evolutionary science, and developments in assisted reproductive technology.

The result is **Maternal Continuity Theory (MCT)**.

This book should therefore not be understood simply as a republication or expansion of my earlier theory. Nor do I regard it as a rejection of that work. Rather, it represents its **modern reconstruction**. The intellectual question that initiated the earlier theory remains, but the conceptual vocabulary, evidentiary architecture, theoretical boundaries, and testable propositions have been substantially reformulated.

The most important change concerns the meaning of **continuity** itself.

My earlier work placed considerable emphasis on the navel and umbilical relationship as evidence of maternal connection. In the present theory, I distinguish more carefully between the anatomical evidence of an individual's prenatal history and the much broader question of ancestry. The umbilicus is evidence of a previous fetal-placental relationship, but it cannot by itself identify a mother, grandmother, remote ancestor, or prehistoric maternal lineage. The scientific journey from an observable gestational relationship to deep human ancestry therefore requires several distinct forms of evidence.

This realization led me to formulate three central dimensions of Maternal Continuity Theory: **gestational continuity, genealogical continuity, and maternal genetic continuity.**

Gestational continuity concerns the embodied relationship established during pregnancy. Genealogical continuity concerns relationships of descent that can be reconstructed across generations. Maternal genetic continuity concerns the particular forms of genetic transmission associated with maternal descent, especially mitochondrial DNA. These dimensions frequently overlap, but they are not identical. This distinction fundamentally changes the theoretical structure.

A woman may gestate a daughter who later gestates another child. These are not parts of one physically continuous pregnancy. They are separate biological events. Yet when placed genealogically in sequence, they constitute what I describe in this book as **serial maternal links**. Thus, maternal continuity is not the persistence of one umbilical cord, placenta, organ, or physiological connection across generations. It is the recurrence of identifiable maternal relationships within an intergenerational pathway.

Symbolically, this may be represented as:

Each arrow represents a distinct reproductive relationship. Together, however, they constitute a maternal pathway.

This reformulation also required me to reconsider the position of male descendants. A son does not become disconnected from his mother simply because his own children are gestated by another woman. He remains her genealogical descendant and carries genetic material inherited from her.

What ordinarily does not continue through him is her direct mitochondrial transmission pathway to his offspring. The distinction between **transmission and relatedness** consequently became one of the central principles of the revised theory.

Mitochondrial genetics provided another important reason for modernization. The predominantly maternal transmission of mitochondrial DNA offers an extraordinary molecular means of investigating female-line ancestry. Yet mitochondrial ancestry must not be confused with total human ancestry. Human beings inherit the overwhelming majority of their genetic material through biparental processes, and every person's genealogy expands through both maternal and paternal branches.

For this reason, this book makes a distinction that I consider fundamental:

Maternal Continuity Theory therefore does not propose maternal exclusivity. It identifies one biologically distinctive pathway within the vastly more complex network of human descent.

The same caution became necessary when considering the concept popularly known as **“mitochondrial Eve.”** The possibility of tracing surviving mitochondrial lineages toward a common maternal ancestor is highly relevant to the questions that originally motivated my theory. Nevertheless, mitochondrial coalescence does not identify the first woman, the only woman living at a particular time, or necessarily the first anatomically modern human female. A mitochondrial common ancestor represents a particular genetic coalescence point within surviving maternal lineages.

Accordingly, one of the most significant intellectual transitions represented by this book is the movement from the question of a single “first woman” toward the scientifically more defensible investigation of **maternal lineage continuity and coalescence**.

This change does not diminish my original question. In my view, it makes the question more precise.

The book also retains a Qur'anic dimension because the theological questions surrounding human creation, gestation, generations, kinship, and common human origin formed part of the intellectual context from which my original thinking developed. However, I have attempted here to establish a much clearer epistemological boundary. Qur'anic statements are considered within a comparative theological framework; they are not presented as substitutes for biomedical or genetic evidence. Similarly, contemporary discoveries in genetics or embryology should not automatically be treated as scientific proof of a particular scriptural interpretation.

I believe meaningful interdisciplinary inquiry becomes stronger, rather than weaker, when the boundaries between different forms of knowledge are made explicit.

For this reason, the book places reproductive medicine, genetics, genealogy, evolutionary science, population genetics, and theology into dialogue without assuming that they employ identical methods or answer identical questions. Biomedical science investigates mechanisms and testable relationships. Population genetics reconstructs demographic and genetic history probabilistically. Genealogy examines relationships of descent. Theology addresses questions that may include creation, meaning, human commonality, and purpose. Maternal Continuity Theory occupies a deliberately interdisciplinary position among these conversations.

An important part of this reconstruction is the multigenerational family example from Bangladesh that contributed to the development of my original thinking. In this book, that family is no longer presented as proof of universal maternal ancestry. Instead, it serves as an **illustrative genealogical model** through which different forms of continuity can be distinguished. Its female-line branches illustrate serial maternal relationships; its male-mediated branches demonstrate why genealogical relatedness must not be confused with mitochondrial transmission; and the pedigree as a whole provides a foundation for designing future empirical tests.

Indeed, perhaps the most important difference between my earlier work and this book concerns **falsifiability**.

I do not wish Maternal Continuity Theory to be accepted merely because its central idea appears intuitively compelling. A scientific theory should expose itself to evidence capable of supporting, modifying, or challenging it. For that reason, this book develops explicit propositions, boundary conditions, counterarguments, limitations, and possible empirical tests.

The next stage of this work should therefore occur not only in theoretical discussion but also in the laboratory, the clinic, the archive, and the field.

Multigenerational pedigrees can be independently reconstructed. Reproductive histories can be documented. Maternal relationships can be evaluated using autosomal evidence where appropriate. Complete mitochondrial genomes can be sequenced. Female-line branches can be compared with male-mediated genealogical branches. Multiple families and populations can be studied. Assisted reproductive technologies can provide important boundary cases in which gestational and genetic maternal relationships no longer coincide.

Such studies may support some propositions of MCT and require revision of others. I welcome both possibilities. This is why I regard this book not as the conclusion of the theory but as the beginning of a new phase of its development.

The intellectual transition represented here may be summarized as:

I have deliberately preserved the history of the earlier theory rather than concealing it. Scientific and scholarly development should permit authors to revisit their own ideas. To revise a theory in response to advances in knowledge is not to erase its intellectual history; it is to make that history visible.

The present work therefore records both **continuity and change** in my own thinking.

The continuity lies in the question that has remained with me: how should we understand the extraordinary recurrence of maternal relationships through human generations?

The change lies in how that question is now approached.

Rather than moving directly from an anatomical observation to universal human origins, the present framework proceeds through progressively different evidentiary levels:

At every stage, the strength of the conclusion must remain proportional to the strength and type of evidence available.

This principle is perhaps the most important lesson I have drawn from revisiting my earlier work.

I offer **Maternal Continuity Theory** neither as a final answer to the question of human origins nor as an alternative to evolutionary biology. I offer it as an interdisciplinary framework through which one distinctive dimension of human continuity-the recurring maternal pathway-can be described more precisely, investigated empirically, and situated within the broader complexity of human ancestry.

If this book succeeds, its contribution will not be measured by whether every proposition remains unchanged. Its value will lie in whether it generates better questions, clearer distinctions, testable hypotheses, and further empirical investigation.

I therefore invite scholars in reproductive medicine, genetics, genomics, genealogy, anthropology, evolutionary biology, population genetics, philosophy of science, and theology to engage critically with the theory. Agreement is not a prerequisite for productive scholarship. Careful criticism, independent testing, and alternative explanations are precisely what can determine whether Maternal Continuity Theory develops into a useful scientific framework.

This book represents my effort to reconsider an earlier idea in the light of contemporary knowledge while preserving the question that originally inspired it. It is, in that sense, both a continuation and a reconstruction-a movement **from Matriarchism to Maternal Continuity**.

**Prof. Dr Kazi Abdul Mannan**
*Author*

## Publisher’s Note

KMF Publishers is pleased to present this scholarly work, which represents a significant intellectual development of the author's earlier theoretical inquiry into maternal descent and human origins. In this volume, the original **Theory of Matriarchism** is revisited, critically reassessed, and substantially reconstructed as **Maternal Continuity Theory (MCT)**-an interdisciplinary framework bringing reproductive biology, genealogy, mitochondrial genetics, population genetics, evolutionary science, and comparative theological reflection into a structured scholarly dialogue.

An important characteristic of this book is the author's willingness to return critically to his earlier theoretical propositions in light of advances in scientific knowledge. Rather than simply reproducing or defending the original theory, the present volume identifies areas requiring clarification, modifies earlier interpretations, establishes new conceptual boundaries, and develops propositions capable of future empirical investigation. This process of reassessment reflects an important principle of scholarship: theories should remain open to refinement when new evidence, methods, and perspectives become available.

At the centre of the revised framework is a distinction among three dimensions of maternal continuity: **gestational continuity, genealogical continuity, and maternal genetic continuity**. By separating these domains, the author seeks to distinguish the embodied biological relationship of pregnancy from broader genealogical descent and from the predominantly maternal transmission of mitochondrial DNA. The resulting framework also acknowledges the essential role of paternal ancestry and situates maternal continuity within the wider, complex, and population-based history of human descent.

The book is particularly noteworthy for establishing boundaries around its own claims. Maternal Continuity Theory is not presented as a replacement for evolutionary biology or population genetics, nor does it claim that mitochondrial ancestry constitutes the entirety of human ancestry. The distinction between mitochondrial coalescence and the concept of a unique “first woman,” the recognition of male-mediated genealogical descent,

and the discussion of assisted reproduction and other boundary conditions demonstrate the author's effort to make the revised theory scientifically testable rather than conceptually unrestricted.

The inclusion of the Bangladesh multigenerational family example provides continuity with the author's earlier work while also illustrating the transition in his thinking. In the present volume, the family genealogy is employed as an illustrative model through which different forms of maternal relationship can be examined, rather than as independent proof of universal human ancestry. This shift from illustration to testable proposition is central to the modernization of the theory.

Another distinctive dimension of the book is its engagement with the Qur'anic perspective on human creation, gestation, kinship, and generations. The author treats this material as a **comparative theological and epistemological perspective**, while maintaining a methodological distinction between revelatory interpretation and empirical biomedical evidence. In doing so, the volume seeks interdisciplinary dialogue without treating different systems of knowledge as methodologically interchangeable.

From a publishing perspective, KMF Publishers considers the transition represented in this volume particularly significant:

This progression reflects the broader scholarly principle that theoretical development is not necessarily linear. Intellectual advancement may require scholars to revisit their own assumptions, acknowledge limitations, incorporate new knowledge, and formulate more precise and falsifiable propositions.

The present book should therefore be read neither as the final resolution of questions concerning maternal ancestry nor as a definitive account of human origins. It is better understood as the presentation of a **developing interdisciplinary theory and an associated research programme**. Its propositions invite examination through verified multigenerational pedigrees, reproductive histories, mitochondrial genome analysis, population-genetic methods, and other forms of independent empirical evidence.

KMF Publishers particularly welcomes this aspect of the work. Scholarly publishing should provide space not only for established knowledge but also for carefully formulated new theories that are transparent about their assumptions, evidence, limitations, and conditions for revision. The value of such theoretical scholarship ultimately depends upon the critical engagement it generates and the evidence produced by subsequent research.

We therefore publish this volume with an invitation to researchers and scholars in reproductive medicine, genetics and genomics, genealogy, anthropology, evolutionary biology, population genetics, philosophy of science, and comparative theology to examine Maternal Continuity Theory critically. Independent testing, constructive criticism, alternative interpretations, and empirical replication will be essential to determining the theory's longer-term scholarly significance.

KMF Publishers recognizes this volume as an important stage in the evolution of an author's original theoretical inquiry-from an earlier concept of **Matriarchism** toward the more differentiated and empirically oriented framework of **Maternal Continuity**. The book documents not only a theory of intergenerational relationships but also the process through which a theory itself can evolve.

It is our hope that this work will encourage further discussion, empirical investigation, and interdisciplinary scholarship concerning maternal relationships, genealogy, genetic inheritance, and the broader scientific and philosophical questions surrounding human continuity and origins.

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## Contents

**Limitations**

## 1. Introduction

Human reproduction represents a continuous biological process through which genetic information, cellular components, physiological interactions, and genealogical relationships are transmitted across generations. Although the evolutionary origins of *Homo sapiens* have been extensively investigated through palaeoanthropology, comparative anatomy, archaeology, molecular genetics, and population genomics, comparatively less theoretical attention has been directed toward integrating the immediate maternal-fetal relationship with longer-term genealogical and genetic patterns of human descent. From a biomedical perspective, every gestational pregnancy establishes a distinctive physiological relationship between the pregnant individual and the developing fetus, mediated principally through the placenta and umbilical cord. This relationship provides an observable biological starting point from which maternal continuity may be examined across individual, familial, and population levels.

During pregnancy, the placenta functions as a highly specialized maternal-fetal interface that supports fetal growth and development through respiratory gas exchange, nutrient transfer, waste removal, endocrine signalling, immunological regulation, and other physiological processes. The fetus is connected to the placenta through the umbilical cord, which contains the vascular structures required for fetoplacental circulation. Following delivery, the cord is separated and the umbilicus remains as an anatomical consequence of this prenatal connection. Importantly, the umbilicus should not itself be interpreted as evidence of genetic ancestry extending into the distant past. Rather, it constitutes an anatomical marker of an individual's previous fetoplacental connection during gestation. This distinction is fundamental to developing a scientifically testable theory of maternal continuity.

The biological relationship becomes theoretically more significant when considered across successive generations. A person who undergoes gestation was themselves, under ordinary reproductive circumstances, previously gestated by another individual. If a female-line descendant subsequently undergoes pregnancy, another maternal-fetal relationship is

established. Repetition of this process creates potentially traceable chains of maternal relationships across generations. Such chains can be examined genealogically, while molecular genetics provides an independent but related dimension of maternal inheritance. The present framework therefore distinguishes **embodied or gestational continuity**, **genealogical continuity**, and **genetic continuity**, rather than treating these phenomena as biologically equivalent.

This distinction is particularly important in relation to mitochondrial DNA (mtDNA). Human mtDNA is transmitted overwhelmingly through the maternal line, making it an important molecular system for investigating maternal inheritance, population history, migration, and disease transmission [1-4]. Molecular research has identified biological mechanisms contributing to the exclusion or elimination of paternal mitochondrial genomes, reinforcing maternal inheritance as the predominant pattern in humans [1,5]. Recent molecular evidence has further clarified mechanisms underlying maternal mtDNA inheritance in humans [5]. Nevertheless, reports of paternal or biparental transmission have generated debate, and some apparent cases may reflect analytical artefacts involving nuclear mitochondrial DNA sequences rather than genuine paternal mtDNA inheritance [2,6]. Consequently, maternal inheritance of mtDNA should be understood as the overwhelmingly established biological pattern while acknowledging the continuing investigation of rare or disputed exceptions.

Maternal genetic continuity is also more complex than simple transmission of an unchanged mitochondrial genome. Heteroplasmy-the coexistence of more than one mtDNA genotype within an individual-can vary between tissues and generations, and mitochondrial genetic bottlenecks can substantially alter variant frequencies during maternal transmission [2,3]. These mechanisms are clinically important because pathogenic mtDNA variants may produce mitochondrial disorders with variable penetrance, severity, and recurrence risks [2,4]. Thus, maternal genetic continuity simultaneously represents an evolutionary, genealogical, and medically relevant phenomenon.

However, mitochondrial inheritance and gestational continuity should not be conflated with total biological ancestry. Nuclear DNA is inherited from both biological parents, and paternal genetic contributions are indispensable components of human heredity. Likewise, a person's genealogical ancestry contains both maternal and paternal branches. Maternal Continuity Theory therefore does not propose that paternal ancestry is absent, biologically secondary, or unnecessary. Instead, it identifies a particular asymmetry within human reproduction: gestation creates a direct embodied maternal-fetal relationship, while mitochondrial inheritance provides a predominantly maternal molecular lineage. These phenomena represent specific dimensions of descent rather than a complete explanation of human genetic ancestry.

### 1.1 Problem Statement

Contemporary biomedical knowledge provides detailed explanations of reproductive physiology, placental function, embryonic and fetal development, nuclear inheritance, mitochondrial genetics, and population ancestry. Nevertheless, these fields are usually investigated within separate disciplinary frameworks. Reproductive medicine principally examines pregnancy and maternal-fetal physiology; medical genetics investigates mechanisms of inheritance and genetic disease; population genetics reconstructs demographic history and ancestry; and anthropology and genealogy examine kinship and intergenerational relationships.

The resulting conceptual problem is therefore not an absence of evidence concerning maternal reproduction or inheritance but the limited integration of these different forms of evidence into a common theoretical framework. An observable gestational relationship exists at the individual level; maternal relationships can potentially be reconstructed across generations at the genealogical level; and mtDNA provides a predominantly maternally transmitted molecular lineage at the genetic level. Each phenomenon is well recognized independently, but their relationships and explanatory boundaries require clearer theoretical differentiation.

This issue was central to the earlier formulation from which the present framework developed. The original model used the umbilicus as a

universal anatomical observation and subsequently extended this observation into a maternal genealogical argument. It also recognized the importance of maternally inherited mitochondrial DNA in reconstructing human maternal ancestry. The present study advances that initial concept by separating anatomical observation from genealogical reconstruction and molecular inference.

A particularly important problem concerns the limits of inference. The existence of a maternal-fetal connection in one generation does not, by itself, establish the identity of a prehistoric common ancestor. Similarly, a mitochondrial most recent common ancestor should not be interpreted as the only woman living at a particular historical period or automatically equated with a hypothetical "first woman." Maternal continuity must therefore be investigated through evidence appropriate to different temporal scales, while distinguishing direct observation from genealogical reconstruction and population-genetic inference.

### 1.2 Research Gap

Despite substantial research on pregnancy, maternal-fetal biology, mitochondrial inheritance, human genetics, genealogy, and evolutionary ancestry, there remains an interdisciplinary conceptual gap concerning how these different dimensions of maternal continuity relate to one another. Biomedical research explains the mechanisms through which pregnancy sustains fetal development, whereas molecular genetics demonstrates the predominantly maternal transmission of mtDNA and its importance for inherited disease and population studies [1-5]. However, these processes are rarely incorporated into a unified theoretical model extending from an individual's embodied gestational history to genealogical maternal relationships and, ultimately, molecular evidence of maternal-line ancestry.

A second gap concerns the analytical separation of different meanings of "maternal descent." Gestational descent, genealogical descent, mitochondrial inheritance, and overall genetic ancestry are related concepts but are not synonymous. Failure to distinguish them can lead to biological overinterpretation. A theoretically rigorous model is therefore required to specify which aspects of maternal continuity are directly

observable, which can be reconstructed genealogically, which can be tested genetically, and which remain historical hypotheses.

The present study addresses this gap by proposing **Maternal Continuity Theory (MCT)**, an interdisciplinary biomedical framework that conceptualizes maternal continuity at three interconnected levels: **(i) embodied or gestational continuity, (ii) genealogical continuity, and (iii) genetic continuity**. Rather than challenging evolutionary biology or conventional genetics, MCT is intended to operate within these established scientific frameworks and provide an additional conceptual structure for examining the persistence of maternal relationships across generations.

### 1.3 Research Objectives

The primary objective of this study is to develop an interdisciplinary theoretical framework for understanding maternal continuity across embodied, genealogical, and genetic dimensions of human descent.

The specific objectives are to:

- define the maternal-fetal gestational relationship as an embodied dimension of biological continuity;
- distinguish gestational continuity from nuclear genetic inheritance, genealogical ancestry, and mitochondrial inheritance;
- examine how sequential maternal-offspring relationships may form traceable maternal genealogical chains across generations;
- evaluate the relevance of mitochondrial inheritance to the concept of maternal genetic continuity;
- integrate evidence from reproductive biology, medical genetics, population genetics, and human evolutionary research within a coherent conceptual framework;
- identify the empirical boundaries separating directly observable maternal relationships from genealogical and genetic inference; and
- formulate a set of theoretically testable propositions for subsequent biomedical, genealogical, and population-based investigation.

### 1.4 Research Questions

The study addresses the following research questions:

- **RQ1.** How can the maternal-fetal relationship established during gestation be conceptualized as a form of embodied biological continuity?
- **RQ2.** What are the conceptual and biological distinctions among gestational, genealogical, and genetic maternal continuity?
- **RQ3.** To what extent can successive maternal-offspring relationships be reconstructed as continuous maternal genealogical pathways across generations?
- **RQ4.** How does predominantly maternal mitochondrial DNA inheritance contribute to the molecular understanding of maternal continuity?
- **RQ5.** How can Maternal Continuity Theory be integrated with established knowledge in reproductive medicine, human genetics, population genetics, and evolutionary biology without conflating maternal-line continuity with total human ancestry?
- **RQ6.** What empirical evidence would be required to test, support, modify, or falsify the principal propositions of Maternal Continuity Theory?

By addressing these questions, the study moves beyond the elementary observation that human development occurs through gestation and instead examines whether recurring maternal-offspring relationships constitute a scientifically meaningful form of intergenerational biological continuity. The proposed theory therefore does not attempt to replace evolutionary explanations of human origins. Rather, it introduces a multilevel framework through which observable gestational relationships, documented maternal genealogies, and predominantly maternal molecular inheritance can be investigated together while maintaining clear boundaries between anatomical evidence, genetic evidence, and historical inference.

## 2. Literature Review

Understanding maternal continuity requires an interdisciplinary synthesis because no single field adequately explains the biological, genealogical, and evolutionary dimensions of human descent. Evolutionary biology and palaeoanthropology describe the emergence and diversification of *Homo sapiens*; reproductive biology explains the physiological processes through which each new individual develops; molecular genetics provides evidence concerning patterns of inheritance; genealogy reconstructs relationships between individuals across generations; and anthropological studies of kinship demonstrate how biological descent interacts with social systems of relatedness. Maternal Continuity Theory (MCT) draws upon these literatures while maintaining an important distinction among **gestational continuity, genealogical continuity, and genetic continuity**.

### 2.1 Human Evolution and Biological Continuity

Modern evolutionary theory explains human origins as the outcome of population-level evolutionary processes rather than a single linear progression from an ancestral species to modern humans. Fossil morphology, comparative genomics, archaeological evidence, and increasingly ancient DNA have demonstrated that human evolutionary history involved population differentiation, migration, admixture, extinction, and repeated interactions among different hominin populations [7-10].

The emergence of *Homo sapiens* is strongly associated with Africa, although contemporary evidence increasingly supports a complex population history rather than an overly simplified model involving a single geographically isolated ancestral population. Population structure within Africa, subsequent dispersals, and interactions with archaic hominins contributed to the genomic architecture of present-day populations [8-10]. Ancient genomic studies have particularly transformed understanding of these relationships by demonstrating gene flow between modern humans, Neanderthals, Denisovans, and other ancestral populations [8,9].

These developments are important for MCT because they establish that human ancestry should not be represented as a simple unbranched

biological line. Human populations repeatedly separated, migrated, encountered one another, and exchanged genetic material. Any theory of maternal continuity must therefore be compatible with reticulate population histories and cannot assume that an anatomically observable mother-offspring relationship alone reconstructs the complete evolutionary history of the species.

At the same time, evolutionary explanations operate predominantly at the level of populations over extended periods. Individual reproduction represents the biological mechanism through which populations themselves persist. Evolution therefore depends upon repeated reproductive events occurring across generations. From this perspective, MCT addresses a different explanatory scale: rather than seeking to replace evolutionary models, it asks whether a recurring feature of individual human reproduction-the embodied relationship between a gestational parent and offspring-can be conceptualized systematically across successive generations.

This distinction between evolutionary history and reproductive continuity is fundamental. Evolutionary ancestry encompasses both maternal and paternal genetic contributions and includes population-level processes such as mutation, recombination, genetic drift, natural selection, migration, and admixture. Maternal continuity, as proposed here, concerns a specific pathway within this much broader evolutionary system.

### 2.2 Human Origins and Population Genetics

The reconstruction of human origins has undergone a methodological transformation with advances in molecular genetics and ancient DNA sequencing. Earlier models relied primarily on fossils, archaeological evidence, comparative morphology, and genetic variation among living populations. Ancient DNA now provides direct molecular evidence from individuals who lived thousands or tens of thousands of years ago and has substantially refined models of migration, population replacement, admixture, and evolutionary relationships [8-10].

Population-genetic evidence indicates that present-day humans carry complex genomic signatures generated by numerous ancestral

populations. Ancient genomic research has demonstrated, for example, substantial contributions from prehistoric migrations to the genetic structure of contemporary populations [9]. Genomic evidence has also established episodes of admixture between anatomically modern humans and archaic hominins, demonstrating that human evolutionary ancestry cannot adequately be represented by a single linear genealogical tree [8,10].

Population-genetic inference nevertheless requires careful interpretation. Demographic conclusions depend partly on assumptions concerning population structure, mutation rates, migration, effective population size, and statistical models. Recent work has demonstrated that failure to account adequately for ancestral population structure can even generate misleading interpretations of ancient admixture events [10]. Genetic reconstruction therefore represents probabilistic historical inference rather than direct observation of every ancestor.

This epistemological distinction has particular relevance to maternal ancestry. An individual's mother can generally be identified through direct or documentary evidence, whereas increasingly remote maternal ancestors must be reconstructed genealogically or inferred genetically. The confidence and nature of evidence consequently change as temporal distance increases.

The concept of a most recent common ancestor must also be distinguished from the concept of a unique first human. Population-genetic common ancestors represent individuals from whom particular genetic lineages surviving in present populations can be traced. They were members of larger reproductive populations and should not be interpreted as necessarily representing the first or only humans existing at their respective times. This distinction is especially important when considering mitochondrial ancestry.

Thus, MCT adopts a hierarchical evidentiary approach: **direct biological observation** for individual gestational relationships, **documentary reconstruction** for recent genealogy, and **population-genetic inference** for deeper ancestry.

### 2.3 Reproductive Biology and the Maternal-Fetal Interface

The strongest directly observable biological foundation for maternal continuity occurs during pregnancy. Human development begins following fertilization and proceeds through implantation, embryogenesis, fetal development, and birth. Implantation and placentation involve highly coordinated interactions among trophoblast populations, maternal decidual tissues, immune cells, vascular systems, and developing fetal structures [11-14].

The placenta occupies a particularly important position in this relationship. It is a transient, highly specialized organ composed predominantly of fetal-derived structures operating within a maternal physiological environment. It facilitates nutrient and respiratory gas exchange, metabolic waste transfer, endocrine signalling, immune regulation, and adaptations necessary for fetal growth [11,13]. Placental development therefore establishes a complex physiological interface rather than a simple physical attachment.

The maternal-fetal interface is also immunologically distinctive. Because the fetus contains paternal as well as maternal genetic material, it is partially allogeneic relative to the pregnant individual. Successful pregnancy consequently requires sophisticated mechanisms of immune regulation and tolerance while preserving maternal and fetal protection against pathogens [12,14]. This further demonstrates why gestational continuity should not be interpreted as genetic identity between mother and offspring.

The umbilical cord forms the vascular connection between the fetus and placenta and enables fetoplacental circulation. At delivery, separation of the cord ends this direct anatomical connection. The resulting umbilicus therefore represents a developmental consequence of fetal dependence upon the placental system. However, the umbilicus itself does not reveal the genetic identity of earlier ancestors and cannot independently establish deep genealogical history.

This distinction modifies the interpretation employed in the original formulation of the theory, in which the navel was treated as a universal

observational sample connecting individuals with their mothers. The original analysis correctly emphasized the observable relationship between birth and maternal gestation, but its extension from individual anatomy to universal historical ancestry requires additional evidentiary stages. MCT therefore reconceptualizes the umbilical relationship as evidence of **embodied gestational continuity**, not as independent proof of a particular prehistoric ancestor.

Pregnancy may also produce biological effects extending beyond delivery. Placental function, maternal metabolism, intrauterine exposures, epigenetic processes, and developmental programming can influence later health outcomes [13]. In this broader biomedical sense, maternal-fetal continuity includes not only physical gestation but also developmental interactions capable of influencing health trajectories across the life course.

### 2.4 Mitochondrial DNA and Maternal Genetic Continuity

Mitochondrial DNA provides the most direct molecular basis for defining a specifically maternal genetic lineage in humans. Human mtDNA is a small, circular genome located within mitochondria and is inherited overwhelmingly through the maternal line [1-4,15]. Unlike autosomal nuclear DNA, which undergoes recombination and is inherited from both biological parents, mtDNA provides a comparatively direct means of reconstructing maternal genetic relationships.

The biological mechanisms underlying maternal mtDNA inheritance have become increasingly well characterized. Evidence indicates that although sperm mitochondria enter the oocyte during fertilization, mechanisms exist that prevent paternal mitochondrial genomes from contributing substantially to the offspring's mitochondrial lineage. Recent molecular investigation has reported that mature human spermatozoa lack intact mtDNA and that redistribution of mitochondrial transcription factor A during spermatogenesis contributes to elimination of the paternal mitochondrial genome [15].

These findings strengthen the molecular basis for predominantly maternal mitochondrial inheritance. Reports suggesting biparental mtDNA

transmission have generated considerable scientific debate; however, subsequent analyses have indicated that some apparent paternal inheritance may result from technical artefacts, including nuclear sequences of mitochondrial origin [16]. The predominant model of human mitochondrial inheritance therefore remains maternal, although continuing investigation of exceptional observations remains scientifically appropriate.

Maternal mitochondrial transmission is not equivalent to the transmission of an entirely unchanged genetic sequence. Heteroplasmy-the presence of multiple mtDNA variants within an individual-is widespread and may differ between tissues and generations [2,3]. The mitochondrial genetic bottleneck occurring during germline development can produce substantial shifts in variant frequencies between a mother and her offspring. These processes have important implications for mitochondrial disease, penetrance, recurrence risk, and genetic counselling [2-4].

For evolutionary and population-genetic studies, accumulated mtDNA variation can be used to reconstruct maternal phylogenies and haplogroups. Such analyses contributed historically to the concept commonly termed **mitochondrial Eve**, referring to the most recent woman from whom the mitochondrial lineages of living humans ultimately coalesce. This concept is frequently misunderstood. It does not imply that this woman was the first anatomically modern human, the only woman alive at that time, or the sole female ancestor of contemporary humanity. Rather, other contemporary women may have contributed extensive nuclear DNA to later populations while their uninterrupted female-line mtDNA lineages eventually became extinct.

This distinction provides a crucial boundary for MCT. Mitochondrial evidence supports the scientific existence of long-term maternal genetic lineages, but it cannot independently establish a singular biological "first mother." MCT therefore treats mtDNA as evidence of **maternal genetic continuity**, while distinguishing this concept from embodied gestational continuity and complete genealogical ancestry.

### 2.5 Genealogy and Intergenerational Maternal Descent

Genealogy provides the intermediate analytical level between directly observable reproduction and deep genetic ancestry. Every individual occupies a position within a network of biological ancestors. Moving backwards through conventional genealogy produces both maternal and paternal branches, with the number of genealogical positions expanding rapidly across generations. Consequently, MCT does not conceptualize total human genealogy as exclusively maternal.

Instead, the theory isolates one specific path within the broader ancestral network: repeated mother-to-offspring relationships. Beginning with an individual, the maternal pathway can theoretically be followed through that individual's mother, maternal grandmother, maternal great-grandmother, and progressively earlier maternal ancestors. This constitutes a **matrilineal genealogical pathway**. Its biological significance differs depending on the dimension being considered. All children participate in a mother-offspring gestational relationship, whereas uninterrupted transmission of a particular maternal mtDNA lineage to subsequent generations occurs through reproduction involving female-line transmission.

This distinction resolves an important limitation in the earlier formulation of the theory. In the original genealogical example, a Bangladeshi family was used to illustrate how maternal lines continued through daughters while certain lines were described as terminating through sons. The later analysis similarly treated descendants of sons as disconnected from the focal woman's maternal line because those children were gestated by other women.

Under the revised MCT framework, these relationships require greater precision. A son does not cease to be genealogically or genetically related to his mother. He remains her biological descendant and carries approximately half of his autosomal nuclear DNA from her. What changes is the transmission pathway: although he inherits his mother's mtDNA, under the predominant pattern of human mitochondrial inheritance he does not transmit that mtDNA to his offspring. His children are also gestated through another maternal-fetal relationship. Consequently, **genealogical**

**relatedness, gestational continuity, and matrilineal mitochondrial transmission must be represented as different networks**.

This conceptual separation makes maternal continuity empirically testable. Documentary family records can reconstruct genealogical relationships; birth and reproductive histories can reconstruct gestational relationships; and molecular analysis can identify mitochondrial haplotypes and maternal genetic relationships. Where multiple evidence types are available, their convergence or divergence can be examined rather than assumed.

### 2.6 Kinship, Biological Descent, and Social Relatedness

Kinship adds another necessary dimension because human relationships cannot be reduced entirely to genetics or gestation. Anthropological scholarship has long demonstrated that societies organize kinship through culturally variable systems of descent, marriage, residence, inheritance, caregiving, adoption, and social recognition. Some societies emphasize patrilineal descent, others matrilineal descent, and many employ bilateral or more complex systems of relatedness.

The terms **maternal**, **matrilineal**, and **matriarchal** must therefore be distinguished carefully. Maternal refers broadly to relationships associated with motherhood; matrilineal describes descent or inheritance traced through a female line; and matriarchy generally refers to forms of social organization in which women or mothers occupy particular positions of authority. Biological maternal continuity does not demonstrate the existence of matriarchal social organization.

This distinction is especially relevant to the naming and scope of the proposed theory. MCT concerns biological and genealogical continuity rather than a claim that human societies originated universally as matriarchies. It consequently separates biological descent from political authority and cultural kinship structures.

Modern reproductive medicine further demonstrates why such conceptual precision is necessary. Assisted reproductive technologies can separate genetic, gestational, and social dimensions of parenthood. An individual may contribute an oocyte without carrying the pregnancy, another

individual may gestate the fetus, and another person or couple may assume the social parental role. Donor conception, gestational surrogacy, adoption, and related family formations therefore demonstrate that **genetic motherhood, gestational motherhood, genealogical relationship, and social motherhood cannot always be represented by a single category**.

Rather than weakening Maternal Continuity Theory, these cases provide important boundary conditions through which its propositions can be tested. They require MCT to specify precisely which type of continuity is under examination. A gestational carrier establishes embodied maternal-fetal continuity without necessarily providing the oocyte or mtDNA; an oocyte donor may establish genetic maternal continuity without experiencing gestation; and an adoptive mother may establish profound social and kinship continuity without either genetic or gestational connection.

### 2.7 Synthesis and Theoretical Positioning

The literature therefore identifies three interconnected but non-equivalent dimensions relevant to maternal continuity. First, reproductive biology demonstrates an **embodied gestational relationship** established through implantation, placentation, maternal-fetal interaction, and fetal development [11-14]. Second, genealogy demonstrates that mother-offspring relationships can be reconstructed across generations as one pathway within the much larger network of human ancestry. Third, mitochondrial genetics demonstrates a predominantly maternal mechanism of molecular inheritance capable of preserving information about maternal-line population history [1-4,15,16].

These three dimensions operate at different evidentiary and temporal scales. Gestational continuity can be directly observed within contemporary reproduction; genealogical continuity can be documented across generations where adequate records exist; and genetic continuity can be inferred over considerably greater timescales through molecular variation and population-genetic models. None should be treated as a substitute for another.

Accordingly, MCT can be summarized conceptually as:

**Embodied maternal continuity → Genealogical maternal continuity → Genetic maternal-line continuity**

The arrows indicate conceptual relationships rather than proof that one level automatically establishes the next. This qualification is critical. The anatomical evidence of gestation cannot independently establish a prehistoric maternal genealogy, just as mitochondrial coalescence cannot identify the complete genealogical ancestry of humanity.

The literature consequently reveals the principal theoretical gap addressed by the present study. Reproductive biology, genealogy, mitochondrial genetics, and evolutionary anthropology each contain extensive evidence concerning different aspects of intergenerational continuity, but these dimensions have rarely been organized within a single framework that explicitly distinguishes their mechanisms, evidence, and inferential limits. **Maternal Continuity Theory** is proposed to address this gap by integrating these levels while remaining compatible with contemporary evolutionary biology and population genetics. Its scientific value therefore depends not upon demonstrating that maternal ancestry replaces biparental human ancestry, but upon determining whether embodied, genealogical, and genetic maternal continuity constitute a coherent and empirically examinable dimension of human descent.

## 3. Conceptual Foundations

Maternal Continuity Theory (MCT) is founded on the proposition that human descent can be examined through multiple forms of biological and relational continuity that operate simultaneously but are not interchangeable. The central conceptual distinction is among **gestational continuity, genetic continuity, and genealogical continuity**. This distinction is necessary because gestation, genetic inheritance, and ancestry describe different biological or relational processes. The original formulation emphasized the visible mother-offspring relationship represented by the umbilical connection and subsequently extended this relationship through successive female generations. The revised framework retains this central observation while defining more precisely what each form of continuity can-and cannot-demonstrate.

### 3.1 Conceptualizing Maternal Continuity

In the present framework, **maternal continuity** refers to the persistence of identifiable maternal relationships across one or more generations through gestational, genealogical, or genetic pathways. It does not imply that human inheritance is exclusively maternal, nor does it suggest that paternal biological ancestry is secondary. Instead, the concept isolates specific features of reproduction and inheritance that possess a maternal directionality.

This distinction is particularly important because several forms of biological connection coexist within human reproduction. Nuclear genetic inheritance is biparental, with offspring normally receiving approximately half of their autosomal nuclear DNA from each biological parent. By contrast, gestation creates a direct physiological relationship between the fetus and the gestational parent through the placenta and fetoplacental circulation. Mitochondrial DNA (mtDNA), meanwhile, follows a predominantly maternal inheritance pattern [1-3,15]. These mechanisms therefore produce different forms of continuity and should not be collapsed into a single concept.

MCT consequently proposes a **three-domain model**:

**Gestational continuity → Genealogical continuity → Genetic maternal-line continuity**

The arrows indicate conceptual relationships rather than a deterministic causal sequence. Evidence within one domain does not automatically prove continuity within another. For example, evidence that an individual experienced gestation does not by itself establish the identity of distant maternal ancestors, while shared mitochondrial ancestry does not reconstruct every gestational relationship connecting two individuals.

### 3.2 Gestational Continuity

**Gestational continuity** is defined here as the embodied developmental relationship established between a gestational parent and the developing embryo and fetus during pregnancy. It represents the most immediate and biologically observable level of MCT.

Following implantation, the developing conceptus establishes a complex relationship with maternal tissues. The placenta subsequently functions as the principal maternal-fetal interface, facilitating respiratory gas exchange, nutrient transport, waste elimination, endocrine communication, vascular adaptation, and immunological regulation required for fetal development [11-14]. The fetus is connected to the placenta through the umbilical cord, making this system central to prenatal development.

Gestational continuity is therefore considerably broader than the anatomical presence of the umbilicus. The umbilicus is better interpreted as a **postnatal anatomical consequence of prenatal umbilical attachment**, rather than as genetic evidence of ancestry. This represents an important refinement of the original theory, which treated the navel as a universal observable sample because humans experience separation of the umbilical connection at birth.

Within MCT, the evidentiary significance of the umbilicus is therefore deliberately restricted. It supports the proposition that an individual previously possessed an umbilical connection during fetal development; it cannot independently identify previous generations or demonstrate prehistoric ancestry.

Gestational continuity nevertheless possesses an important intergenerational characteristic. Consider three sequential generations:

**Generation 1:** Woman A gestates Woman B
**Generation 2:** Woman B later gestates Woman C
**Generation 3:** Woman C later gestates Individual D

There are three independently occurring gestational relationships:

**A → B; B → C; C → D**

These relationships can conceptually be linked as:

**A → B → C → D**

The continuity therefore does not mean that the same placenta, umbilical cord, cells, or physiological connection physically persists across all

generations. Each pregnancy creates a new maternal-fetal interface. The continuity lies instead in the **recurrence of the same relational biological process across successive generations**.

This distinction makes gestational continuity a potentially testable concept rather than a metaphorical claim.

### 3.3 Genetic Continuity

Genetic continuity refers to the transmission of inherited biological information between generations. Within MCT, it must be divided into at least two components: **biparental nuclear inheritance** and **maternal mitochondrial inheritance**.

Most human genetic information is contained within the nuclear genome and is inherited from both biological parents. Meiotic recombination further reshuffles genetic material across generations. Consequently, overall human genetic ancestry cannot accurately be represented as an exclusively maternal lineage.

Mitochondrial inheritance differs substantially. Human mtDNA is transmitted overwhelmingly through the maternal line [1-3]. Molecular studies have identified mechanisms contributing to the exclusion of paternal mitochondrial genomes, and recent research has provided further mechanistic evidence explaining maternal mtDNA inheritance in humans [15]. This makes mtDNA particularly useful for studying maternal genetic relationships, mitochondrial disorders, population history, and maternal-line phylogenies.

MCT therefore defines **maternal genetic continuity** narrowly as the intergenerational transmission of maternally inherited genetic information, particularly mtDNA, rather than as the entirety of an individual's genome.

This distinction also clarifies what occurs in male descendants. A son receives mtDNA from his mother and therefore participates in maternal genetic continuity in the receiving generation. Under the predominant pattern of human mitochondrial inheritance, however, he does not transmit

this mtDNA to his offspring [1-3,15]. A daughter both receives maternal mtDNA and may transmit it to her offspring.

Thus:

**Mother → Daughter → Granddaughter → Great-granddaughter**

can represent an uninterrupted mtDNA transmission pathway, whereas:

**Mother → Son → Grandchild**

normally represents transmission to the son followed by termination of that particular mtDNA transmission route.

Importantly, termination of the mitochondrial transmission pathway does **not** mean termination of genealogical or overall genetic relatedness. This qualification revises a potentially problematic interpretation in the original model, where descendants through sons appeared to become disconnected from the focal maternal line. They remain genealogical descendants and retain nuclear genetic inheritance from the earlier female ancestor; what normally terminates is the direct transmission of her mtDNA through that male descendant.

Genetic continuity is also dynamic rather than genetically static. Mutation, heteroplasmy, mitochondrial bottlenecks, selection, and genetic drift can alter mtDNA variant frequencies between generations [2,3]. Consequently, MCT does not assume molecular identity across generations; it refers to **lineal transmission despite genetic variation**.

### 3.4 Genealogical Continuity

**Genealogical continuity** refers to identifiable descent relationships connecting individuals across generations. Unlike gestational continuity, which concerns pregnancy, or genetic continuity, which concerns inherited biological material, genealogy concerns the relational structure of ancestry.

Every individual has both maternal and paternal genealogical ancestry. Moving backward one generation identifies two biological parents; moving further backward produces progressively expanding ancestral

networks. Maternal genealogy therefore constitutes one pathway within this larger network rather than the entirety of human descent.

For MCT, the relevant pathway can be expressed as:

**Individual → Mother → Maternal grandmother → Maternal great-grandmother → ...**

This represents a matrilineal genealogical sequence. In principle, the pathway can be extended for as many generations as reliable evidence permits. In practice, documentary records become increasingly incomplete with temporal distance. Genealogical continuity therefore has an important epistemological limitation: the existence of an ancestral relationship may be biologically plausible without the identity of the ancestor being historically recoverable.

The family example in the original article attempted to demonstrate this phenomenon by tracing descendants of a woman through several generations. In the revised framework, such family structures are valuable as **illustrative genealogical models**, but they cannot independently establish universal prehistoric ancestry.

Genealogical continuity also differs fundamentally from genetic continuity because genealogical ancestors do not necessarily contribute identifiable genetic material to every distant descendant. As generations accumulate and recombination occurs, a person may remain a genuine genealogical ancestor even when identifiable autosomal DNA inherited from that ancestor is no longer detectable in a particular descendant. Genealogical descent and genetic inheritance must therefore remain analytically separate.

### 3.5 Relationship Among the Three Forms of Continuity

The conceptual strength of MCT lies not in treating gestational, genetic, and genealogical continuity as equivalent, but in examining where they converge and where they diverge.

For a conventional mother-child relationship in which the same individual contributes the oocyte and carries the pregnancy, all three forms may coincide:

**Gestational relationship + genealogical relationship + maternal genetic relationship**

However, contemporary reproductive medicine demonstrates that this convergence is not universal. Assisted reproductive technologies can separate these dimensions. For example, where an embryo created using a donor oocyte is carried by another individual, the oocyte donor contributes the maternal nuclear genome and mtDNA, while the gestational carrier provides the intrauterine environment and maternal-fetal physiological relationship. The social or legally recognized mother may potentially be another relational category.

Such cases provide useful natural tests of the conceptual boundaries of MCT because they demonstrate that **gestational motherhood, genetic motherhood, genealogical descent, and social motherhood are conceptually separable**.

Accordingly, the three principal domains can be defined as follows:

| Domain | Core mechanism | Primary evidence | What it establishes | What it does not establish |
|---|---|---|---|---|
| **Gestational continuity** | Pregnancy, placenta, | Clinical, anatomical and | Embodied prenatal | Complete genetic |

| Domain | Core mechanism | Primary evidence | What it establishes | What it does not establish |
|---|---|---|---|---|
| | maternal-fetal interface and umbilical circulation | reproductive evidence | relationship | ancestry |
| **Genetic continuity** | Transmission of inherited biological information; specifically, mtDNA for maternal-line analysis | Molecular/genomic evidence | Maternal molecular lineage | Complete genealogy or a unique "first mother" |
| **Genealogical continuity** | Parent-offspring relationships across generations | Family records, demographic data, pedigrees and genetic corroboration | Ancestral relationships | Necessarily detectable DNA from every distant ancestor |

This differentiation establishes an **evidentiary hierarchy rather than a hierarchy of biological importance**. Gestational relationships are observable at the individual level; genealogy extends those relationships historically where records permit; molecular genetics allows particular inherited lineages to be investigated across substantially deeper timescales.

### 3.6 Convergence and Divergence within Maternal Continuity

The three domains may therefore either converge or diverge.

**Convergence** occurs when the same woman provides the oocyte, carries the pregnancy, gives birth, and occupies the corresponding genealogical

maternal position. In such a case, gestational, genealogical, and mitochondrial genetic continuity are aligned.

**Divergence** occurs when these roles are separated, as may happen through oocyte donation, gestational surrogacy, embryo donation, adoption, or other reproductive and family arrangements. These circumstances demonstrate why maternal continuity cannot scientifically be reduced to the statement that "every person comes from one mother" without defining what *mother* means biologically and analytically.

The revised MCT therefore replaces a singular maternal category with a multidimensional framework:

**Maternal continuity = f ($G_s$, $G_e$, $G_n$)**

where:

- **$G_s$ = gestational continuity**
- **$G_e$ = genealogical continuity**
- **$G_n$ = maternal genetic continuity**

The expression is conceptual rather than a quantitative mathematical equation. It indicates that maternal continuity may contain different combinations of these dimensions depending on reproductive circumstances and the level of analysis.

### 3.7 Temporal and Evidentiary Boundaries

A further foundation of MCT concerns the relationship between temporal distance and evidentiary certainty. The theory distinguishes three broad evidentiary levels.

At the **proximal level**, contemporary mother-offspring gestational relationships can be directly observed and documented clinically. At the **intermediate level**, maternal relationships across several generations can be reconstructed through birth records, family documentation, demographic records, pedigrees, and potentially genetic corroboration. At the **deep-time level**, direct genealogical documentation becomes unavailable, and ancestry must increasingly be inferred through

population genetics, ancient DNA, archaeological evidence, and evolutionary models.

The strength and type of inference therefore change with temporal depth:

**Direct observation → documentary reconstruction → molecular/population inference**

This principle prevents a major logical error: extrapolating directly from the observable gestational relationship of contemporary individuals to the identity of a specific prehistoric maternal ancestor.

The original article acknowledged that detailed information concerning distant maternal lines was unavailable and suggested that additional ascending genealogical research would be necessary. MCT formalizes this limitation by treating the transition from documented genealogy to deep ancestry as an explicit **epistemological boundary**.

### 3.8 Boundary Conditions of the Theory

MCT is subject to several boundary conditions.

First, the theory does not propose that maternal continuity constitutes the entirety of human ancestry. Paternal genetic and genealogical contributions remain fundamental.

Second, gestational continuity is not equivalent to genetic continuity. A gestational carrier and fetus can share a profound physiological relationship without the carrier providing the oocyte or mtDNA.

Third, mitochondrial continuity is not equivalent to genealogical continuity. A male inherits maternal mtDNA but normally does not transmit it, although his descendants remain genealogically related to his mother.

Fourth, mitochondrial common ancestry does not establish a unique historical “first woman.” A mitochondrial most recent common ancestor represents the point at which surviving contemporary mtDNA lineages coalesce, not necessarily the first female member of *Homo sapiens* or the only woman alive at that time.

Fifth, the framework applies most directly to human reproduction involving gestation. Developments in assisted reproductive technologies require the separate identification of genetic, gestational, and social parental roles rather than assumptions based solely on conventional reproduction.

### 3.9 Conceptual Definition of Maternal Continuity Theory

Based on the preceding distinctions, **Maternal Continuity Theory** is formally defined in this study as:

> ***An interdisciplinary framework proposing that human intergenerational continuity contains a distinct maternal dimension that can be investigated through recurring gestational relationships, reconstructable maternal genealogies, and predominantly maternally inherited genetic lineages, while recognizing that these dimensions operate through different biological mechanisms and constitute different forms of evidence.***

The theoretical contribution of MCT therefore lies not in proposing a competing mechanism of human evolution but in identifying and integrating three forms of continuity that are normally studied independently. The theory predicts that the strongest scientific interpretation of maternal continuity will emerge where **gestational, genealogical, and molecular evidence converge**, while discrepancies among these domains should be treated as informative evidence rather than exceptions that invalidate the framework.

This conceptual foundation provides the basis for the formal theoretical propositions developed in the following section.

## 4. The Maternal Continuity Theory

The **Maternal Continuity Theory (MCT)** developed in this study originates from a simple but theoretically consequential observation advanced in the original formulation: every gestated human individual begins postnatal life following an embodied developmental relationship with the individual who carried the pregnancy. The earlier theory used the

umbilicus as the visible anatomical point from which this relationship could be recognized and argued that successive mother-offspring relationships could be followed backward through generations. The original model subsequently represented this continuity through hypothetical female lines and an empirical family genealogy, attempting to demonstrate how maternal relationships could extend from contemporary individuals toward progressively earlier generations.

The present theory retains this **original theoretical contribution** but reformulates it within contemporary reproductive biology, genealogy, and genetics. Rather than treating the umbilicus as proof of an uninterrupted physical connection to a single ancestral woman, MCT proposes that human continuity contains a distinctive maternal pathway produced through the **serial recurrence of mother-offspring relationships across generations**. The theory further proposes that this pathway can be examined at three analytically distinct levels: embodied gestational continuity, genealogical maternal continuity, and maternal genetic continuity.

### 4.1 The Central Theoretical Proposition

The central proposition of MCT can be stated as follows:

> ***Every gestated human individual participates in an embodied mother-offspring relationship; when such relationships are considered sequentially across generations, they constitute potentially reconstructable maternal pathways that may be investigated through gestational, genealogical, and genetic evidence.***

This proposition begins with an observable reproductive event rather than an assumption concerning prehistoric ancestry. During pregnancy, the developing fetus exists within a maternal physiological environment and interacts with the gestational parent through the placenta and fetoplacental circulation [11-14]. Following birth, this specific physiological relationship ends, but the individual who has been born may subsequently participate in another reproductive generation.

The theoretical innovation lies in treating these reproductive events not merely as isolated pregnancies but as **serial biological relationships**.

Suppose that:

$$\mathbf{F_0 \rightarrow F_1 \rightarrow F_2 \rightarrow F_3 \rightarrow \ldots \rightarrow F_n}$$

where each arrow represents a mother-offspring relationship involving gestation and each F represents a successive female-line generation. Each pregnancy is biologically independent: a new placenta develops, a new umbilical connection forms, and a new fetus undergoes development. Nevertheless, when the relationships are ordered genealogically, they form a continuous relational sequence.

Accordingly, MCT does not claim the persistence of one physical umbilical connection across generations. It proposes the **continuity of a recurring biological relationship**.

### 4.2 From the Umbilical Observation to a Theory of Continuity

The umbilicus was the starting point of the original theoretical argument. The earlier paper described it as a universal anatomical observation resulting from separation of the newborn from the maternal reproductive system and proposed it as a common point through which individuals could recognize their maternal origin.

The revised MCT assigns the umbilicus a narrower but scientifically stronger role. The umbilicus is not a genealogical record and contains no visible information identifying a maternal grandmother, great-grandmother, or prehistoric ancestor. Instead, it is an **anatomical consequence of an individual's prenatal umbilical connection**.

The theoretical reasoning therefore proceeds through separate evidentiary steps:

**Umbilical evidence → prior gestational relationship → documented mother-offspring relationship → maternal genealogy → molecular investigation of deeper maternal-line ancestry.**

The significance of this sequence is methodological. Each step requires a different type of evidence. The existence of an umbilicus cannot substitute

for genealogical documentation, and genealogical documentation cannot substitute for molecular evidence when investigating deep population history.

This reformulation preserves the original insight while avoiding an evidentiary leap from contemporary anatomy directly to prehistoric ancestry.

### 4.3 The Serial Maternal-Link Principle

The principal original mechanism proposed by MCT is termed here the **Serial Maternal-Link Principle (SMLP)**.

The principle states that a gestated individual is linked directly to one gestational event and that successive female-line reproduction can create a serial sequence of such events across generations.

Consider four generations:

$$\mathbf{F_0 \text{ gestates } F_1}$$
$$\mathbf{F_1 \text{ gestates } F_2}$$
$$\mathbf{F_2 \text{ gestates } F_3}$$

There is no single physiological connection running continuously from $F_0$ to $F_3$. Rather, there are three separate biological relationships:

$$\mathbf{R_1 = F_0 \rightarrow F_1}$$
$$\mathbf{R_2 = F_1 \rightarrow F_2}$$
$$\mathbf{R_3 = F_2 \rightarrow F_3}$$

The maternal pathway can therefore be expressed conceptually as:

$$\mathbf{MCP = R_1 + R_2 + R_3 + \ldots + R_n}$$

where **MCP** represents the Maternal Continuity Pathway and $\mathbf{R_n}$ represents the maternal relationship occurring in generation *n*.

This is a conceptual representation rather than a quantitative biological equation. Its purpose is to distinguish **continuity by serial recurrence** from continuous physical attachment. This principle develops the central intuition of the original paper, where successive female descendants were represented as branches extending from earlier women. The revised model

replaces the earlier tree-root analogy with a relational structure that can be operationalized using reproductive histories, pedigrees, genealogical records, and genetic evidence.

### 4.4 The Maternal Continuity Pathway

MCT proposes that every individual occupies a position within multiple ancestry networks. The maternal continuity pathway is one analytically identifiable pathway within this larger ancestry structure.

For a contemporary individual $\mathbf{P_0}$, the retrospective maternal pathway may be represented as:

$$\mathbf{P_0 \leftarrow M_1 \leftarrow M_2 \leftarrow M_3 \leftarrow \ldots \leftarrow M_n}$$

where:

- $\mathbf{P_0}$ = focal contemporary individual;
- $\mathbf{M_1}$ = biological/gestational mother, depending on the dimension being analysed;
- $\mathbf{M_2}$ = maternal grandmother;
- $\mathbf{M_3}$ = maternal great-grandmother; and
- $\mathbf{M_n}$ = the earliest maternal ancestor identifiable by the evidence available.

Theoretically, this pathway has no arbitrary genealogical starting point within the life of the focal individual. Every identified maternal ancestor was herself produced through an earlier reproductive event. However, **the theoretical continuity of the pathway must be distinguished from our empirical ability to reconstruct it**.

This produces a central distinction:

**Existence of a maternal relationship ≠ identification of every maternal ancestor.**

For recent generations, identities may be documented through clinical records, birth certificates, population registers, family records, or oral histories. For deeper generations, documentary evidence becomes increasingly incomplete. At considerably greater temporal depth,

population genetics and ancient DNA replace individual genealogy as the primary forms of inference.

Thus, MCT predicts continuity of reproductive relationships without claiming that the complete chain can presently be reconstructed.

### 4.5 Ascending and Descending Maternal Analysis

Another feature retained and refined from the original theory is the distinction between **ascending** and **descending** approaches. The earlier article suggested that tracing maternal relationships backward from contemporary individuals could be particularly useful for identifying earlier female lines.

Within MCT, **ascending maternal analysis** begins with a known contemporary individual:

**Individual → Mother → Maternal grandmother → Maternal great-grandmother → earlier maternal generations.**

This approach is empirically attractive because the investigation begins with an identifiable person and proceeds toward progressively less certain historical evidence.

By contrast, **descending maternal analysis** begins with a known or hypothesized historical woman and examines her descendants:

**Earlier female ancestor → daughter(s) → granddaughter(s) → subsequent descendants.**

The two approaches answer different questions. Ascending analysis asks, *"How far backward can this individual's maternal pathway be reliably reconstructed?"* Descending analysis asks, *"Which subsequent individuals can be demonstrated to descend from this particular woman, and through which pathways?"*

The two methods may converge when adequate genealogical and genetic evidence is available.

### 4.6 Transmission, Branching, and Termination

The original model placed considerable emphasis on the observation that daughters and sons occupy different positions in maternal-line continuation. In the family example, a focal woman had five daughters and several sons, and the analysis attempted to show how the female descendants generated continuing birth lines.

MCT retains the importance of this observation but revises its biological interpretation.

Both sons and daughters are descendants of their mother. Both normally inherit nuclear genetic material from her, and both normally receive her mtDNA. Therefore, neither becomes biologically "disconnected" from the mother.

The distinction concerns **subsequent transmission**.

Under predominant human mitochondrial inheritance:

**Mother → Daughter → Daughter's child ✓**

permits continuation of the maternal mtDNA pathway, whereas:

**Mother → Son → Son's child ×**

normally does not transmit the original mother's mtDNA beyond the son [1-3,15].

Genealogically, however:

**Mother → Son → Son's child ✓**

remains a valid descent pathway.

The revised theory therefore distinguishes three outcomes:

**Continuation** - the relevant form of maternal continuity persists into another generation;

**Branching** - one woman produces multiple descendants, creating several genealogical pathways;

**Transmission termination** - a particular maternal molecular pathway, such as mtDNA transmission through a male descendant, normally ends even though genealogical descent continues.

This distinction substantially strengthens the original theory because it prevents *line termination* from being incorrectly interpreted as loss of biological relatedness.

### 4.7 The Three-Layer Maternal Continuity Model

The complete theory can therefore be represented through three superimposed layers.

**Layer I: Embodied/Gestational Continuity**

$$\mathbf{G_0 \rightarrow G_1 \rightarrow G_2 \rightarrow \ldots \rightarrow G_n}$$

Each arrow represents a distinct gestational relationship.

**Layer II: Genealogical Continuity**

$$\mathbf{M_0 \rightarrow D_1 \rightarrow D_2 \rightarrow \ldots \rightarrow D_n}$$

Each connection represents documented or inferable descent.

**Layer III: Maternal Genetic Continuity**

$$\mathbf{mtDNA_0 \rightarrow mtDNA_1 \rightarrow mtDNA_2 \rightarrow \ldots \rightarrow mtDNA_n}$$

Each connection represents maternal molecular transmission, subject to mutation, heteroplasmy, bottlenecks, drift, and selection [1-3]. The three layers may overlap in conventional reproduction but should never be assumed to be identical.

Accordingly:

$$\mathbf{MCT = Gestational\ Continuity \cap Genealogical\ Continuity \cap Maternal\ Genetic\ Continuity}$$

where the intersection represents circumstances in which all three forms of evidence identify the same maternal pathway.

This intersection constitutes the **strongest evidentiary state of MCT**, although the theory remains applicable when only one or two dimensions can be established.

### 4.8 The Maternal Continuity Convergence Principle

A second major theoretical contribution is therefore the **Maternal Continuity Convergence Principle (MCCP)**.

It proposes that:

> ***Confidence in a reconstructed maternal pathway increases when independently derived gestational, genealogical, and genetic evidence converge on the same intergenerational relationships.***

For example, a documented pedigree may establish:

$$\mathbf{A \rightarrow B \rightarrow C \rightarrow D}$$

Historical birth records may independently confirm the maternal relationships. Molecular analysis may then demonstrate mtDNA compatibility among appropriate female-line descendants.

No single evidence type performs the work of all three. Rather, confidence increases through triangulation.

Conceptually:

$$\mathbf{C_m \propto E(g_s) + E(g_e) + E(g_n)}$$

where $\mathbf{C_m}$ denotes confidence in the maternal pathway and the three evidence terms represent gestational, genealogical, and genetic evidence respectively.

Again, this is not intended as a statistical formula but as an epistemological representation that can subsequently be operationalized.

### 4.9 Maternal Continuity and the Question of Human Origins

The most ambitious implication of MCT concerns human origins. However, this implication requires careful definition.

If every contemporary maternal-line relationship can theoretically be extended backward to an earlier maternal relationship, then maternal pathways must extend into progressively deeper human history. Population genetics independently demonstrates that surviving human mtDNA lineages coalesce when traced backward through maternal inheritance [1-3,5,6].

This provides an important point of convergence between the original theoretical intuition and molecular population genetics. The original article already recognized research suggesting a maternal common ancestor through mitochondrial evidence.

MCT nevertheless distinguishes three propositions that should not be conflated:

- all gestated humans have an immediate gestational predecessor;
- maternal genealogical pathways extend backward across generations; and
- surviving contemporary mtDNA lineages eventually coalesce to a mitochondrial most recent common ancestor.

None of these propositions independently demonstrates the identity of the **first female human**.

This is a critical theoretical boundary. The mitochondrial most recent common ancestor was not necessarily the first *Homo sapiens* woman, the only woman alive at that time, or the sole genealogical female ancestor of contemporary humans. Other women living during the same period may have contributed extensively to present-day nuclear genomes even if their uninterrupted mtDNA transmission lines later disappeared.

MCT therefore reframes the original question from:

**“Can the navel prove that all humans originated from one first woman?”**

to the scientifically testable question:

> ***“How far can serial maternal relationships be reconstructed across gestational, genealogical, and molecular levels, and at***

***what point does direct evidence give way to population-level inference?"***

This reformulation preserves the originality of the theory while making it compatible with contemporary biomedical and evolutionary science.

### 4.10 Maternal Continuity Does Not Replace Evolution

MCT is not proposed as an alternative to evolutionary theory. Evolutionary biology explains changes in allele frequencies, populations, phenotypes, and species across generations through mechanisms including mutation, natural selection, genetic drift, recombination, migration, and admixture. MCT addresses a narrower but complementary question: **through what recurring maternal relationships are successive human generations biologically produced and connected?**

The explanatory levels can therefore coexist:

**Evolutionary theory:** explains population and species change across generations.

**Population genetics:** reconstructs genetic ancestry and demographic history.

**Reproductive biology:** explains pregnancy, fetal development, and maternal-fetal interaction.

**Genealogy:** reconstructs descent relationships.

**Maternal Continuity Theory:** integrates the maternal dimension across these levels.

MCT therefore does not ask evolutionary biology to explain gestational relationships, nor does it use gestational anatomy to replace evolutionary evidence. Its purpose is interdisciplinary integration.

### 4.11 The Original Contribution of MCT

The originality of MCT lies not in separately discovering that humans undergo gestation, that maternal genealogies exist, or that mtDNA is maternally inherited. Each of these phenomena is already well established.

The theoretical contribution lies instead in **connecting these independently established phenomena through a unified multilevel model of maternal continuity while explicitly defining their evidentiary boundaries**.

The theory makes four principal original contributions.

First, it conceptualizes repeated gestational events as **serial embodied continuity** rather than isolated reproductive episodes.

Second, it introduces the **Serial Maternal-Link Principle**, through which successive maternal relationships can be represented as an ordered intergenerational pathway.

Third, it separates **gestational, genealogical, and maternal genetic continuity**, allowing convergence and divergence among them to be scientifically examined.

Fourth, it introduces the **Maternal Continuity Convergence Principle**, according to which confidence in reconstructed maternal pathways increases when independent biological, documentary, and molecular evidence converge.

Consequently, the revised MCT transforms the original anatomical observation into a broader, falsifiable interdisciplinary theory:

> ***Human maternal continuity is not the persistence of a single physical connection across generations; it is the serial recurrence of biologically identifiable mother-offspring relationships that can form reconstructable genealogical pathways and, along particular female lines, correspond with predominantly maternally transmitted molecular lineages*.**

This formulation constitutes the central theoretical proposition to be evaluated through the formal propositions and empirical framework developed in the following sections.

## 5. Propositions and Conceptual Model

Building on the conceptual distinctions developed in Sections 3 and 4, Maternal Continuity Theory (MCT) can be translated into a set of explicit theoretical propositions. The purpose of these propositions is to move the framework beyond descriptive observation and make its central claims **conceptually testable, empirically examinable, and potentially falsifiable**. This is particularly important because the original formulation moved from the observable umbilical relationship toward increasingly remote maternal connections. The revised model separates these stages and specifies the evidence required at each level.

MCT proposes that maternal continuity operates through three distinct but potentially convergent domains: **gestational continuity (GC), genealogical continuity (GeC), and maternal genetic continuity (MGC)**. These domains operate over different temporal scales and require different forms of evidence. Their convergence constitutes the strongest empirical support for a reconstructed maternal pathway, whereas divergence between them provides information about the biological and genealogical structure of descent rather than necessarily contradicting the theory.

### 5.1 Proposition 1: Universal Gestational Predecessor Principle

> ***P1. Every gestated human individual has an identifiable gestational predecessor with whom a direct maternal-fetal physiological relationship existed during prenatal development.***

This proposition represents the most proximal and directly observable component of MCT. During pregnancy, fetal development depends upon a complex maternal-fetal system involving implantation, placentation, endocrine signaling, immunological adaptation, nutrient and gas exchange, and fetoplacental circulation [11-14]. The umbilical cord forms part of this developmental system, while the postnatal umbilicus remains an anatomical consequence of the previous fetal-placental connection.

The original theory identified the navel as the universal anatomical starting point of the maternal relationship. MCT retains the insight but modifies its evidentiary interpretation. The umbilicus is not itself proof of genealogical

or prehistoric ancestry; rather, it provides anatomical evidence consistent with an earlier gestational process.

Accordingly:

$$\textbf{Individual } (I_0) \leftarrow \textbf{Gestational predecessor } (G_1)$$

P1 establishes the first biological link in the model but makes no claim concerning the identity of earlier ancestors.

### 5.2 Proposition 2: Serial Maternal-Link Principle

> ***P2. When a female-line descendant subsequently undergoes gestation, successive mother-offspring relationships generate a serial maternal pathway across generations.***

If $F_0$ gestates $F_1$ and $F_1$ later gestates $F_2$, two distinct pregnancies occur, yet they can be arranged genealogically as a sequential relationship:

$$F_0 \rightarrow F_1 \rightarrow F_2$$

Extending the model:

$$F_0 \rightarrow F_1 \rightarrow F_2 \rightarrow F_3 \rightarrow \ldots \rightarrow F_n$$

Each arrow represents an independent gestational event rather than a persistent physical connection.

This proposition captures one of the central ideas of the original theory, which represented successive female descendants as maintaining a line extending from an earlier woman. The revised model defines this more precisely as **serial relational continuity**.

Thus:

where **MCP** represents the Maternal Continuity Pathway and each represents a separate gestational mother-offspring relationship.

The theoretical claim is therefore not that a single biological structure persists through generations, but that the same category of reproductive relationship recurs serially.

### 5.3 Proposition 3: Genealogical Reconstruction Principle

> ***P3. Serial maternal relationships can form genealogically reconstructable pathways, but the empirical completeness of such reconstruction decreases as temporal distance increases.***

Every focal individual can theoretically be positioned within a maternal genealogical sequence:

$$\mathbf{I_0 \leftarrow M_1 \leftarrow M_2 \leftarrow M_3 \leftarrow \ldots \leftarrow M_n}$$

where $M_1$ represents the mother, $M_2$ the maternal grandmother, $M_3$ the maternal great-grandmother, and $M_n$ an increasingly remote maternal ancestor.

The original study illustrated this reasoning using a multigenerational family from Bangladesh, tracing relationships from a focal woman through daughters and subsequent descendants. Under MCT, such a pedigree provides evidence for a particular documented family pathway rather than proof of universal prehistoric descent.

P3 therefore contains two separate claims: maternal relationships can be reconstructed where adequate evidence exists, but the absence of records for remote generations prevents direct identification of every maternal ancestor.

This produces the evidentiary sequence:

**Direct observation → clinical/civil records → documented genealogy → historical reconstruction → genetic inference**

The confidence associated with individual identification generally decreases as analysis moves backward through these levels.

### 5.4 Proposition 4: Maternal Genetic Transmission Principle

> ***P4. Predominantly maternal transmission of mitochondrial DNA provides a molecular pathway that may correspond with, and independently support, particular female-line genealogical relationships.***

Human mtDNA is transmitted overwhelmingly through the maternal line [1-3,15]. Consequently, where a female-line pedigree is correctly reconstructed, mtDNA provides a potentially independent molecular source for evaluating maternal genetic relationships.

A simplified transmission pathway can be represented as:

$$\mathbf{M_0(mtDNA_0) \rightarrow D_1(mtDNA_1) \rightarrow D_2(mtDNA_2) \rightarrow \ldots \rightarrow D_n(mtDNA_n)}$$

The notation does not imply absolute sequence identity. Mutation, heteroplasmy, mitochondrial bottlenecks, drift, and selection may generate variation across generations [2,3]. Continuity therefore concerns **lineal transmission**, not molecular invariance.

This proposition also requires a critical qualification. A male descendant normally inherits his mother's mtDNA but does not transmit that mtDNA to his offspring [1-3,15]. Therefore:

**Mother → Son ✓ inheritance**

but ordinarily:

**Mother → Son → Son's offspring ✕ mtDNA-line transmission**

This does not terminate genealogical relatedness or nuclear genetic inheritance.

### 5.5 Proposition 5: Domain Independence Principle

> ***P5. Gestational, genealogical, and maternal genetic continuity are analytically distinct; evidence of continuity in one domain does not necessarily establish continuity in the others.***

This proposition protects MCT against overinterpretation.

A gestational relationship establishes that one individual carried a pregnancy but does not necessarily establish that the gestational parent contributed the oocyte. A genetic relationship may exist without gestation by the genetic mother, as in oocyte donation. Genealogical or social maternal relationships may likewise exist without either gestational or genetic continuity.

Therefore:

where:

- **GC** = gestational continuity;
- **GeC** = genealogical continuity;
- **MGC** = maternal genetic continuity.

The three domains may overlap, but none should be used automatically as a proxy for another.

This proposition becomes particularly important in contemporary reproductive medicine, where oocyte donation, embryo donation, gestational surrogacy, and related technologies can separate gestational and genetic parental roles.

### 5.6 Proposition 6: Maternal Continuity Convergence Principle

> ***P6. Confidence in a reconstructed maternal continuity pathway increases when independent gestational, genealogical, and genetic evidence converge on the same intergenerational relationships.***

This proposition provides the principal evidentiary mechanism of MCT.

Suppose genealogical documentation identifies:

$$\mathbf{F_0 \rightarrow F_1 \rightarrow F_2 \rightarrow F_3}$$

and independent reproductive records support these mother-offspring relationships. If mtDNA analysis is also compatible with the proposed female-line relationships, three independent evidentiary domains converge.

Conceptually:

where denotes confidence in a reconstructed Maternal Continuity Pathway and the three terms represent evidence from the gestational, genealogical, and maternal genetic domains.

This expression is conceptual rather than a validated statistical equation. Future empirical research could develop quantitative weighting procedures for different evidence types.

### 5.7 Proposition 7: Transmission-Relatedness Distinction

> ***P7. Termination of a particular maternal transmission pathway does not imply termination of genealogical or overall genetic relatedness.***

This proposition directly refines an important element of the original model. In the earlier family analysis, descendants through sons were described as no longer being directly connected with the focal female line because their children were gestated by other women.

The revised theory distinguishes **transmission** from **relatedness**.

Consider:

$$\mathbf{F_0 \rightarrow S_1 \rightarrow C_2}$$

$S_1$ remains the biological son of $F_0$ and $C_2$ remains her genealogical grandchild. Nuclear genetic inheritance can therefore continue from $F_0$ through $S_1$ to $C_2$. However, $F_0$'s mtDNA is normally not transmitted by $S_1$ to $C_2$.

Thus:

**Genealogical continuity = retained**

**Autosomal genetic contribution = potentially retained**

**Direct mtDNA transmission = normally terminated**

This distinction permits the original branching model to be retained without contradicting established principles of human genetics.

### 5.8 Proposition 8: Deep-Time Inference Boundary

> ***P8. Maternal continuity can be extended theoretically into deep human history, but individual-level claims become progressively inferential and cannot identify a unique first human female without independent evidence.***

This proposition defines the most important epistemological boundary of MCT.

The original theory hypothesized that successive maternal relationships could ultimately lead toward a first female ancestor. Contemporary population genetics provides strong evidence that surviving mtDNA lineages coalesce backward toward a mitochondrial most recent common ancestor, an issue also recognized in the original article.

However:

and:

Consequently, MCT supports investigation of increasingly ancient maternal-line relationships but does not infer a unique historical “first mother” from contemporary anatomical or mitochondrial evidence alone.

This makes P8 both a theoretical proposition and a **boundary condition preventing unfalsifiable extrapolation**.

### 5.9 Integrated Conceptual Model of Maternal Continuity Theory

The eight propositions can now be integrated into a single conceptual model.

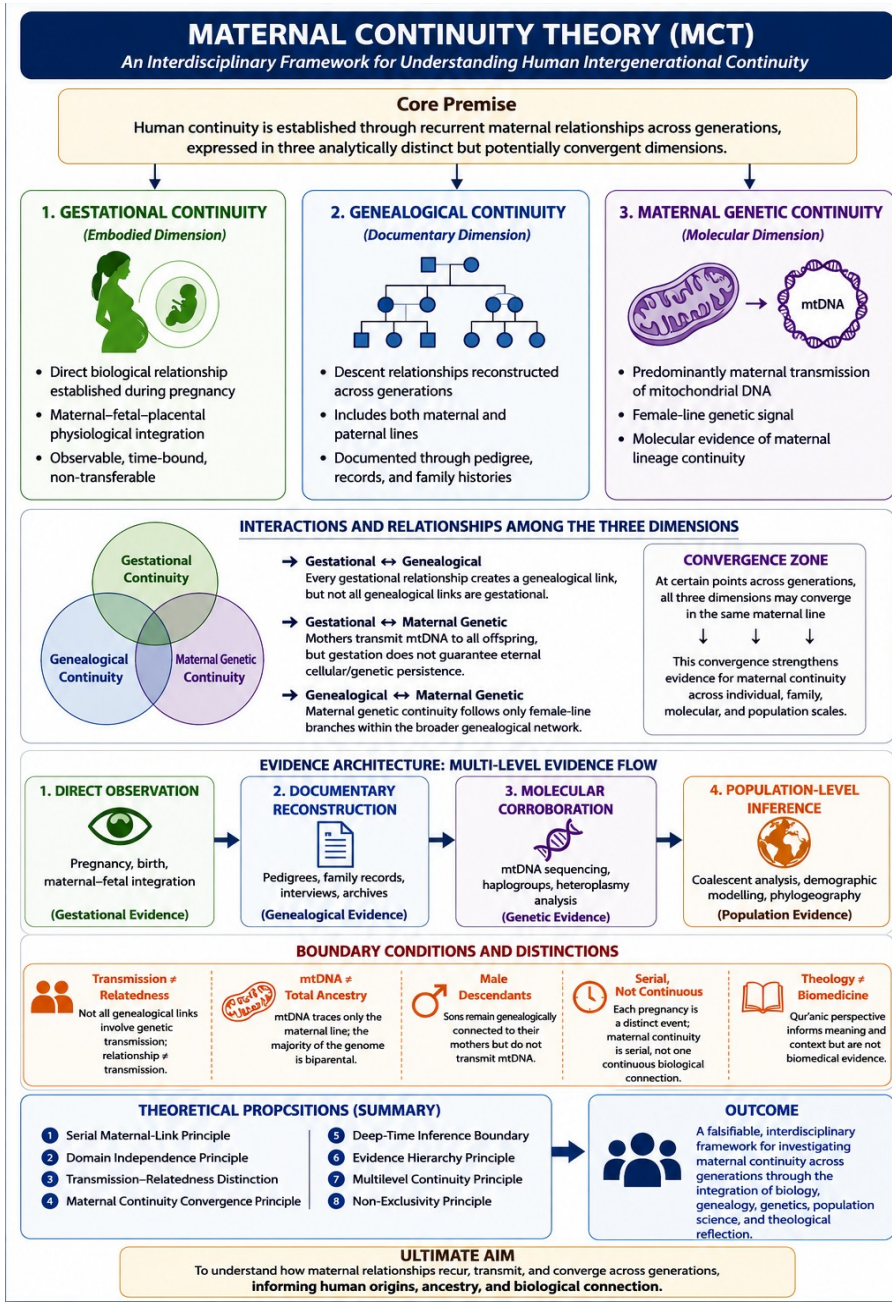



Figure 1. Integrated Conceptual Model of Maternal Continuity Theory (MCT)

### 5.10 Three-Level Evidence Architecture

The model can additionally be represented through three evidentiary levels:

| Level | Maternal-continuity domain | Principal evidence | Typical temporal reach | Evidentiary status |
|---|---|---|---|---|
| **Level I** | Gestational continuity | Clinical/ reproductive records, maternal-fetal physiology | Individual/current generation | Directly observable |
| **Level II** | Genealogical continuity | Birth records, pedigrees, civil/family records | Multiple documented generations | Reconstructable |
| **Level III** | Maternal genetic continuity | mtDNA, population genetics, ancient DNA | Deep ancestry/population history | Molecularly inferential |

The three levels should not be interpreted as a simple progression in which one automatically proves the next. Instead, they represent **different evidentiary windows into the same broader problem of maternal continuity**.

### 5.11 Falsifiability and Empirical Expectations

For MCT to function as a scientific theory rather than solely as a philosophical interpretation, its propositions must permit empirical challenge. Several observations could require rejection or substantial modification of particular components of the framework.

For example, P4 would require revision if robust population-level evidence demonstrated that human mtDNA is routinely inherited biparentally. P6 could be evaluated by determining whether genealogically documented female-line relatives display the predicted mitochondrial

relationships. P5 can be examined directly through assisted reproductive cases in which genetic and gestational maternal roles are separated.

Likewise, reconstructed pedigrees can test P2 and P3 by determining whether hypothesized serial maternal relationships correspond to independently verifiable birth and family records.

The theory therefore generates an important methodological principle:

> ***The farther a maternal-continuity claim extends from directly observed reproduction, the greater the requirement for independent genealogical and molecular corroboration.***

This principle prevents anatomical observation from being used as sufficient evidence for deep historical claims and transforms MCT into a framework in which the **strength of conclusions is proportional to the convergence and quality of evidence**.

### 5.12 Summary of Theoretical Propositions

The complete theoretical architecture can be summarized as:

- **P1 - Universal Gestational Predecessor:** every gestated individual has a direct gestational predecessor.
- **P2 - Serial Maternal Link:** successive female-line reproductive events can form serial maternal pathways.
- **P3 - Genealogical Reconstruction:** such pathways can be reconstructed where appropriate records exist, although completeness declines with temporal distance.
- **P4 - Maternal Genetic Transmission:** predominantly maternal mtDNA inheritance provides a molecular dimension of female-line continuity.
- **P5 - Domain Independence:** gestational, genealogical, and maternal genetic continuity are related but non-equivalent.
- **P6 - Evidence Convergence:** confidence in maternal-pathway reconstruction increases when independent evidence from the three domains converges.

- **P7 - Transmission-Relatedness Distinction:** termination of mtDNA transmission does not terminate genealogical or broader genetic relatedness.
- **P8 - Deep-Time Inference Boundary:** maternal pathways can be investigated into deep history, but current evidence cannot infer a unique “first human female” merely from umbilical, genealogical, or mtDNA continuity.

Together, these propositions transform the original maternal-line hypothesis into a structured theoretical framework capable of generating empirical research questions and testable predictions. The resulting conceptual model preserves the original insight-that successive human generations contain a recurring maternal relationship-while distinguishing direct biological observation from genealogical reconstruction and molecular inference. This distinction provides the foundation for the methodological strategy developed in the next section.

## 6. Methodology

This chapter outlines the methodological framework employed to develop and examine Maternal Continuity Theory (MCT). Given the interdisciplinary and theory-building nature of the study, the methodology integrates conceptual synthesis, comparative evidence assessment, genealogical modelling, and interdisciplinary interpretation rather than relying on a single empirical design. Evidence from reproductive biology, genetics, mitochondrial inheritance, genealogy, population genetics, and evolutionary research is systematically connected to evaluate the proposed dimensions of maternal continuity. An illustrative multigenerational Bangladeshi family is additionally used to demonstrate the genealogical model and generate propositions for subsequent empirical testing.

### 6.1 Study Design

This study adopts an **interdisciplinary conceptual synthesis and genealogical modelling approach** to develop and evaluate Maternal Continuity Theory (MCT). The study is theoretical rather than experimental and does not attempt to estimate the prevalence of a clinical condition, test an intervention, or establish a new molecular mechanism.

Instead, it integrates established knowledge from reproductive biology, maternal-fetal medicine, human genetics, population genetics, evolutionary biology, genealogy, and kinship research to determine whether gestational, genealogical, and maternal genetic continuity can be represented within a coherent analytical framework.

This methodological approach is appropriate because the principal research problem concerns relationships among concepts that are generally investigated separately. Maternal-fetal physiology establishes one level of biological connection; genealogical records provide another form of intergenerational evidence; and predominantly maternal mitochondrial DNA (mtDNA) inheritance provides a molecular pathway that can extend maternal-line inference considerably further into the past [1-3,11-15]. MCT therefore does not treat these sources of evidence as interchangeable. Instead, the methodology examines their **conceptual compatibility, evidentiary independence, convergence, and limits of inference**.

The original formulation approached the problem through the observable umbilicus and a multigenerational family example. The umbilicus was treated as a universal sample representing separation from the mother at birth, while a Bangladeshi family genealogy was subsequently used to illustrate the continuation and branching of maternal relationships across generations. The present methodology retains these elements as the historical foundation of the theory but substantially restructures them within a reproducible conceptual and genealogical framework.

### 6.2 Methodological Framework

The methodological framework consists of four sequential components:

**(1) interdisciplinary evidence identification → (2) conceptual synthesis → (3) genealogical modelling → (4) theoretical evaluation and boundary testing.**

These components correspond directly to the three domains defined in MCT:

where:

- **GC** = gestational continuity;
- **GeC** = genealogical continuity; and
- **MGC** = maternal genetic continuity.

The methodology does not assume that evidence supporting one domain automatically establishes another. Rather, each domain is evaluated according to the forms of evidence appropriate to it.

### 6.3 Interdisciplinary Conceptual Synthesis

The first methodological component involves a structured conceptual synthesis of biomedical and interdisciplinary evidence relevant to maternal continuity. The synthesis is organized around six knowledge domains: **(i) human evolution and origins, (ii) reproductive and maternal-fetal biology, (iii) mitochondrial genetics, (iv) population genetics, (v) genealogy, and (vi) kinship and reproductive relationships**.

The objective is not to conduct a quantitative meta-analysis because the evidence encompasses fundamentally different study designs, biological mechanisms, outcomes, and units of analysis. Instead, evidence is examined according to its relevance to the propositions of MCT.

For reproductive biology, the principal analytical question is whether pregnancy establishes a biologically definable and observable relationship between the gestational parent and fetus. Evidence concerning implantation, placentation, maternal-fetal exchange, immune regulation, fetoplacental circulation, and umbilical development is therefore used to evaluate the concept of gestational continuity [11-14].

For molecular genetics, evidence concerning mtDNA inheritance, heteroplasmy, mitochondrial bottlenecks, paternal mitochondrial elimination, and exceptional or disputed patterns of inheritance is considered in relation to maternal genetic continuity [1-3,15,16].

Population-genetic and evolutionary evidence is used to establish the appropriate limits of deep-time inference, particularly the distinction between maternal-line coalescence and the identification of a unique first human female. Genealogical and kinship literature is used to differentiate

biological ancestry from matrilineal descent, social motherhood, and culturally defined kinship relationships.

### 6.4 Concept Identification and Operational Definition

Following evidence synthesis, the principal concepts are operationally differentiated. This step is necessary to avoid using terms such as *maternal relationship*, *maternal ancestry*, *maternal lineage*, and *motherhood* as though they represented the same phenomenon.

Three primary analytical constructs are specified.

**Gestational continuity (GC)** is operationally defined as a documented or biologically established relationship in which an individual underwent prenatal development within a gestational parent. Evidence may include obstetric or birth documentation, reproductive history, or other reliable evidence of gestation.

**Genealogical continuity (GeC)** is defined as an identifiable mother-offspring relationship positioned within an intergenerational pedigree. Evidence may include civil registration, birth records, family records, historical documentation, validated pedigrees, or corroborating genetic information.

**Maternal genetic continuity (MGC)** is defined specifically as maternal-line molecular transmission, principally evaluated through mtDNA. It is distinguished from total genetic ancestry because nuclear inheritance is biparental.

The operational distinction can be represented as:

while allowing:

That is, the three forms of continuity are conceptually distinct but may converge in the same mother-offspring pathway.

### 6.5 Unit of Analysis

The primary unit of analysis is the **maternal link**, defined as a relationship between two adjacent generations in which the younger individual is

connected to an identified maternal predecessor according to one or more MCT domains.

A single link is represented as:

where represents the maternal predecessor and the descendant.

Each link can be characterized according to the evidence available:

For example, a conventional biological mother-daughter relationship may contain evidence for all three domains:

whereas a gestational-surrogacy relationship could contain gestational continuity without maternal genetic continuity:

depending on how genealogy is defined for the particular research question.

These numerical values are **categorical indicators for conceptual modelling**, not validated clinical or probabilistic scores.

### 6.6 Construction of the Genealogical Model

The second major methodological component is genealogical modelling. A focal individual is designated as $\mathbf{P_0}$, from whom maternal ancestry can be examined retrospectively.

The ascending maternal pathway is represented as:

where represents the maternal predecessor of $P_0$, the maternal predecessor in the previous generation, and the most distant maternal ancestor supported by the available evidence.

The model may alternatively be examined prospectively or historically through a descending pathway:

where represents a focal ancestral woman and subsequent nodes represent descendants.

The earlier article employed a related descending approach in which a focal woman and her five daughters were followed through subsequent generations. In the revised model, however, descendants are not removed

from the genealogical network merely because descent occurs through a son. Instead, different transmission pathways are coded separately.

### 6.7 Branching and Transmission Rules

Genealogical modelling distinguishes **descent branching** from **maternal-line molecular transmission**.

If a woman has both a daughter and a son:

both $D_1$ and $S_1$ remain genealogical descendants of $F_0$ and both normally inherit nuclear genetic material and mtDNA from her.

If both subsequently have children, however:

may preserve $F_0$'s maternal mtDNA transmission pathway, whereas:

normally does not transmit $F_0$'s mtDNA to $C_2$ [1-3,15].

The dashed arrow therefore indicates **termination of the focal mtDNA transmission pathway**, not termination of genealogical relatedness.

This rule represents an important methodological revision of the original family model, in which descendants through sons were interpreted as no longer directly connected with the focal woman's maternal line. The revised approach permits simultaneous representation of genealogical, nuclear genetic, gestational, and mitochondrial relationships.

### 6.8 Illustrative Genealogical Case

The multigenerational family described in the original study is retained as an **illustrative genealogical case**, rather than being treated as a representative population sample or empirical proof of universal human maternal ancestry.

The original family included an older couple, five daughters, surviving sons, and multiple grandchildren and later descendants. The earlier analysis subsequently identified 62 women within the extended lineage and attempted to demonstrate their relationship with the focal female ancestor.

Under the revised methodology, this family is used for three purposes: to demonstrate construction of serial maternal links, to illustrate branching and transmission termination, and to show how gestational, genealogical, and maternal genetic relationships may require different graphical representations.

No population-level generalization is made from the family. The case functions as a **worked theoretical model** illustrating the operation of MCT.

### 6.9 Evidence Classification

To prevent overextension of conclusions, evidence used in maternal-pathway reconstruction is classified into three broad levels.

| Evidence level | Primary source | Type of inference |
|---|---|---|
| **Level I: Direct** | Clinical reproductive evidence, documented birth/gestation | Directly observable relationship |
| **Level II: Reconstructed** | Birth certificates, civil records, validated family records, pedigrees | Genealogically reconstructed relationship |
| **Level III: Molecular/inferential** | mtDNA, ancient DNA, population-genetic models | Genetic or deep-time inference |

A maternal relationship supported at Level I should therefore not be interpreted as automatically establishing Level III ancestry.

The methodological principle applied throughout the study is:

Consequently, the evidentiary requirements become more stringent as claims extend further into the past.

### 6.10 Convergence Analysis

The third methodological element examines whether independent forms of evidence converge.

For a hypothesized maternal pathway:

evidence is considered separately for each link and each domain. A conceptual evidence matrix can therefore be constructed:

| Link | Gestational evidence | Genealogical evidence | mtDNA evidence | Overall interpretation |
|---|---|---|---|---|
| $F_0 \rightarrow F_1$ | Present/absent | Present/absent | Compatible/not tested/incompatible | Evaluated |
| $F_1 \rightarrow F_2$ | Present/absent | Present/absent | Compatible/not tested/incompatible | Evaluated |
| $F_2 \rightarrow F_3$ | Present/absent | Present/absent | Compatible/not tested/incompatible | Evaluated |

This approach operationalizes the **Maternal Continuity Convergence Principle (P6)**.

Importantly, mtDNA compatibility is not treated as sufficient proof of a specific mother-offspring relationship because many individuals can share the same maternal haplogroup or closely related mitochondrial sequences. Conversely, incompatible high-quality molecular evidence may challenge a proposed direct maternal genetic relationship and require re-evaluation of the pedigree.

### 6.11 Proposition-Based Evaluation

The eight propositions developed in Section 5 provide the analytical framework for evaluating MCT.

P1 and P2 are evaluated primarily through reproductive biological evidence concerning gestation and sequential reproduction. P3 is examined through genealogical modelling and the availability of intergenerational documentation. P4 is evaluated against established mechanisms of mitochondrial inheritance. P5 is examined through situations in which gestational, genetic, and genealogical roles diverge, particularly assisted reproduction. P6 is assessed conceptually through evidence convergence. P7 is evaluated by distinguishing mtDNA

transmission from broader genealogical and nuclear genetic relatedness. P8 is examined against population-genetic and evolutionary evidence concerning deep ancestry and coalescence.

This proposition-based strategy prevents the theory from being assessed as one indivisible claim. Individual propositions can be supported, modified, restricted, or rejected without necessarily invalidating every other component of MCT.

### 6.12 Boundary-Case Analysis

Boundary cases are deliberately incorporated because they provide particularly strong tests of the conceptual model.

These include **oocyte donation, gestational surrogacy, embryo donation, adoption, male-line descent, mitochondrial heteroplasmy, disputed paternal mtDNA transmission, and incomplete genealogical documentation**.

For example, gestational surrogacy separates gestational continuity from maternal genetic continuity. Oocyte donation separates the genetic contributor from the gestational parent. Male descendants distinguish genealogical continuity from continued mtDNA transmission. Adoption demonstrates the distinction between biological continuity and social kinship.

Rather than being treated as exceptions to be excluded, these cases are used to examine whether MCT remains internally coherent when conventional correspondence among genetic, gestational, genealogical, and social motherhood is absent.

### 6.13 Deep-Time Analysis and Inferential Limit

For deep human history, genealogical modelling cannot identify every maternal relationship directly. At this point, the methodology shifts from individual pedigree reconstruction to population-level molecular inference.

mtDNA phylogenies can identify relationships among surviving maternal genetic lineages and estimate their coalescence, while ancient DNA can provide additional evidence concerning prehistoric populations and

migration. However, molecular coalescence cannot establish that a mitochondrial most recent common ancestor was the first female *Homo sapiens*, the only woman living at the time, or the sole female genealogical ancestor of living humans.

Accordingly:

and:

This inferential boundary is incorporated explicitly into the methodology rather than being treated only as a study limitation.

### 6.14 Validity and Falsifiability

The conceptual validity of MCT is assessed through four criteria: **internal consistency, compatibility with established biomedical evidence, explanatory utility, and falsifiability**.

Internal consistency requires that the three continuity domains remain conceptually distinct throughout the model. Biomedical compatibility requires that propositions concerning gestation and inheritance do not contradict established reproductive physiology or human genetics. Explanatory utility concerns whether MCT provides a useful framework beyond existing descriptions of reproduction, genealogy, and mtDNA inheritance.

Falsifiability is particularly important for the theory's scientific status. For example, consistent high-quality evidence demonstrating routine paternal mtDNA inheritance would require substantial revision of P4. Reliable genealogical evidence systematically contradicting the proposed serial maternal relationships would challenge particular pathway reconstructions. Likewise, failure to maintain conceptual distinction between gestational and genetic relationships in assisted reproduction would undermine P5.

The framework therefore permits both confirmation and revision.

### 6.15 Ethical Considerations

The present study is principally a theoretical and conceptual analysis and does not involve clinical intervention, biological specimen collection, or

prospective recruitment of human participants. The historical family genealogy derived from the original theoretical work is used only as an illustrative model.

For any future empirical testing of MCT involving identifiable family pedigrees, medical records, reproductive histories, or genomic information, appropriate institutional ethical approval and informed consent would be required. Genetic genealogy presents particular ethical concerns because information obtained from one participant can reveal biological relationships involving relatives who have not themselves consented to testing. Future investigations should therefore address confidentiality, data protection, incidental findings, family disclosure, genetic discrimination, and culturally sensitive interpretations of parentage and kinship.

### 6.16 Methodological Scope

This methodology is designed to evaluate whether maternal continuity constitutes a coherent and empirically examinable dimension of human intergenerational descent. It does not reconstruct the complete genealogy of humanity, establish the identity of a first human female, or substitute a maternal lineage for the biparental genetic structure of human ancestry.

Its principal methodological contribution is the creation of a framework in which:

can be applied systematically.

Through this sequence, the original observation of maternal connection is transformed into an interdisciplinary research methodology in which every extension of the theory requires evidence appropriate to the level of inference being made. This approach provides the methodological basis for the **illustrative genealogical analysis and evaluation of the MCT propositions** presented in the subsequent section.

## 7. Illustrative Genealogical Analysis: The Bangladesh Family Example

his chapter applies **Maternal Continuity Theory (MCT)** to an illustrative multigenerational family from Bangladesh to demonstrate how maternal

continuity can be represented within an actual genealogical structure. The analysis distinguishes among **direct female-line descent, broader genealogical relatedness, and predicted maternal mitochondrial transmission**, while examining how these pathways converge or diverge across successive generations. Rather than treating the family case as population-level evidence, it is used as an illustrative model to operationalize the theoretical propositions of MCT, clarify the transmission–relatedness distinction, and establish a foundation for future molecular and genealogical validation.

### 7.1 Purpose of the Illustrative Analysis

To demonstrate how Maternal Continuity Theory (MCT) can be applied to an actual multigenerational family structure, this section re-examines the Bangladesh family described in the original study. The case is used strictly as an **illustrative genealogical model**, rather than as a representative population sample or empirical proof of universal maternal ancestry. This distinction is important because a single extended family can demonstrate how maternal relationships branch and continue across generations, but it cannot establish population-level patterns or deep human ancestry.

The original study described a family from a village in Bangladesh centred on an approximately 60-year-old woman and her approximately 86-year-old husband. The woman had given birth to five daughters (D1-D5) and six sons, one of whom died during infancy, leaving five surviving sons (S1-S5). The family subsequently expanded through grandchildren and later descendants.

The earlier analysis initially represented **121 individuals** as connected within the extended family structure and then differentiated descendants according to whether the subsequent reproductive pathway proceeded through daughters or sons. A subsequent female-line representation identified **62 women** connected through successive generations, beginning with the focal woman and continuing through her daughters and later female descendants.

Under the revised MCT framework, these data are reinterpreted according to three separate dimensions: **gestational continuity (GC), genealogical continuity (GeC), and maternal genetic continuity (MGC)**.

### 7.2 Identification of the Focal Maternal Ancestor

For modelling purposes, the focal woman in the original study is retained as **F70**, following the notation used in the original analysis. She represents the starting node for the **descending genealogical analysis**.

The first documented reproductive level can be represented as:

with the additional son who died in infancy recognized as part of her reproductive history but not as a source of subsequent descent in the observed genealogy.

This first generation provides the clearest illustration of the distinction among the three MCT domains.

For every child gestated by F70, there is **gestational continuity**, because each pregnancy constituted a direct maternal-fetal relationship. There is also **genealogical continuity**, because every son and daughter remains a descendant of F70. Assuming conventional biological maternity, each child would additionally receive nuclear genetic material and mtDNA from F70.

Thus, at the immediate mother-offspring level:

for both daughters and sons.

The distinction emerges only when transmission is examined in subsequent generations.

### 7.3 First Maternal Branching: Daughters and Sons

The original theory placed particular emphasis on the five daughters because they were capable of creating subsequent gestational maternal links. This insight remains relevant, but its interpretation must be separated from genealogical relatedness.

Consider a daughter:

where represents a child subsequently gestated by D1.

Two serial gestational relationships now exist:

and

These constitute a two-link **Serial Maternal Pathway**.

If is a daughter who subsequently reproduces:

the pathway can extend into further generations.

The situation differs for a son:

F70 gestated S1, but S1 does not gestate. The child's gestational relationship is instead with another individual. Therefore, the **serial gestational pathway originating through F70's reproductive relationship does not continue through S1 in the same form**.

However:

remains a valid **genealogical pathway**.

This distinction corrects the original interpretation in which descendants through F70's sons were described as no longer connected to F70 because those children were born from other women. Under MCT, they remain genealogical descendants and may retain autosomal genetic material inherited ultimately from F70. What normally does not continue through the son is F70's mtDNA transmission pathway.

### 7.4 Reconstruction of the Female-Line Pathway

The original analysis reported that F70's five daughters subsequently produced **18 daughters**, followed by a later generation containing **35 female descendants**, with two of those women subsequently producing four additional daughters.

Using the figures exactly as reported in the source, the female-line structure can be summarized conceptually as:

The reported female total is:

However, the original text separately states that **62 women** were represented in the female-line figure. This numerical inconsistency is important and should **not be silently corrected** in the revised manuscript. The original pedigree/figure and underlying family records should be rechecked before publication to establish whether the focal F70 woman was excluded from the reported total of 62, whether one descendant was counted differently, or whether the narrative contains a numerical error.

For the present theoretical analysis, therefore, the reported **62-person female-line structure is retained as the original study's figure**, while the precise generational count is treated as requiring source verification.

### 7.5 Gestational Continuity within the Family

The Bangladesh example illustrates the Serial Maternal-Link Principle particularly clearly.

Suppose one pathway in the family follows:

This does not represent one continuous physiological connection. Instead:

Each represents a separate pregnancy involving a distinct placenta, umbilical system, and maternal-fetal interface.

Therefore:

The family example consequently illustrates the central MCT proposition that **maternal continuity is produced through serial recurrence rather than persistence of a single physical connection**.

### 7.6 Genealogical Continuity within the Family

The genealogical model produces a substantially larger network than the strict female-line gestational or mitochondrial pathway.

All daughters and sons of F70 are genealogical descendants. Their children are also genealogical descendants, regardless of whether descent proceeds through a male or female intermediate.

Thus:

and

are both genealogically valid.

This is particularly important because the original family diagram reportedly contained **121 connected individuals** before the earlier analysis separated the male-mediated branches from the focal maternal pathway.

Under MCT, those branches should no longer be deleted from the genealogy. Instead, they should be retained and **coded according to the type of continuity they represent**.

This produces two overlapping structures:

**Total genealogical network**

versus:

**Serial maternal/female-line network**

The second is therefore a subset of the first:

where **MCP** represents the Maternal Continuity Pathway and **GeN** represents the complete genealogical network.

### 7.7 Predicted Maternal Genetic Pattern

The original family example did not include molecular testing. Consequently, **no claim can presently be made that the reported descendants were genetically tested for mtDNA concordance**. This limitation must be explicit in a medical-journal version.

Nevertheless, MCT generates a testable prediction.

If the documented female-line pedigree is correct and conventional biological maternity applies throughout the relevant pathway, individuals connected through uninterrupted female-line descent should demonstrate mitochondrial relationships compatible with their common maternal lineage.

For example:

predicts:

subject to expected mutation, heteroplasmy, and mitochondrial bottleneck effects [1-3].

By contrast:

predicts that S2 inherits F70's mtDNA but normally does not transmit that mitochondrial genome to his child [1-3,15].

Thus, the existing family genealogy produces an empirically testable molecular prediction without claiming that such testing has already occurred.

### 7.8 An MCT Evidence Matrix for the Bangladesh Family

The case can therefore be reconstructed using the evidence architecture developed in Section 6.

| Relationship | Gestational continuity | Genealogical continuity | Predicted F70 mtDNA transmission | Current evidentiary status |
|---|---|---|---|---|
| F70 → | Yes | Yes | Yes | Genealogy |

| Relationship | Gestational continuity | Genealogical continuity | Predicted F70 mtDNA transmission | Current evidentiary status |
|---|---|---|---|---|
| daughter | | | | reported; molecular testing not reported |
| F70 → son | Yes | Yes | Yes, to son | Genealogy reported; molecular testing not reported |
| Daughter → her daughter | Yes | Yes | Expected | Genealogy reported for female-line descendants |
| Daughter → her son | Yes | Yes | Expected to son | Transmission normally stops through him |
| Son → his child | No serial gestational continuation through son | Yes | F70 mtDNA normally not transmitted | Genealogical branch remains |
| Female-line descendant → next female generation | Yes | Yes | Expected | Principal testable MCT pathway |

The table demonstrates why the revised theory should not classify people simply as “connected” or “disconnected.” The scientifically appropriate question is:

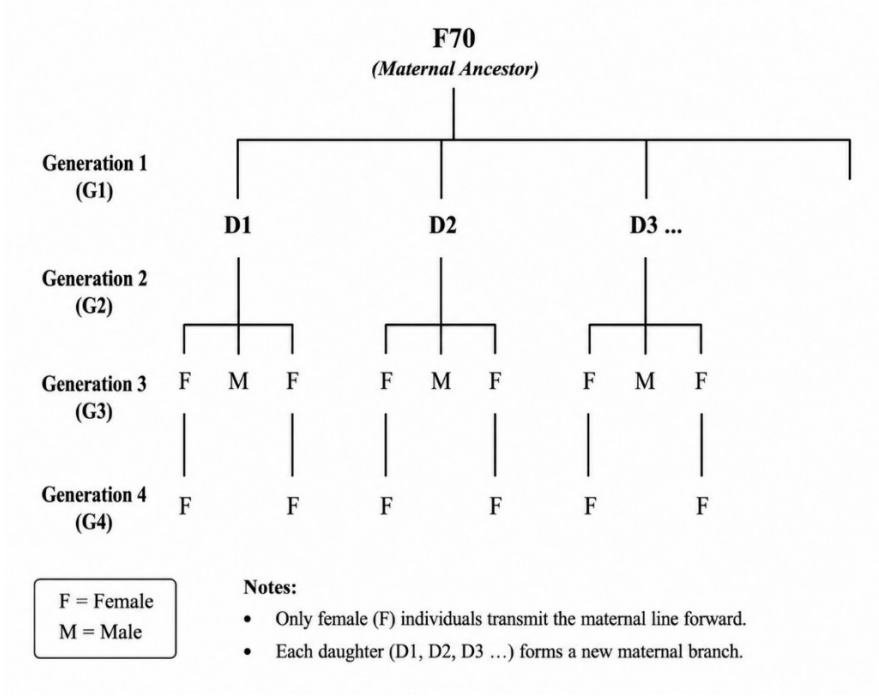
**Connected through which biological or genealogical pathway?**

This is one of the major conceptual advances from the original model.

## 7.9 Branching of the Maternal Network

The Bangladesh case also demonstrates that maternal continuity is not necessarily a single linear chain. Once a woman has more than one daughter who subsequently reproduces, the pathway branches.

For example:




Each female descendant capable of subsequent reproduction can create another serial maternal link. The appropriate structure is therefore better conceptualized as a **branching maternal network** than as one uninterrupted vertical line.

This modifies the creeping-tree analogy used in the original paper, where female descendants were described as remaining connected to a common root. The network model is more compatible with genealogy and genetics

because it permits branching, lineage extinction, and differential transmission without implying continuing physical attachment.

### 7.10 Line Persistence and Line Extinction

The family also illustrates another important feature of maternal-line dynamics: not every female lineage necessarily continues indefinitely.

A woman may have no children, may have only sons, or her daughters may not reproduce. In these circumstances, the particular uninterrupted female-line pathway terminates.

This phenomenon was partially recognized in the original study. For example, the paper described the mother of the approximately 86-year-old man as having only one son and concluded that she could not establish a subsequent female birth line because she had no daughters.

The revised interpretation is more precise:

**Her genealogical lineage did not terminate** if her son had descendants.

**Her nuclear genetic contribution may persist** among later descendants.

However, **her direct mtDNA transmission pathway normally terminated with her son**, because he would not ordinarily transmit her mtDNA to his offspring.

Thus, MCT distinguishes:

This distinction is also fundamental to understanding why a mitochondrial most recent common ancestor should never be interpreted as the only female ancestor of contemporary humans.

### 7.11 Ascending Analysis from a Contemporary Descendant

The same Bangladesh genealogy can be analysed in the opposite direction.

Suppose a contemporary female descendant is designated $\mathbf{P_0}$. Her maternal ancestry could be reconstructed as:

If documentary evidence verifies each maternal relationship, the pathway provides genealogical support for continuity between $P_0$ and F70.

If mtDNA were then collected from appropriate consenting descendants from different surviving female branches, molecular analysis could examine whether their mitochondrial sequences are compatible with the proposed pedigree.

This produces a triangulation model:

Such an empirical study would provide a considerably stronger test of MCT than anatomical observation alone.

### 7.12 What the Bangladesh Example Demonstrates

The Bangladesh family example provides illustrative support for several MCT propositions.

It demonstrates **P2 (Serial Maternal-Link Principle)** because multiple generations of mother-offspring relationships can be represented sequentially.

It illustrates **P3 (Genealogical Reconstruction Principle)** because a multigenerational family structure can be reconstructed where family information is available.

It provides a framework for testing **P4 (Maternal Genetic Transmission Principle)**, although the original study did not collect mtDNA evidence.

It strongly illustrates **P5 (Domain Independence Principle)** because descendants through sons remain genealogically related even when the focal mtDNA pathway does not continue through them.

It also illustrates **P7 (Transmission-Relatedness Distinction)** because termination of a female-line mitochondrial pathway is not equivalent to termination of biological ancestry.

### 7.13 What the Bangladesh Example Does Not Demonstrate

Equally important are the conclusions that cannot be drawn from this case.

The family does **not** establish that all humans descend genealogically from one identifiable woman.

It does **not** provide molecular confirmation of the maternal relationships because mtDNA testing was not reported in the original study.

It does **not** demonstrate the identity of a mitochondrial most recent common ancestor.

It does **not** establish a prehistoric “first human mother.”

It does **not** represent the demographic or reproductive structure of Bangladesh as a whole.

Finally, it does not establish that maternal ancestry is more biologically important than paternal ancestry.

> The case instead demonstrates something narrower but empirically useful: ***how repeated maternal relationships can generate a branching intergenerational structure and how gestational, genealogical, and predicted mitochondrial pathways can be distinguished within that structure.***

### 7.14 Revised Interpretation of the Original Family Model

The principal difference between the original and revised interpretations can therefore be summarized as follows:

| Original interpretation | Revised MCT interpretation |
|---|---|
| Navel demonstrates connection to mother | Umbilicus indicates prior fetal-placental/umbilical development |
| Female descendants remain | Female-line descendants can form serial |

| Original interpretation | Revised MCT interpretation |
|---|---|
| connected to focal woman | gestational and mtDNA pathways |
| Male-mediated lines become disconnected | Male-mediated descendants remain genealogically and genetically related |
| Daughter line represents continuing birth line | Daughter line may continue serial gestational and maternal mtDNA transmission |
| Family model supports universal maternal connection | Family model illustrates how MCT operates locally |
| Maternal pathway can be extended toward a first woman | Extension beyond records requires population-genetic inference |
| Visual connection establishes continuity | Independent evidence should be triangulated |

This reinterpretation does not abandon the central insight of the original Bangladesh family analysis. Instead, it transforms that insight into a model compatible with contemporary reproductive biology and genetics.

### 7.15 Implications for Empirical Testing

The Bangladesh family provides a practical foundation for a future empirical test of MCT. A follow-up study could reconstruct the pedigree using independently verified civil and birth records, identify surviving female-line branches, collect reproductive histories, and-with informed consent and appropriate ethical approval-conduct mtDNA sequencing among selected descendants.

The central empirical prediction would be:

> ***Documented descendants connected to F70 through uninterrupted biological female-line descent should exhibit mitochondrial genetic relationships compatible with the reconstructed maternal pedigree, whereas descendants***

***connected exclusively through intervening male lines should not be expected to carry F70's transmitted mtDNA lineage.***

If molecular findings systematically contradicted a well-documented female-line pedigree after technical error and known mitochondrial complexities were excluded, the relevant MCT propositions would require modification. Conversely, concordance between documentary genealogy and molecular evidence would support the **Maternal Continuity Convergence Principle**, although it would still not prove universal or prehistoric maternal ancestry.

Accordingly, the Bangladesh example functions as a bridge between the **original theoretical observation and a future testable biomedical research programme**. Its value lies not in proving the universal origin of humanity from one family structure, but in demonstrating how maternal continuity can be operationalized, reconstructed, differentiated, and eventually tested through independent genealogical and molecular evidence.

## 8. Relationship with Evolutionary and Population-Genetic Evidence

Maternal Continuity Theory (MCT) is intended to complement, rather than replace, contemporary evolutionary biology and population genetics. Its central proposition-that repeated mother-offspring relationships create serial maternal pathways-operates at a different explanatory level from theories describing species evolution, population divergence, migration, admixture, natural selection, and genomic change. This distinction is essential because the original formulation sought to extend contemporary maternal relationships toward the earliest human female lineage. The revised MCT evaluates that proposition against evolutionary and population-genetic evidence while explicitly distinguishing what is directly observable from what can only be inferred.

### 8.1 MCT within the Evolutionary Framework

Evolutionary theory explains biological change through processes operating across populations and generations, including mutation, natural selection, genetic drift, recombination, gene flow, and demographic

change. Human evolution therefore cannot be reduced to a sequence of individual mother-offspring relationships. The evolutionary history of *Homo sapiens* involves population structure, divergence, migration, admixture, and interaction with other hominin groups [7-10].

MCT addresses a narrower question. Evolution requires reproduction across successive generations, and every gestational reproductive event establishes a developmental relationship between a gestational parent and offspring. MCT conceptualizes the recurrence of these relationships as one identifiable component of intergenerational biological continuity.

The relationship can therefore be expressed as:

MCT is consequently **nested within the broader evolutionary process**. It does not provide an alternative mechanism for speciation or population evolution.

This positioning substantially modifies the relationship between the theory and Darwinian evolution presented in the original paper, where questions were raised about whether conventional evolutionary explanations adequately incorporated physiology, reproduction, life cycles, psychology, and other dimensions of human existence. The revised framework does not treat these considerations as evidence against evolution. Instead, it proposes that evolutionary theory and MCT address different levels of biological explanation.

### 8.2 Human Origins as a Population Process

Contemporary evidence does not support a model in which modern humanity appeared instantaneously from a single reproductively isolated couple. Instead, *Homo sapiens* emerged through evolutionary processes operating within populations. Fossil, archaeological, genomic, and palaeogenomic evidence supports an African origin of modern humans while increasingly indicating substantial population structure and interaction rather than a single geographically isolated ancestral population [7-10].

This distinction has direct implications for MCT. The theory can propose that every individual occupies a maternal genealogical pathway without

requiring all maternal pathways to converge recently on a single woman who was the first biological member of the species.

Species boundaries themselves emerge over evolutionary time rather than necessarily appearing at one discrete reproductive event. Consequently, asking for the biological identity of the exact "first *Homo sapiens* woman" may impose a categorical boundary on what was, biologically, a gradual population-level evolutionary process.

MCT therefore distinguishes:

An individual's gestational origin can be directly identified. A recent maternal lineage may be genealogically reconstructed. A deep maternal lineage may be genetically inferred. Species origins, however, require population-level evolutionary evidence.

### 8.3 Population Structure and Human Ancestry

Population genetics further demonstrates that human ancestry is not adequately represented by a single bifurcating family tree. Populations can divide and later exchange genetic material, creating reticulate patterns of ancestry. Ancient DNA has provided particularly important evidence of admixture between modern humans and archaic hominins, including Neanderthals and Denisovans [8,9].

These findings do not contradict maternal continuity. Rather, they demonstrate that maternal pathways exist within a much larger network of ancestry.

Conceptually:

MCT isolates one path through this network:

but each individual within that sequence simultaneously possesses paternal and additional genealogical ancestry. $M_2$, for example, herself had two biological parents, four genealogical grandparents, and a much larger network of more distant ancestors.

The maternal pathway should therefore be interpreted as an **analytical lineage embedded within a reticulated ancestry network**, not as the complete ancestry of the individual.

### 8.4 Genealogical Ancestry versus Genetic Ancestry

A particularly important contribution of population genetics to MCT is the distinction between **genealogical ancestry and genetic ancestry**.

Genealogically, every individual has ancestors through both maternal and paternal branches. The number of ancestral positions increases rapidly backward through generations:

where represents generations under a simplified pedigree model without pedigree collapse.

However, this mathematical expansion does not imply that all ancestral positions correspond to different people. In finite populations, the same ancestors appear through multiple genealogical routes-a phenomenon known as **pedigree collapse**.

Moreover, not every genealogical ancestor necessarily contributes identifiable autosomal DNA to a particular living descendant. Recombination causes inherited chromosomal segments to be reshuffled and progressively diluted across generations. Consequently:

for sufficiently remote ancestry.

This distinction supports the conceptual architecture of MCT. Genealogical maternal continuity can remain valid even when a particular distant ancestor's autosomal DNA is no longer identifiable in a contemporary descendant.

### 8.5 Mitochondrial DNA as a Maternal-Line Marker

Mitochondrial DNA provides a fundamentally different form of ancestry information. Because human mtDNA is transmitted overwhelmingly through the maternal line, it permits reconstruction of a particular maternal genetic pathway [1-3,15].

For an uninterrupted female-line sequence:

the corresponding mitochondrial pathway can be represented as:

subject to mutation, heteroplasmy, bottleneck effects, drift, and selection [1-3].

This provides molecular support for one of the central intuitions underlying the original theory. The original article itself referred to mtDNA as a means of tracing maternal ancestry and discussed the proposition that contemporary humans can be connected through maternal genetic ancestry.

However, mtDNA represents only a very small component of the human genome. It therefore cannot reconstruct an individual's complete ancestry.

This distinction can be expressed as:

MCT treats mtDNA as a **lineage-specific molecular tracer**, not as evidence that human inheritance is exclusively maternal.

### 8.6 Mitochondrial Coalescence and “Mitochondrial Eve”

When the mtDNA sequences of contemporary humans are analysed retrospectively using population-genetic methods, surviving mitochondrial lineages eventually coalesce toward a most recent common maternal ancestor. This individual is conventionally described as **mitochondrial Eve** [5,6].

The concept is highly relevant to MCT because it demonstrates that contemporary maternal genetic lineages can be analysed backward toward common ancestry. Nevertheless, its interpretation requires considerable caution.

Mitochondrial Eve was not necessarily:

- the first woman;
- the first anatomically modern human woman;
- the only woman alive during her lifetime;
- the only female ancestor of contemporary humanity; or
- the woman from whom all contemporary nuclear DNA originated.

Instead, she represents the most recent woman through whom the **uninterrupted maternal mtDNA lineages surviving in living humans coalesce**.

Other women living at the same time could have numerous living descendants today through sons, or through female lines that subsequently

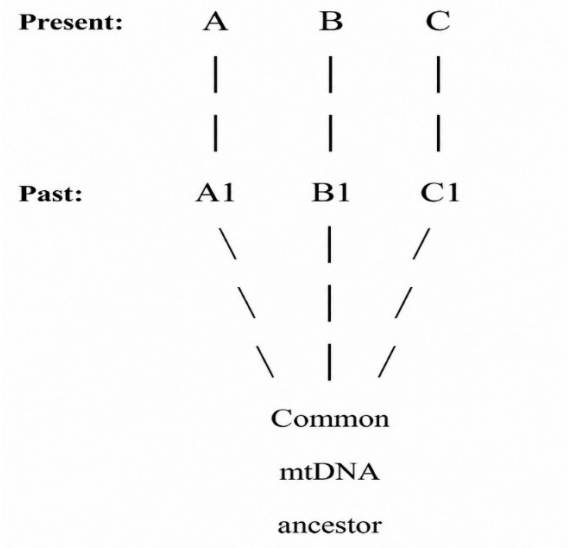
became extinct in the strict mtDNA sense. They may therefore contribute substantially to contemporary nuclear genomes despite not being ancestors along surviving direct mitochondrial lines.

This observation provides population-genetic support for MCT Proposition 7:

### 8.7 Lineage Coalescence versus the First Maternal Ancestor

The distinction between **coalescence** and **origin** represents perhaps the most important modification of the original theory.

Suppose three contemporary maternal lineages are represented as:




The common node represents the point at which surviving mitochondrial lineages converge when traced backward. It does not necessarily represent the origin of the population or species.

The original theoretical model hypothesized increasingly early female nodes and ultimately considered the possibility of reaching a first female lineage. Population genetics supports the **backward-tracing logic**, but it does not support equating the resulting coalescence point with the first biological woman.

The revised theory therefore replaces:

with:

This is a scientifically stronger and empirically testable formulation.

### 8.8 Why Maternal Lineages Disappear

Population genetics also explains how maternal-line diversity decreases over long periods. A woman's direct mtDNA lineage will continue only if transmission proceeds through reproducing female descendants.

Consider:

The maternal molecular lineage can continue.

By contrast:

normally represents the final generation carrying $F_0$'s mtDNA through that particular descendant.

Similarly:

followed by no offspring from $D_1$ also terminates that transmission branch.

Across thousands of generations, reproductive variation, demographic events, migration, population bottlenecks, drift, and lineage extinction progressively alter the number and distribution of surviving mitochondrial lineages.

This mechanism provides a population-level counterpart to the phenomenon illustrated by the Bangladesh family example in Section 7. The original paper observed that a woman with only a son could not continue a female birth line. The revised interpretation is that her **direct mtDNA transmission lineage** would normally terminate through that son, while her genealogical and nuclear-genetic legacy could continue.

### 8.9 Maternal Continuity and Ancient DNA

Ancient DNA provides an additional evidentiary bridge between recent genealogy and deep population history. Whereas family records may document several generations, ancient genomic material permits direct

genetic investigation of individuals who lived hundreds, thousands, or tens of thousands of years ago.

Ancient DNA has demonstrated that human evolutionary history included substantial population movement and admixture [8,9]. For MCT, ancient mtDNA can potentially identify maternal haplogroups of historical individuals and establish their relationship to broader maternal population lineages.

However, ancient DNA generally cannot reconstruct every mother-daughter relationship linking a prehistoric individual to contemporary descendants. Sampling is incomplete, preservation is uneven, and most historical individuals have never yielded recoverable genetic material.

Ancient DNA therefore occupies an intermediate epistemological position:

It extends the empirical reach of maternal-line research without eliminating the inferential gaps between individual generations.

## 8.10 Population Structure and the Interpretation of Common Ancestry

Coalescent estimates are also influenced by demographic history and population structure. Population subdivision, migration, changes in effective population size, and admixture can affect estimates of ancestral relationships. Contemporary research has emphasized that inadequate modelling of population structure can generate misleading interpretations of ancient population interactions [10].

MCT therefore treats deep maternal ancestry probabilistically rather than deterministically.

At recent temporal levels:

may be established with high confidence.

At deep temporal levels, conclusions instead take the form:

within a model-dependent temporal interval.

The type of scientific statement must therefore change with evidentiary depth.

### 8.11 Compatibility with Natural Selection and Genetic Drift

MCT is also compatible with natural selection and genetic drift. Maternal lineages are not transmitted independently of evolutionary processes. mtDNA variants can be affected by mutation, selection, drift, heteroplasmy, and demographic bottlenecks [2,3].

Accordingly, maternal continuity does not imply molecular constancy:

in absolute sequence terms across sufficiently large numbers of generations.

Instead:

may indicate phylogenetic continuity despite accumulated variation.

This distinction is medically relevant because pathogenic mitochondrial variants may change in heteroplasmic frequency between generations, contributing to substantial phenotypic variability in mitochondrial disease [2-4].

Thus, continuity within MCT means **descent with modification**, not genetic immutability-placing the framework squarely within evolutionary principles.

### 8.12 Maternal Continuity and Archaic Admixture

The genomic evidence for Neanderthal and Denisovan admixture presents another useful test of MCT [8,9]. Contemporary human nuclear genomes can contain ancestry derived from archaic hominin populations, yet the surviving mtDNA lineages of contemporary humans do not necessarily preserve the same ancestry patterns.

This demonstrates why different genetic systems can produce different pictures of human history.

An individual may simultaneously possess:

***a contemporary maternal mtDNA lineage + paternal ancestry + multiple autosomal ancestral components + archaic genomic contributions.***

There is no contradiction among these components because they describe different pathways through the ancestry network.

MCT therefore should not be interpreted as proposing that maternal mitochondrial ancestry captures the complete evolutionary history of an individual. Instead, it identifies **one biologically coherent pathway embedded within a multidimensional genomic history**.

## 8.13 Evolutionary Interpretation of the Serial Maternal-Link Principle

The Serial Maternal-Link Principle introduced in Section 4 can now be placed explicitly within evolutionary theory.

At the individual level:

represents reproduction.

Across generations:

represents serial reproduction along one maternal pathway.

At the population level, thousands or millions of such pathways coexist, branch, terminate, and occasionally coalesce retrospectively:

MCT therefore scales from individual reproduction toward population ancestry without claiming that one observed family pathway alone explains species history.

This provides the bridge between the Bangladesh genealogical model and population genetics.

## 8.14 An Integrated Evolutionary-MCT Model

The relationship among the relevant explanatory levels can be summarized as follows:

| Analytical level | Primary process | Principal evidence | Contribution to MCT |
|---|---|---|---|
| Individual | Gestation and birth | Clinical/reproductive biology | Establishes direct maternal-fetal relationship |
| Family | Intergenerational descent | Pedigrees, civil records | Reconstructs maternal pathways |
| Molecular lineage | mtDNA transmission | Molecular genetics | Tests maternal-line inheritance |
| Population | Migration, drift, selection, admixture | Population genomics | Places lineages within demographic history |
| Deep ancestry | Coalescence and ancient population relationships | Ancient DNA, phylogenetics | Estimates common maternal ancestry |
| Species | Human evolutionary emergence | Fossils, archaeology, genomics | Provides the broader evolutionary framework |

The model illustrates why no single evidentiary domain can independently answer every question concerning human origins.

### 8.15 Theoretical Convergence with Population Genetics

The relationship between MCT and population genetics can consequently be summarized through three areas of convergence.

First, both recognize **intergenerational transmission**. MCT begins with observable reproductive relationships, while population genetics models the transmission and transformation of genetic variants across populations.

Second, both recognize **branching and extinction of lineages**. The Bangladesh family provides a micro-level illustration; coalescent genetics examines the consequences of such processes over much greater timescales.

Third, both permit **retrospective reconstruction**. MCT's ascending method traces maternal relationships backward from contemporary individuals, while coalescent methods similarly infer ancestral relationships backward from observed genetic variation.

The major difference lies in the unit of evidence. MCT begins with identifiable mother-offspring relationships; population genetics begins principally with patterns of genetic variation across individuals and populations.

## 8.16 Theoretical Boundary between MCT and Evolutionary Evidence

The relationship can therefore be represented as:

Each downward movement represents an increase in explanatory scale but also an increase in inferential complexity.

Consequently, the strongest formulation of MCT is not that contemporary anatomy directly reveals the first human mother. Rather:

> ***Observable maternal-fetal relationships provide the proximal biological foundation of maternal continuity; documented genealogy can extend this relationship across identifiable generations; mitochondrial inheritance provides an independent molecular pathway for investigating deeper female-line descent; and population genetics situates these lineages within the branching, coalescing, and admixed evolutionary history of human populations.***

## 8.17 Implications for Maternal Continuity Theory

Evolutionary and population-genetic evidence therefore both **supports and constrains** MCT.

It supports the theory by demonstrating that reproduction creates genuine intergenerational biological transmission; mtDNA is predominantly maternally inherited [1-3,15]; maternal genetic lineages can be reconstructed; and surviving mitochondrial lineages can be examined through coalescent approaches [5,6].

At the same time, it constrains the theory by demonstrating that total human ancestry is biparental and reticulate, mitochondrial ancestry represents only one component of genetic history, lineage coalescence does not identify the first human female, and the emergence of *Homo sapiens* occurred through population-level evolutionary processes rather than through a maternal pathway that can presently be reconstructed individual by individual.

These constraints do not weaken the central contribution of MCT. Instead, they define its scientifically defensible scope.

The theory can therefore be positioned as a **meso-level interdisciplinary framework** connecting the micro-level biology of pregnancy and birth with the macro-level reconstruction of maternal population ancestry. Its central contribution is the conceptual bridge:

Within this framework, MCT becomes compatible with evolutionary theory rather than a competing explanation of human origins. The theory's distinctive contribution lies in demonstrating how an observable reproductive relationship can be followed conceptually across increasing biological and temporal scales, while maintaining explicit boundaries between **direct observation, genealogical reconstruction, molecular evidence, and evolutionary inference**.

## 9. Comparative and Theological Perspective: The Qur’anic Component

This chapter examines the Qur’anic perspective on human origin, gestation, maternal relationships, reproduction, and intergenerational descent in relation to Maternal Continuity Theory (MCT). The analysis is comparative rather than evidentiary: Qur’anic descriptions are not treated as substitutes for biomedical, genetic, or evolutionary evidence. Instead,

relevant verses are considered as a distinct theological and epistemological perspective that may conceptually intersect with questions addressed by MCT. Particular attention is given to the womb, successive human generation, common ancestry, and maternal experience, while maintaining a clear methodological boundary between scriptural interpretation and empirical scientific inquiry.

### 9.1 Rationale for Including a Theological Perspective

Questions concerning human origins occupy an unusual intellectual space because they have historically been addressed through both empirical investigation and theological reflection. Evolutionary biology, reproductive medicine, genetics, and paleoanthropology investigate human origins through observable or inferential evidence, whereas religious traditions address questions of creation, human identity, purpose, and the relationship between humanity and its Creator. These domains need not be treated as methodologically interchangeable.

The original formulation of the theory included an extensive Qur'anic discussion of human creation and reproductive development. In particular, it considered Qur'anic references to creation from *turāb* (dust/soil), *mā'* (water), *ṭīn* (clay), *nutfah* (a small quantity/drop of reproductive fluid), and subsequent developmental stages. In the revised Maternal Continuity Theory (MCT), this material is retained as a **comparative theological and epistemological perspective**, rather than being presented as biomedical evidence for the propositions developed in Sections 3-8.

This distinction is essential for a medical-journal audience. Scientific propositions within MCT must remain open to evaluation using reproductive, genealogical, genetic, and population-level evidence. Qur'anic passages are therefore not employed as substitutes for clinical or molecular evidence. Instead, they are examined to determine whether the Qur'anic representation of human generation contains conceptual themes that can be compared with the biological framework of intergenerational continuity developed in MCT.

## 9.2 Epistemological Distinction between Revelation and Biomedical Evidence

The methodological relationship between theology and biomedical science requires explicit definition. Biomedical knowledge is established through observation, experimentation, measurement, replication, and evidence-based inference. Qur'anic knowledge, within Islamic theology, derives from revelation and addresses dimensions of existence that extend beyond the methodological boundaries of empirical science.

Accordingly:

and:

The purpose of comparison is therefore not to claim that a Qur'anic verse scientifically validates mtDNA inheritance, placental physiology, evolutionary population genetics, or MCT. Nor is it appropriate to use contemporary biomedical findings as definitive proof of a particular interpretation of a scriptural passage.

Instead, the two domains can be placed in **conceptual dialogue** where they address related phenomena from different epistemological positions.

This approach also avoids retrospective scientific concordism-the practice of reading highly specific modern scientific findings into ancient religious terminology when the text itself does not explicitly make such claims.

## 9.3 Qur'anic Representation of Human Creation

The Qur'an describes human creation through several formulations rather than through one uniform biological description. Among these are creation from dust or soil (Qur'an 3:59; 30:20; 35:11), clay (15:26; 23:12), water (21:30; 25:54), and *nutfah* (16:4; 18:37; 22:5; 23:13; 35:11; 40:67; 53:46; 75:37; 76:2; 80:19).

These references operate at different conceptual levels and should not automatically be interpreted as descriptions of identical biological stages.

Of particular relevance to reproduction is Qur'an 22:5, which presents a sequence involving *turāb*, *nutfah*, *ʿalaqah*, *muḍghah*, gestation, birth, maturation, and death. Qur'an 23:12-14 similarly describes a

developmental sequence involving *nutfah*, *ʿalaqah*, and *muḍghah*. These passages formed part of the reproductive discussion in the original theory.

For the purposes of MCT, their principal relevance is not that they provide a technical account of modern embryology. Rather, they portray human existence as involving **successive processes of generation and development**, including an intrauterine phase before birth.

This process-oriented representation provides the first conceptual point of comparison with MCT.

### 9.4 Reproduction through Male and Female Contribution

A scientifically important feature of the revised MCT is its explicit recognition that maternal continuity does not eliminate paternal biological contribution. The Qur'anic material can likewise be interpreted without constructing reproduction as an exclusively female biological process.

Qur'an 53:45-46 states that male and female are created from *nutfah* when emitted, while Qur'an 75:37-39 connects reproductive fluid with subsequent formation and differentiation into male and female. Qur'an 76:2 refers to human creation from *nutfatin amshāj*, conventionally understood in terms of a mixed reproductive substance.

These passages are relevant because they prevent the theological component of MCT from being interpreted as a doctrine of exclusively maternal biological origin.

The conceptual relationship is therefore:

This formulation is consistent with the distinction established in Sections 3-8: nuclear genetic ancestry is biparental, whereas gestation establishes a biologically asymmetric maternal-fetal relationship.

The theological perspective therefore does not require denial or minimization of paternal ancestry in order to recognize the distinctive role of maternal gestation.

### 9.5 The Womb as a Site of Human Development

The Qur'anic concept most directly relevant to gestational continuity is **raḥim** (womb), with its plural form *arḥām*. Several passages explicitly locate human formation within the womb.

Qur'an 3:6 states that God shapes human beings in the wombs as He wills. Qur'an 39:6 refers to creation within the wombs through successive stages, while Qur'an 22:5 describes what is established in the womb until an appointed term before birth.

These passages provide a theological representation in which prenatal human development occurs within a maternal reproductive environment.

MCT approaches the same broad phenomenon from reproductive biology. Implantation, placentation, fetal development, maternal physiological adaptation, fetoplacental circulation, and immune regulation establish the biological basis of the gestational relationship [11-14].

The two descriptions should nevertheless remain epistemologically differentiated:

**Qur'anic perspective:** the womb as a divinely governed site of human formation.

**Biomedical perspective:** the intrauterine environment as a physiological system within which embryonic and fetal development occurs.

**MCT perspective:** gestation as the first directly identifiable level of embodied maternal continuity.

Thus, there is conceptual correspondence around **intrauterine development**, without requiring the Qur'anic text to function as a biomedical textbook.

### 9.6 Maternal Gestation, Birth, and Dependency

The Qur'an also explicitly recognizes pregnancy as a demanding embodied maternal process. Qur'an 31:14 describes the mother as carrying the child through successive weakness, while Qur'an 46:15 refers to the mother carrying and delivering the child with hardship.

These passages are particularly relevant to the **embodied** component of MCT because they focus on the physical experience of pregnancy and birth rather than simply identifying a genealogical mother.

Qur'an 46:15 states, in conceptual sequence:

MCT similarly begins at the embodied level but describes it biologically:

The correspondence is therefore primarily structural rather than technical. Both frameworks recognize gestation as a process preceding independent postnatal existence, while only the biomedical framework specifies the physiological mechanisms involved.

### 9.7 The Qur'anic Concept of *Arḥām* and Genealogical Relatedness

A particularly significant conceptual relationship exists between **raḥim/arḥām** and kinship.

In Qur'anic usage, *arḥām* can refer not merely to anatomical wombs but also to relationships of kinship. Qur'an 4:1 places the concept within a passage describing humanity, reproduction, men and women, and relationships of kinship. Qur'an 8:75 and 33:6 likewise use *ulū al-arḥām* in relation to relatives or those connected through kinship.

This semantic relationship between womb and kinship is highly relevant to MCT because the theory similarly moves from:

However, the comparison must be made carefully. Qur'anic kinship is not reducible to mitochondrial descent, nor does *arḥām* mean mtDNA. The theological concept encompasses familial relatedness at a level broader than a specific molecular inheritance system.

Nevertheless, the association provides an important comparative insight: **embodied reproduction and intergenerational relatedness are conceptually linked within Qur'anic discourse**.

This parallels MCT's attempt to distinguish yet connect gestational and genealogical continuity.

### 9.8 Humanity from a Common Origin: Interpreting Qur'an 4:1

Qur'an 4:1 is especially relevant to any theological discussion of human common origin. The verse refers to humanity being created from *nafs wāḥidah* ("a single self/soul/person"), from which its *zawj* (mate/pair) was created, and from the two of them many men and women were spread.

For MCT, this verse requires particular caution.

A medical or population-genetic paper should **not** present *nafs wāḥidah* as empirical proof that the entire contemporary human population descends genetically from one historical female individual. The Qur'anic statement is theological, while the genetic structure of ancestral human populations is investigated through a different evidentiary system.

Moreover, the wording *nafs wāḥidah* should not simply be translated into "first woman" for the purpose of supporting MCT. Such an interpretation would require separate linguistic and exegetical argument.

The appropriate conclusion is narrower: Qur'an 4:1 expresses a theological conception of **shared human origin and subsequent reproductive multiplication**.

Conceptually:

Population genetics, by contrast, investigates common ancestry through populations, genomic inheritance, coalescence, and demographic modelling.

The two should not be collapsed.

### 9.9 Maternal Continuity and Qur'anic Genealogy

The Qur'an also demonstrates repeated concern with genealogy, parentage, offspring, descendants, and generations. Terms associated with parents (*wālidayn*), mothers (*ummahāt*), fathers (*ābāʾ*), offspring (*dhurriyyah*), and kinship appear in numerous contexts.

This is important for MCT because the Qur'anic representation of human relationships is **not exclusively matrilineal**. Both maternal and paternal genealogical relationships are recognized.

Consequently, the Qur’anic component supports an important boundary already established in the scientific model:

rather than:

MCT therefore isolates the maternal pathway analytically without claiming that the Qur'an presents all human descent as exclusively maternal.

### 9.10 A Qur’anic Reading of Serial Maternal Continuity

The Serial Maternal-Link Principle can nevertheless be considered from a Qur’anic conceptual perspective.

Every woman who gives birth was herself born through an earlier reproductive process. Where a daughter subsequently becomes a mother, another maternal gestational relationship occurs.

MCT represents this as:

The Qur’an does not present this mathematical model, and it would be inappropriate to attribute the formal theory itself to the scripture. However, Qur’anic references to pregnancy, wombs, offspring, generations, and kinship provide a theological conceptual environment within which intergenerational reproduction is repeatedly recognized.

The relationship is therefore one of **conceptual compatibility**, not textual derivation:

rather than:

This distinction substantially strengthens the interdisciplinary credibility of the theory.

### 9.11 Qur’anic Perspective and Mitochondrial Inheritance

No Qur’anic passage explicitly describes mitochondrial DNA, mitochondrial genomes, heteroplasmy, mitochondrial bottlenecks, or maternal molecular inheritance. Therefore, MCT should not attempt to claim direct Qur’anic prediction of mtDNA.

The relationship can only be formulated at different levels:

**Qur'anic level:** recognition of reproduction, maternal gestation, wombs, generations, and kinship.

**Molecular level:** predominantly maternal transmission of human mtDNA [1-3,15].

**MCT level:** integration of maternal genetic inheritance as one independently measurable dimension of maternal continuity.

This separation is methodologically important because mtDNA is an empirical discovery of modern molecular biology. Its inclusion in MCT derives from genetic evidence, not from theological interpretation.

### 9.12 Qur'anic Perspective and Mitochondrial Eve

An even stronger distinction is required between Qur'anic accounts of common human origin and the population-genetic concept of mitochondrial Eve.

As established in Section 8:

Mitochondrial Eve represents the most recent woman through whom surviving contemporary human mtDNA lineages coalesce [5,6]. She was not necessarily the only woman alive at that time, and population genetics does not identify her as a theological figure.

Therefore:

MCT should not attempt to establish an identity between these concepts.

This distinction is especially important for a medical journal because conflating theological anthropology with mitochondrial coalescence would undermine the scientific credibility of the paper.

### 9.13 Comparative Epistemological Model

The relationship among the three major knowledge domains considered in this study can be represented as follows:

| Domain | Central question | Principal evidence | Relevance to MCT |
|---|---|---|---|
| **Reproductive medicine** | How does a | Clinical, | Embodied/ |

| Domain | Central question | Principal evidence | Relevance to MCT |
|---|---|---|---|
| | human develop during gestation? | physiological, anatomical | gestational continuity |
| **Genetics and genealogy** | How are biological relationships transmitted and reconstructed ? | DNA, mtDNA, pedigrees, records | Genetic and genealogical continuity |
| **Evolutionary/ population science** | How did human populations emerge and change? | Genomics, ancient DNA, fossils, models | Deep-time ancestry and boundaries |
| **Qur'anic theology** | What is the theological meaning and framework of human creation, reproduction, and kinship? | Revelation/ textual analysis | Comparative theological interpretation |

The domains overlap in subject matter but not necessarily in method.

This can be represented as:

The central arrow denotes interdisciplinary dialogue, not evidentiary equivalence.

### 9.14 Areas of Conceptual Convergence and Distinction

The comparison identifies several areas of conceptual convergence.

Both perspectives recognize that human beings emerge through reproductive processes; intrauterine development occupies a distinctive stage of human existence; pregnancy establishes a maternal embodied relationship; birth marks transition from prenatal dependence to postnatal existence; reproduction generates successive generations; and human beings exist within networks of genealogy and kinship.

However, several distinctions are equally important. Biomedical science explains mechanisms through empirically testable evidence, whereas the Qur’anic account embeds reproduction within a theological framework of creation and purpose. Population genetics models ancestry probabilistically, whereas scripture addresses common human origin within a theological discourse. mtDNA inheritance is a molecular phenomenon not explicitly described in the Qur'an.

Consequently:

This principle governs the theological component of MCT.

### 9.15 Theological Implications for Maternal Continuity Theory

The Qur’anic perspective adds a dimension to MCT that cannot be supplied by molecular biology alone: it situates reproduction within a broader conception of human relatedness, continuity, and shared origin.

At the same time, the revised framework deliberately limits the theological claim. The Qur'an is not used to prove the Serial Maternal-Link Principle, mtDNA inheritance, mitochondrial coalescence, or the biological identity of a first human female. Those propositions must be evaluated through their appropriate empirical methods.

The comparative theological contribution is therefore better summarized as follows:

> ***The Qur’anic representation of human generation emphasizes reproductive development within the womb, maternal embodied experience, intergenerational reproduction, kinship, and shared human origin. These themes are conceptually relevant to Maternal Continuity Theory, particularly its gestational and genealogical dimensions, but they constitute a theological***

***framework rather than independent biomedical evidence for its genetic or evolutionary propositions.***

### 9.16 Position of the Qur'anic Component within MCT

The complete relationship can therefore be represented as:

This arrangement preserves the distinctive theological contribution of the original article while establishing an essential boundary between **revelatory interpretation and empirical validation**.

For a medical-journal audience, this positioning is particularly important. It allows the Qur'anic component to contribute to the interdisciplinary character and intellectual origins of MCT without requiring theological propositions to function as scientific evidence. Conversely, biomedical findings are not presented as definitive validation of scriptural meaning.

In this revised form, the Qur'anic component therefore becomes a **comparative epistemological extension of Maternal Continuity Theory**: one that recognizes meaningful conceptual correspondences concerning gestation, generation, kinship, and human commonality while maintaining methodological independence between theology and biomedical science.

## 10. Discussion

The present study reformulates Maternal Continuity Theory (MCT) as an interdisciplinary framework for examining one specific dimension of human intergenerational continuity through **gestational, genealogical, and maternal genetic pathways**. The principal contribution of the revised theory is not the observation that humans undergo gestation, that family relationships can be reconstructed, or that mitochondrial DNA (mtDNA) is predominantly maternally inherited; these are independently established phenomena [1-3,11-15]. Rather, MCT proposes that these phenomena can be organized into a multilevel explanatory framework while maintaining clear distinctions between their biological mechanisms, evidentiary bases, and inferential limits. This reconstruction is important because the original formulation moved comparatively directly from the universal observation of the umbilical relationship to increasingly remote maternal ancestry. The

revised theory preserves that original insight while subjecting each inferential transition to separate biological, genealogical, and population-genetic evaluation.

## 10.1 From Anatomical Observation to Embodied Maternal Continuity

The most immediate proposition of MCT concerns gestational continuity. The original theory identified the navel as a universal anatomical feature linking an individual conceptually to the mother from whom separation occurred at birth. This observation remains theoretically useful, but its scientific meaning requires qualification. The umbilicus cannot identify a mother, reconstruct genealogy, or demonstrate deep ancestry. Its significance lies instead in being an anatomical consequence of the prenatal umbilical connection within the fetal-placental system.

Contemporary reproductive biology provides a substantially richer basis for this proposition than anatomy alone. Pregnancy involves dynamic interactions among maternal tissues, fetal-derived placental structures, vascular systems, endocrine pathways, and immune mechanisms [11-14]. The fetus is therefore not simply physically “attached” to the pregnant individual; development occurs through a highly regulated maternal-fetal interface. MCT consequently replaces the narrower concept of **navel connection** with **embodied gestational continuity**.

This reformulation strengthens the theory in two ways. First, it grounds the initial maternal relationship in established reproductive physiology. Second, it avoids attributing to the umbilicus evidentiary properties that it does not possess. The observable anatomy establishes a proximal developmental history; subsequent ancestral claims require independent evidence.

## 10.2 Serial Maternal Continuity as the Principal Theoretical Contribution

The distinctive theoretical proposition of MCT is the **Serial Maternal-Link Principle**. Individual pregnancies are normally studied as discrete reproductive events. MCT instead asks what becomes visible when these events are arranged intergenerationally.

If:

represent three separate gestational relationships, they can simultaneously be represented genealogically as:

The continuity resides not in persistence of the same placenta, umbilical cord, or physiological connection but in the **serial recurrence of the mother-offspring relationship**.

This distinction addresses a potential conceptual objection. Biological continuity need not require physical continuity of one structure. Reproduction itself is inherently discontinuous at the organismal level: individuals are born, reproduce, and die, while genetic and genealogical relationships persist across generations. MCT proposes that gestational relationships can similarly be conceptualized as recurrent units forming an intergenerational pathway.

The original article anticipated this idea by representing successive women as connected through maternal birth lines. The revised formulation, however, avoids describing later descendants as remaining physically connected to an earlier woman. They are instead related through a **sequence of independently occurring biological relationships**.

### 10.3 Distinguishing Maternal Continuity from Maternal Exclusivity

A major conceptual risk for any theory centred on maternal descent is that it may be interpreted as minimizing paternal contribution. MCT explicitly rejects such an interpretation.

Most human nuclear genetic inheritance is biparental. Each generation therefore incorporates maternal and paternal ancestry, and recombination produces increasingly complex genomic combinations. Maternal genealogy is consequently one pathway within a much larger ancestry network.

This can be expressed as:

where **MCP** represents a maternal continuity pathway and **TGA** represents total genealogical ancestry.

The theoretical significance of maternal continuity therefore arises not from exclusivity but from **reproductive asymmetry**. Under conventional reproduction, both biological parents contribute nuclear genetic material, whereas only one individual undergoes pregnancy. Likewise, mtDNA is overwhelmingly maternally transmitted [1-3,15]. These biological asymmetries make a specifically maternal pathway analytically identifiable without implying that paternal ancestry is biologically less important.

This distinction also represents an important revision of the original model. The earlier analysis described some male-mediated branches as becoming disconnected from the focal woman because subsequent children were born from other women. The revised framework demonstrates that this is true only for particular forms of transmission, not for ancestry generally.

### 10.4 The Importance of Separating Transmission from Relatedness

The distinction between **transmission and relatedness** is one of the most consequential refinements introduced by MCT.

A son receives mtDNA from his mother but ordinarily does not transmit that mtDNA to his offspring [1-3,15]. Yet the son remains genealogically related to his mother, and his children remain her descendants. Nuclear genetic material originating from the grandmother may also pass through the son to later generations.

Thus:

This distinction resolves an apparent contradiction within female-line genealogical models. A maternal molecular lineage can become extinct while the woman's broader genealogical lineage expands substantially.

The phenomenon is particularly important for interpreting mitochondrial common ancestry. Women whose uninterrupted female-line mtDNA transmission eventually disappeared may nevertheless be ancestors of large numbers of living humans through other genealogical pathways. Consequently, the survival of one mitochondrial lineage should never be

interpreted as evidence that alternative female genealogical ancestry disappeared.

### 10.5 Interpretation of the Bangladesh Family Example

The Bangladesh family described in the original study provides a useful micro-level illustration of these distinctions. The family included a focal woman, five daughters, surviving sons, and multiple subsequent descendants. The original analysis attempted to identify which descendants remained within the focal woman's continuing female birth line.

Under MCT, the same family can be represented as overlapping networks rather than a binary system of connection and disconnection.

The first network contains **all genealogical descendants**. The second contains serial gestational relationships through reproducing female descendants. The third represents the predicted mtDNA transmission network. These networks overlap but are not identical.

This reinterpretation demonstrates the practical value of the Domain Independence Principle. Instead of asking whether a descendant is “connected” to the focal woman, MCT asks:

**What type of continuity connects this descendant to the focal ancestor?**

This seemingly modest change substantially increases biological precision.

The family example also highlights the importance of data verification. The original narrative reports generational female counts that, when summed directly, do not clearly reconcile with the separately reported total of 62 women. This discrepancy should be resolved against the original pedigree records before the case is presented as an empirical dataset in a future study. In the present article, it therefore remains an illustrative model rather than quantitative evidence supporting MCT.

## 10.6 Mitochondrial Genetics Provides Support but Also Defines a Boundary

mtDNA provides the strongest molecular parallel to the proposed maternal continuity pathway. Predominantly maternal inheritance enables mitochondrial variants to be followed through female-line transmission and has long been used to investigate population history and maternal ancestry [1-3,5,6]. Recent molecular evidence has also strengthened understanding of the biological mechanisms contributing to maternal mitochondrial inheritance [15].

Nevertheless, mitochondrial genetics simultaneously places an important restriction on MCT. A mitochondrial lineage represents only one narrow component of an individual's genetic ancestry. It does not capture the enormous number of genealogical relationships represented in the nuclear genome and family pedigree.

Moreover, mtDNA is not transmitted as an entirely invariant molecular entity. Mutation, heteroplasmy, mitochondrial bottlenecks, genetic drift, and selection can alter variant frequencies and sequence characteristics across generations [2,3]. Maternal genetic continuity should therefore be understood as **descent with molecular variation**, rather than exact genetic replication.

This observation has particular biomedical relevance. The intergenerational transmission of pathogenic mtDNA variants can produce highly variable clinical outcomes because heteroplasmy levels can differ among siblings, tissues, and generations [2-4]. Thus, the concept of maternal genetic continuity already has established clinical significance independent of MCT. The contribution of MCT is to position this molecular process within a broader framework connecting gestation and genealogy.

## 10.7 MCT and the Concept of Mitochondrial Eve

The population-genetic concept commonly described as mitochondrial Eve represents an important point of both convergence and divergence with the original theory. Early mtDNA studies demonstrated that surviving contemporary mitochondrial lineages can be traced retrospectively toward

a common maternal ancestor [5]. The original paper recognized this literature when discussing maternal common ancestry.

At first sight, this appears to support the hypothesis that maternal pathways eventually lead to a single woman. However, coalescent ancestry must be interpreted precisely. A mitochondrial most recent common ancestor is the most recent woman whose uninterrupted maternal mtDNA lineage is ancestral to the sampled living lineages. She was not necessarily the first woman, the first *Homo sapiens*, the only woman alive at that time, or the only female genealogical ancestor of living humans.

Accordingly:

This represents one of the most significant theoretical modifications made in the revised MCT. The theory retains the logic of retrospective maternal tracing but removes the unsupported inference that mitochondrial convergence necessarily identifies a unique first human female.

### 10.8 Compatibility with Evolutionary Theory

MCT is compatible with evolutionary biology because the two frameworks operate at different explanatory scales.

Evolutionary theory addresses changes in populations across generations through mutation, selection, drift, recombination, migration, and gene flow. MCT focuses on one recurrent reproductive relationship through which generations themselves are produced. The two therefore answer different questions:

Ancient DNA and population-genomic research further demonstrate that human ancestry includes population subdivision and admixture, including genetic contributions from archaic hominin populations [8-10]. These findings are inconsistent with an overly simple linear model of human ancestry but fully compatible with MCT if maternal pathways are understood as individual trajectories embedded within broader reticulated population histories.

The revised framework therefore moves away from the more adversarial questioning of evolutionary explanation found in the original introduction.

Evolution provides the broader explanatory framework within which serial reproductive relationships occur.

### 10.9 A Micro-to-Macro Bridge

One potential theoretical value of MCT is its capacity to organize evidence across different scales:

The first level is observable clinically. The second can be documented individually. The third can be reconstructed genealogically. The fourth can be investigated molecularly. The fifth requires population-genetic inference.

This progression provides what may be termed a **micro-to-macro bridge**. However, the bridge is epistemological rather than evidentiary continuity in the strict sense: evidence from one level cannot automatically prove the next.

This leads to perhaps the most important methodological principle generated by the theory:

> ***The temporal reach of a maternal-continuity claim should not exceed the evidentiary reach of the methods used to establish it.***

A contemporary pregnancy can establish a direct gestational relationship. A validated pedigree may establish several generations. Molecular evidence can extend maternal-line inference substantially further. Claims about species origins require evolutionary and population-level evidence.

### 10.10 Assisted Reproduction as a Critical Test of MCT

Assisted reproductive technologies provide particularly informative boundary cases because they can separate biological roles that usually coincide.

In conventional reproduction, one woman may provide the oocyte, mtDNA, gestational environment, and genealogical maternal relationship. In gestational surrogacy using another woman's oocyte, however, genetic and gestational maternal relationships are divided between two individuals.

This produces:

Such cases demonstrate that the word *mother* alone is insufficient for rigorous biological modelling. MCT therefore gains explanatory precision by separately coding gestational, genetic, genealogical, and-where relevant-social parental relationships.

Rather than undermining the theory, assisted reproduction provides an opportunity to test its Domain Independence Principle. A framework that continues to function when these relationships diverge is theoretically stronger than one that assumes their universal coincidence.

### 10.11 Medical and Biomedical Relevance

Although MCT is fundamentally a theory of intergenerational continuity, several aspects have potential biomedical relevance.

First, maternal genetic continuity is directly relevant to mitochondrial disease. Pathogenic mtDNA variants exhibit maternal inheritance patterns, while heteroplasmy and bottleneck effects influence recurrence and clinical expression [2-4]. Understanding the distinction between genealogical and mitochondrial transmission is therefore relevant to genetic counselling.

Second, gestational continuity highlights the developmental importance of the maternal-fetal interface. Placental function and intrauterine exposures can influence fetal growth and later health [11-14]. This links MCT conceptually with developmental and life-course approaches to disease, although MCT itself does not establish causal transgenerational health effects.

Third, pedigree reconstruction remains an important component of medical genetics. Distinguishing maternal-line, paternal-line, autosomal, X-linked, and mitochondrial inheritance can inform clinical interpretation. MCT's layered representation may therefore have potential educational or analytical utility when discussing maternal-line inheritance.

These applications should nevertheless remain proportionate. MCT does not currently offer a diagnostic test, therapeutic intervention, or validated clinical prediction tool. Its present contribution is conceptual.

## 10.12 The Qur’anic Component in an Interdisciplinary Framework

The comparative theological analysis adds another dimension to the discussion. The Qur'an refers to human generation, intrauterine development, pregnancy, birth, kinship, and successive generations, themes that formed an important part of the original theoretical formulation.

The revised framework deliberately avoids treating these passages as biomedical data. Instead, they demonstrate that questions of gestation, descent, and common human origin have also been addressed within theological systems of knowledge.

This distinction is important for maintaining scientific rigor:

For example, Qur’anic references to development in the womb may be conceptually compared with MCT's emphasis on gestation, but they do not constitute evidence for placental physiology. Likewise, theological accounts of shared human origin cannot be equated automatically with mitochondrial coalescence.

This positioning allows the theory to retain its interdisciplinary intellectual origins while remaining methodologically appropriate for biomedical evaluation.

## 10.13 Falsifiability and Scientific Status of MCT

A central challenge for any new theoretical framework is distinguishing a scientifically testable theory from a reinterpretation of established facts. MCT addresses this challenge by specifying propositions that can be examined independently.

Some propositions are strongly grounded in existing evidence. The existence of gestational maternal-fetal relationships and predominantly maternal mtDNA inheritance are well established [1-3,11-15]. Other propositions-particularly the usefulness of integrating these phenomena into a single continuity framework-require empirical evaluation.

The Maternal Continuity Convergence Principle is particularly testable. In a well-documented multigenerational family, researchers could reconstruct female-line genealogy independently and then perform

mtDNA analysis among consenting descendants. The prediction would be that uninterrupted biological female-line descendants should exhibit mitochondrial relationships compatible with the documented pedigree.

A failure of concordance would not automatically invalidate MCT because pedigree error, non-maternity events, mutation, heteroplasmy, laboratory error, or reproductive technologies could provide alternative explanations. However, systematic disagreement after such factors were excluded would require modification of the relevant proposition.

Thus, MCT should be regarded as a **provisional theoretical framework whose value depends on future empirical testing**, rather than as a completed explanation of human origins.

### 10.14 Theoretical Contributions

The revised framework makes several conceptual contributions.

First, it introduces **serial gestational continuity**, distinguishing recurring mother-offspring relationships from continuous physical attachment.

Second, it separates three domains that are frequently conflated:

Third, it introduces the **Transmission-Relatedness Distinction**, explaining why extinction of an mtDNA pathway does not imply extinction of genealogical ancestry.

Fourth, it proposes an **Evidence Convergence Principle**, whereby confidence in a maternal pathway increases when independent gestational, documentary, genealogical, and molecular evidence converge.

Fifth, it establishes a **Deep-Time Inference Boundary**, preventing contemporary anatomy or recent genealogy from being extrapolated directly into claims concerning the first human female.

Finally, MCT provides a framework connecting individual reproductive biology with family genealogy and maternal population genetics without attempting to replace biparental ancestry or evolutionary theory.

### 10.15 Alternative Explanations and Potential Criticisms

Several criticisms of MCT should be considered.

The first is that the theory may appear to redescribe established biological knowledge using new terminology. Pregnancy, maternal genealogy, and mitochondrial inheritance are already known phenomena. For MCT to provide genuine theoretical value, it must therefore demonstrate that integrating these domains produces explanatory or empirical insights unavailable when they are considered separately.

A second criticism concerns the term **continuity**. Because each pregnancy represents a new biological event, critics may argue that there is no literal continuous physiological structure across generations. MCT addresses this objection by defining continuity relationally and genealogically rather than anatomically. The proposed continuity is a sequence of maternal links, not persistence of one biological organ.

Third, the theory could be interpreted as privileging maternal ancestry. This interpretation is explicitly rejected. Maternal continuity represents one analytically identifiable pathway within biparental and increasingly complex ancestry networks.

Fourth, deep-time reconstruction is necessarily incomplete. MCT cannot presently reconstruct an unbroken named maternal pedigree from a living individual into prehistoric human populations. At deep temporal scales, individual genealogy gives way to molecular and population-level inference.

These criticisms define the boundaries within which MCT must be evaluated and refined.

### 10.16 Future Empirical Direction

The strongest next step would be a prospective or retrospective **multigenerational pedigree-genomic study**. Several extended families with reliable civil or clinical documentation could be recruited. Maternal relationships would first be reconstructed independently of molecular data. mtDNA sequencing could then be performed among consenting individuals representing multiple female-line branches and male-mediated genealogical branches.

Such a design would permit direct testing of several MCT propositions, including whether documentary maternal pathways correspond to molecular patterns and whether the three-domain framework improves interpretation of complex family structures.

A broader second phase could combine genealogical databases with mitochondrial haplogroup information across geographically diverse populations. Eventually, ancient DNA datasets could be incorporated to examine how individual-level maternal continuity relates to population-level lineage reconstruction.

Importantly, these studies should test MCT rather than assume its correctness.

### 10.17 Overall Interpretation

Taken together, the findings of the conceptual synthesis and genealogical modelling support a substantially narrower but scientifically stronger interpretation of maternal continuity than that proposed in the original formulation.

The evidence supports the existence of direct maternal-fetal physiological relationships, serial maternal reproductive events, reconstructable maternal genealogies, and predominantly maternal mitochondrial inheritance [1-3,11-15]. It also supports the possibility of tracing surviving maternal genetic lineages backward through population-genetic methods [5,6].

The evidence does **not**, however, establish that the human umbilicus identifies remote ancestry, that male-mediated descendants become biologically disconnected from maternal ancestors, that mitochondrial Eve represents the first human woman, or that a contemporary family pedigree can independently demonstrate the universal origin of humanity.

The resulting theoretical position is therefore:

with an explicit evidentiary boundary between each stage.

Accordingly, Maternal Continuity Theory is best understood not as an alternative theory of human evolution, but as an **interdisciplinary**

**framework for identifying, distinguishing, and investigating a persistent maternal dimension of human intergenerational continuity**. Its originality derives from connecting reproductive physiology, genealogy, and maternal molecular inheritance within one testable architecture, while its scientific credibility depends on respecting the limits separating observable biological relationships from increasingly remote historical inference.

## 11. Boundary Conditions, Counterarguments, and Limitations

Maternal Continuity Theory (MCT) proposes that a distinct maternal dimension of human intergenerational continuity can be examined through gestational, genealogical, and predominantly maternally inherited genetic pathways. However, the explanatory value of a new theoretical framework depends not only on the phenomena it can accommodate but also on the clarity with which it defines circumstances in which its propositions do not apply, require modification, or cannot presently be tested. This section therefore identifies the principal **boundary conditions, counterarguments, methodological constraints, and inferential limitations** of MCT. These qualifications are particularly important because the original formulation made broad claims concerning the extension of maternal relationships toward early human ancestry. The revised theory deliberately narrows these claims to those that can be distinguished conceptually and evaluated against appropriate biomedical, genealogical, and population-genetic evidence.

### 11.1 Boundary Condition 1: MCT Does Not Represent Complete Human Ancestry

The first and most important boundary is that maternal continuity represents **one pathway within the much larger structure of human ancestry**. Human nuclear genetic inheritance is biparental, and every individual is embedded within an expanding network of maternal and paternal genealogical relationships.

Thus:

where **MCP** denotes a Maternal Continuity Pathway and **TGA** denotes total genealogical ancestry.

Consequently, MCT should not be interpreted as claiming that maternal ancestry is the only, or necessarily the dominant, biological determinant of human descent. A focal maternal pathway:

captures only one trajectory through a much larger pedigree.

This qualification is particularly important when considering the original model, which focused almost exclusively on female-mediated birth lines. The revised MCT retains this pathway as its analytical focus while explicitly acknowledging paternal and other genealogical branches.

### 11.2 Boundary Condition 2: Gestational Continuity Is Not Genetic Continuity

A second boundary concerns the distinction between carrying a pregnancy and contributing genetic material to the resulting offspring.

In conventional biological reproduction, the individual providing the oocyte commonly also carries the pregnancy. This coincidence can create the impression that gestational and genetic motherhood are biologically inseparable. Assisted reproductive technologies demonstrate that they are not.

With donor-oocyte gestational surrogacy, for example:

The oocyte provider contributes maternal nuclear DNA and ordinarily mtDNA, whereas the gestational carrier provides the intrauterine developmental environment and maternal-fetal physiological interface.

Accordingly:

MCT must therefore identify explicitly which form of maternal continuity is being analysed rather than using the term *mother* as an undifferentiated biological category.

### 11.3 Boundary Condition 3: Genealogical Continuity Is Not Necessarily Genetic Detectability

A genealogical ancestor does not necessarily contribute an identifiable segment of autosomal DNA to every distant descendant. Because meiotic recombination reshuffles chromosomal material across generations, detectable autosomal contributions from particular ancestors become increasingly uncertain with temporal depth.

Thus:

This distinction is fundamental to MCT. An individual may remain a genuine genealogical descendant of an earlier woman even when no identifiable autosomal segment can confidently be attributed to that specific ancestor.

Conversely, mtDNA provides a highly specific maternal transmission pathway but captures only a small fraction of total genetic ancestry [1-3]. Neither autosomal DNA nor mtDNA should therefore be equated with genealogy in its entirety.

### 11.4 Boundary Condition 4: Maternal Genetic Continuity Is Not Molecular Identity

The term *continuity* could incorrectly suggest that the mitochondrial genome remains unchanged across generations. MCT makes no such assumption.

Mutation, heteroplasmy, mitochondrial bottlenecks, genetic drift, and selection can generate differences between maternal relatives [1-4]. Accordingly:

may occur at the sequence or heteroplasmy level while the two individuals remain part of the same maternal genetic lineage.

Maternal genetic continuity therefore refers to **lineal transmission with potential molecular modification**, not perfect molecular replication.

This boundary is also clinically relevant because mitochondrial disorders may exhibit substantial variability among maternally related individuals despite their shared lineage [2-4].

### 11.5 Boundary Condition 5: Male Descendants Do Not Become Genealogically Disconnected

The original formulation suggested that when descent proceeded through sons, subsequent offspring became disconnected from the focal woman's birth line because they were gestated by other women. This interpretation requires substantial qualification.

A son remains the genealogical descendant of his mother, and his children remain her grandchildren. He also inherits nuclear genetic material and normally mtDNA from his mother. What ordinarily terminates through him is **transmission of her mtDNA to his offspring**, not genealogical relatedness.

Therefore:

This Transmission-Relatedness Distinction constitutes a major boundary condition of the revised theory.

### 11.6 Boundary Condition 6: The Umbilicus Has Limited Evidentiary Scope

The umbilicus provided the observational starting point of the original theory and was described as a universal sample from which maternal relationships might be conceptualized. Within the revised MCT, its evidentiary role is intentionally restricted.

The umbilicus is consistent with an individual's prior prenatal umbilical attachment. It does not contain visible information identifying the mother, grandmother, maternal haplogroup, or prehistoric ancestors.

Accordingly:

but:

This distinction prevents a proximal anatomical observation from being extrapolated beyond its evidentiary capacity.

### 11.7 Boundary Condition 7: Maternal-Line Coalescence Is Not the Origin of Womanhood or Humanity

Perhaps the most consequential boundary concerns deep ancestry.

Population-genetic analysis demonstrates that surviving contemporary mtDNA lineages can be traced retrospectively toward a mitochondrial most recent common ancestor [5,6]. The original study discussed this evidence in relation to a common maternal origin.

However:

and:

Women whose direct mtDNA lines became extinct may nevertheless have contributed extensively to contemporary genealogical and nuclear genetic ancestry.

MCT can therefore investigate **maternal-line coalescence**, but current evidence does not permit the theory to identify a biologically unique first woman through mtDNA alone.

### 11.8 Boundary Condition 8: Species Origins Cannot Be Reduced to a Single Genealogical Event

The emergence of *Homo sapiens* was a population-level evolutionary process involving genetic variation, population structure, migration, selection, drift, and admixture [7-10]. Species boundaries developing across evolutionary time need not correspond to one identifiable birth.

This creates a conceptual problem for the phrase **“first human mother.”** If evolutionary change occurs gradually within populations, identifying one generation as fully human and the immediately preceding generation as categorically non-human may not correspond to biological reality.

MCT therefore distinguishes:

The theory's strongest claims concern the first two levels. The latter two remain within evolutionary and population science.

### 11.9 Counterargument 1: MCT Merely Renames Established Biological Facts

Perhaps the strongest theoretical criticism is that MCT combines phenomena that are already well known. Pregnancy establishes maternal-fetal relationships; genealogy describes ancestry; and mtDNA is

maternally inherited. A critic could therefore argue that the theory introduces terminology without generating genuinely new explanatory knowledge.

This criticism deserves serious consideration.

The proposed novelty of MCT is **not discovery of the individual mechanisms**. Instead, its theoretical contribution lies in integrating them into a structured framework in which three different types of maternal continuity are explicitly separated and then examined for convergence.

Thus, MCT proposes:

Whether this integration constitutes sufficient theoretical novelty must ultimately be demonstrated through its explanatory and empirical utility. If MCT does not generate testable predictions, clarify previously ambiguous relationships, or facilitate new research designs, then the criticism that it is primarily terminological would remain valid.

### 11.10 Counterargument 2: There Is No Genuine "Continuity" between Separate Pregnancies

A second objection concerns the use of the word *continuity.* Each pregnancy is biologically independent. A new placenta develops, a new umbilical cord forms, and a distinct maternal-fetal interface is established. Therefore, critics may argue that there is no literal gestational continuity across generations.

MCT accepts the anatomical premise of this criticism.

The proposed continuity is **relational and serial rather than anatomically continuous**:

The term therefore resembles genealogical continuity: a grandchild is connected to a grandparent through an intervening parent even though no single continuous physiological structure links all three individuals.

Whether the term *continuity* adequately captures this serial relationship is nevertheless open to theoretical debate. Future scholarship may determine that terms such as **serial maternal linkage**, **intergenerational maternal pathway**, or **maternal relational continuity** provide greater precision.

### 11.11 Counterargument 3: MCT Artificially Privileges the Maternal Line

Another criticism is that selecting one maternal pathway from an enormous biparental pedigree may create an arbitrary impression of special biological importance.

This criticism is valid if MCT is interpreted as a complete theory of ancestry. It is less compelling if the theory is treated as a **domain-specific framework**.

The maternal line possesses particular analytical characteristics because gestation is biologically asymmetric and mtDNA is predominantly maternally transmitted [1-3,15]. These features make maternal pathways particularly amenable to certain forms of reconstruction.

Nevertheless:

MCT therefore assigns no hierarchy of human value or overall genetic importance to maternal versus paternal ancestry.

### 11.12 Counterargument 4: mtDNA Cannot Validate the Entire Theory

Because mtDNA follows a predominantly maternal transmission pattern, there is a temptation to treat molecular concordance as confirmation of the entire MCT framework. Such an interpretation would be excessive.

Compatible mtDNA can support a hypothesized female-line genetic relationship, but it cannot independently prove each mother-daughter relationship in a pedigree. Unrelated or distantly related individuals may share common haplogroups, while genetic similarity must be interpreted in relation to population frequency, sequence resolution, mutation, and appropriate comparison samples.

Thus:

Molecular evidence should therefore be triangulated with independent genealogical documentation whenever recent family relationships are being reconstructed.

### 11.13 Counterargument 5: Exceptional Paternal mtDNA Findings Challenge a Strict Maternal Rule

Human mtDNA is overwhelmingly described as maternally inherited, but the scientific literature has included exceptional or disputed reports concerning possible paternal mitochondrial contribution. The existence and interpretation of such findings require caution [15,16].

MCT therefore deliberately uses the terms **predominantly** or **overwhelmingly maternal inheritance**, rather than asserting an exceptionless universal rule.

If future high-quality evidence established reproducible paternal mtDNA transmission at a biologically meaningful frequency, P4 would require modification. Importantly, such revision would affect the molecular component of MCT without necessarily invalidating the gestational or genealogical components.

This illustrates the modular falsifiability of the framework.

### 11.14 Counterargument 6: Assisted Reproduction Complicates the Concept of “Mother”

Modern reproductive medicine challenges any theory based on a singular definition of maternity.

A child may have a genetic maternal contributor, a gestational carrier, a legally recognized mother, and a social parent who are not the same individual. Mitochondrial replacement techniques may introduce additional complexity into simple models of maternal genetic contribution.

Consequently, the expression:

is insufficiently precise for all biomedical circumstances.

MCT responds by decomposing the relationship into:

where **SC** may represent social or legally recognized continuity when such a dimension is relevant.

However, the present theory primarily concerns biological and genealogical relationships and does not provide a comprehensive theory of social, legal, or psychological motherhood.

### 11.15 Counterargument 7: Genealogy Is Vulnerable to Documentary Error

Genealogical reconstruction is not inherently equivalent to biological truth. Birth records, family histories, oral accounts, and pedigrees can contain errors. Misattributed parentage, undocumented adoption, informal fostering, incomplete registration, record loss, and incorrect family recollection may all affect reconstructed pedigrees.

Consequently:

This limitation becomes increasingly important as temporal depth increases.

MCT therefore gives greatest weight to **convergent evidence** rather than a single information source. Documentary genealogy, reproductive history, and molecular evidence should ideally be evaluated independently before being integrated.

### 11.16 Limitation 1: The Present Study Is Primarily Conceptual

The most immediate limitation is that the current study develops and refines a theoretical framework rather than conducting a new prospective biomedical investigation.

No new mtDNA sequencing, whole-genome sequencing, ancient DNA analysis, reproductive imaging, or experimental assessment was performed specifically to test MCT.

Accordingly, the present article can establish:

- conceptual coherence;
- compatibility or incompatibility with existing knowledge;
- theoretical propositions;
- potential empirical predictions; and
- boundaries for future testing.

It cannot establish the empirical validity of the entire theory.

This distinction should be made explicit in the interpretation of the study.

### 11.17 Limitation 2: The Bangladesh Family Is Illustrative Rather than Representative

The family example is drawn from the original theoretical work and provides a useful multigenerational demonstration. However, it constitutes neither a representative sample of Bangladesh nor a population-based genealogical dataset.

The original paper reported a network involving 121 individuals and subsequently a female-line representation involving 62 women.

The case therefore cannot be used to estimate:

- maternal-line persistence in Bangladesh;
- reproductive rates;
- mitochondrial haplogroup frequencies;
- genealogical coalescence;
- or population-level ancestry.

Its role is solely to demonstrate how the conceptual model operates within a multigenerational family.

### 11.18 Limitation 3: Numerical Inconsistency in the Original Family Description

A specific limitation concerns the internal numerical reporting of the original genealogy. As noted in Section 7, the reported generational female counts do not clearly reconcile with the stated total of 62 women.

This discrepancy should be resolved before the genealogy is used as a formal empirical dataset.

The appropriate methodological response is **verification rather than retrospective correction**. Original pedigree notes, family records, and figure coding should be re-examined to determine whether the discrepancy arose from inclusion/exclusion of the focal woman, duplicate counting, generational classification, or a simple reporting error.

Until this is resolved, quantitative conclusions should not depend on the exact female-line total.

### 11.19 Limitation 4: Absence of Molecular Verification in the Family Example

The original Bangladesh family analysis did not report mtDNA sequencing. Consequently, the proposed mitochondrial relationships among the female-line descendants remain **predictions derived from established inheritance mechanisms**, not observations from this particular family.

The distinction is important:

A future study should therefore test the genealogy independently through molecular analysis rather than treating genetic continuity as already established.

### 11.20 Limitation 5: Deep-Time Genealogical Reconstruction Is Not Currently Possible

Recent maternal relationships may be reconstructed through records and family evidence, but an uninterrupted individual-by-individual maternal pedigree extending from a living person to early *Homo sapiens* is not presently available.

The evidentiary pathway necessarily changes with temporal depth:

The transition between these stages introduces uncertainty.

MCT therefore cannot currently demonstrate a complete named maternal chain from a contemporary person to a prehistoric individual. At deep temporal levels, it must defer to phylogenetic, coalescent, archaeological, palaeoanthropological, and ancient-DNA evidence.

### 11.21 Limitation 6: Population-Genetic Models Are Inferential

Even molecular evidence does not remove all uncertainty. Estimates of population divergence, migration, effective population size, lineage coalescence, and ancestral relationships depend upon sampling, mutation-rate assumptions, demographic models, population structure, and analytical methods [5-10].

Therefore, deep maternal ancestry should be described probabilistically rather than as a directly observed genealogy.

This reinforces the principle:

MCT must therefore avoid presenting population-genetic estimates as equivalent to documented family relationships.

### 11.22 Limitation 7: The Framework Does Not Fully Address Social and Cultural Kinship

Anthropological kinship can differ substantially from biological genealogy. Adoption, fostering, clan membership, legal parenthood, marriage systems, and culturally defined maternal roles can create meaningful kinship relationships without gestational or genetic continuity.

The present framework acknowledges these distinctions but focuses primarily on **embodied, genealogical, and genetic descent**.

It should therefore not be used to invalidate social parenthood or culturally recognized kinship merely because a relationship lacks a biological link.

This boundary is especially important when applying MCT across culturally diverse populations.

### 11.23 Limitation 8: The Theological Component Has a Different Evidentiary Status

The Qur’anic component discussed in Section 9 provides a comparative theological perspective on creation, gestation, reproduction, kinship, and common human origin. It does not constitute independent biomedical evidence for MCT.

Therefore:

Likewise, contemporary discoveries concerning embryology, mtDNA, or population genetics should not automatically be presented as proof of one specific interpretation of Qur’anic terminology.

This epistemological separation is particularly necessary if the manuscript is intended for a medical or biomedical journal.

### 11.24 Limitation 9: Terminological Ambiguity Requires Continued Refinement

Several terms introduced by MCT-including *maternal continuity*, *gestational continuity*, *serial maternal link*, and *maternal continuity pathway*-are theoretical constructs rather than established biomedical terminology.

Their definitions must therefore remain explicit.

For example, *gestational continuity* might be misunderstood as suggesting that one physiological process continues physically through several generations. MCT instead defines it as a sequence of separate gestational events linked genealogically.

Future conceptual and empirical studies may reveal that alternative terminology improves precision. The theory should remain open to such refinement rather than treating its initial vocabulary as fixed.

### 11.25 Ethical and Privacy Limitations of Future Testing

Empirical testing of MCT using genomic genealogy would raise significant ethical issues. A person's genetic information can reveal biological relationships involving relatives who have not consented to testing. Unexpected parentage, adoption, reproductive history, or familial disease risk could also emerge.

Future studies would therefore require appropriate ethical review, informed consent, secure genomic-data management, privacy protection, procedures for incidental findings, and culturally appropriate approaches to family disclosure.

These considerations are particularly important because MCT proposes combining **genealogical and genetic information**, two categories of data with substantial implications for personal and familial privacy.

### 11.26 Falsification and Revision Criteria

A useful theory should specify conditions under which its propositions would require revision. MCT is therefore deliberately structured as a modular framework.

For example:

| MCT proposition | Evidence requiring modification |
|---|---|
| **P1: Gestational predecessor** | Evidence requiring revision of how gestation is defined in future reproductive technologies |
| **P2: Serial maternal links** | Demonstration that the proposed relational sequence lacks meaningful explanatory utility |
| **P3: Genealogical reconstruction** | Systematic inability to validate proposed maternal pedigrees |
| **P4: Maternal genetic transmission** | Robust evidence of routine biparental mtDNA inheritance |
| **P5: Domain independence** | Evidence showing gestational, genetic, and genealogical roles are biologically inseparable |
| **P6: Evidence convergence** | Demonstration that multimodal evidence does not improve reconstruction reliability |
| **P7: Transmission-relatedness distinction** | Contradiction by established principles of genetic and genealogical inheritance |
| **P8: Deep-time boundary** | Direct evidence permitting individual-level reconstruction beyond present inferential limitations |

The table emphasizes that MCT is not intended to be protected from disconfirming evidence. Its propositions should be modified if future reproductive, genealogical, or genomic evidence requires revision.

### 11.27 Overall Boundary of Maternal Continuity Theory

The scientifically defensible scope of MCT can ultimately be represented as:

but not:

These boundaries are not peripheral qualifications; they are integral components of the theory. By distinguishing **what is observed, what is reconstructed, what is molecularly inferred, and what remains unknown**, MCT becomes more resistant to overinterpretation and more amenable to empirical testing.

Accordingly, the present formulation should be regarded as a **provisional and falsifiable interdisciplinary theory of maternal intergenerational continuity**, rather than a completed theory of human origins. Its future scientific value will depend on whether independent genealogical, reproductive, and genomic investigations confirm the predicted relationships and whether the integrated framework provides explanatory value beyond the established disciplines from which its components are derived.

## 12. Implications and Future Empirical Testing

Maternal Continuity Theory (MCT) has implications across reproductive medicine, medical genetics, genealogy, population genetics, evolutionary anthropology, and interdisciplinary studies of human descent. At its present stage, MCT should be understood as a **conceptual and testable framework rather than a clinically validated model**. Its principal value lies in distinguishing and integrating gestational, genealogical, and maternal genetic continuity while specifying the evidentiary transitions between them. The original theory developed these ideas from the observable umbilical relationship and multigenerational maternal-line reasoning. The revised framework extends that contribution by identifying explicit propositions and empirical designs through which its assumptions can be evaluated.

### 12.1 Implications for Reproductive Medicine

The first implication concerns the conceptualization of pregnancy as an intergenerational biological relationship rather than solely as an isolated reproductive event. Contemporary reproductive medicine already recognizes pregnancy as a complex maternal-fetal physiological process involving placentation, vascular exchange, endocrine regulation, immunological adaptation, and fetal development [11-14]. MCT adds an

intergenerational perspective by asking how such relationships recur serially across generations.

This does not alter existing obstetric physiology, but it provides a conceptual structure through which reproductive histories may be represented longitudinally. For example, a woman who was herself gestated and later carries a pregnancy participates sequentially in two distinct positions:

[
\text{gestated offspring}
\rightarrow
\text{later gestational parent}.
]

Across multiple generations, such relationships generate serial reproductive pathways.

This perspective may be particularly useful in studies examining intergenerational reproductive health, maternal developmental exposures, or family reproductive histories, although MCT does not itself establish transgenerational causal effects.

### 12.2 Implications for Medical Genetics

The strongest immediate biomedical implication concerns the differentiation between **maternal genetic transmission and broader genealogical relatedness**.

Mitochondrial disorders are typically associated with maternal patterns of inheritance, but clinical outcomes can vary substantially because of heteroplasmy, mitochondrial bottlenecks, tissue distribution, and variant-specific effects [1-4]. MCT's distinction between maternal genetic continuity and genealogical continuity reinforces the need to avoid assuming that all descendants of a woman carry the same mitochondrial lineage.

The framework may therefore have conceptual utility in genetic counselling by distinguishing:

[
\text{genealogical descendant}
]

from:

[
\text{carrier of a particular maternal mtDNA transmission pathway}.
]

For example, descendants through a son remain genealogically related to their paternal grandmother but would not ordinarily inherit her mtDNA through that son [1-3,15]. This distinction is already established genetically; MCT incorporates it into a broader model of maternal continuity.

### 12.3 Implications for Pedigree Analysis

Pedigrees in medical genetics are commonly used to identify patterns of inheritance. MCT suggests that maternal pathways could be represented in a **multilayer pedigree** in which different lines indicate different forms of continuity.

A future MCT-informed pedigree might independently encode:

- gestational relationship;
- biological genealogy;
- mtDNA transmission;
- nuclear genetic descent;
- and, where relevant, assisted reproductive relationships.

This would be particularly useful when genetic and gestational maternal roles differ.

For example:

$$
[
\text{oocyte donor}
\rightarrow
\text{genetic maternal continuity}
]
$$

while:

$$
[
\text{gestational carrier}
\rightarrow
\text{gestational continuity}.
]
$$

The conventional use of a single maternal symbol may therefore conceal biologically relevant distinctions in complex reproductive histories.

### 12.4 Implications for Assisted Reproductive Medicine

Assisted reproductive technologies provide one of the most important domains for testing the theoretical precision of MCT.

In conventional reproduction, genetic, gestational, genealogical, legal, and social maternal identities may coincide. In assisted reproduction, however, these roles may be distributed among different individuals.

MCT predicts that such cases should be represented as **divergent continuity domains**, rather than treated as anomalies.

For example:

[
GC=1,\quad MGC=0
]

may occur for a gestational carrier who did not provide the oocyte.

Conversely:

[
GC=0,\quad MGC=1
]

may apply to an oocyte provider whose embryo is gestated by another individual.

These cases provide direct tests of the Domain Independence Principle developed in Section 5.

### 12.5 Implications for Genealogical Research

MCT also has implications for genealogical methodology. Traditional genealogy frequently represents family relationships without distinguishing which dimensions of biological inheritance continue through specific branches.

The Bangladesh family example illustrates this problem. The original analysis distinguished female birth lines from descendants mediated through sons. The revised model shows that these male-mediated descendants should remain within the genealogy while being distinguished from direct mtDNA transmission pathways.

Future genealogical databases could therefore represent:

$$
\text{total pedigree network}
$$

and:

$$
\text{maternal transmission subnetwork}
$$

simultaneously.

Such modelling could improve interpretation of maternal-line genealogies without reducing total ancestry to matrilineal descent.

### 12.6 Implications for Population Genetics

At the population level, MCT provides a conceptual bridge between identifiable mother-offspring relationships and the much deeper maternal histories reconstructed through mtDNA.

The theory predicts that:

$$
\text{individual maternal links}
\rightarrow
\text{family maternal lineages}
\rightarrow
\text{population maternal lineages}.
$$

However, the transition is not empirically continuous at every generation because genealogical documentation eventually disappears. Population genetics therefore becomes necessary for deeper analysis.

This creates an important epistemological distinction:

$$
[
\text{family-level maternal genealogy}
\neq
\text{population-level coalescent genealogy}.
]
$$

The former attempts to identify particular individuals; the latter estimates ancestral relationships among genetic lineages.

MCT could potentially provide terminology for linking these levels while maintaining their methodological differences.

### 12.7 Implications for Human-Origin Research

MCT may also contribute to interdisciplinary discussion of human origins by specifying the difference between **individual reproductive origin and population evolutionary origin**.

Every individual has a specific gestational history. Populations, by contrast, emerge and change through evolutionary processes involving many individuals and multiple generations.

Thus:

$$
[
\text{individual origin}
\rightarrow
\text{specific reproductive event}
]
$$

whereas:

$$
[
\text{species origin}
\rightarrow
\text{population-level evolutionary process}.
]
$$

This distinction is especially important in relation to the original theoretical interest in a first maternal ancestor. The revised theory permits maternal lineages to be traced retrospectively but does not infer that population-genetic coalescence identifies a unique first human woman.

## 12.8 Implications for Interdisciplinary Theory Development

A broader implication of MCT is methodological. The theory illustrates how a phenomenon may be studied simultaneously at several explanatory levels without assuming that those levels are equivalent.

The framework progresses through:

$$
\boxed{
\text{Anatomy and physiology}
\rightarrow
\text{reproductive relationship}
\rightarrow
\text{genealogy}
\rightarrow
\text{molecular inheritance}
\rightarrow
\text{population history}
}
$$

This layered model may be applicable beyond maternal ancestry to other problems where individual biological events scale into population-level processes.

However, interdisciplinary integration should not blur disciplinary standards. Each level requires evidence appropriate to its own methodology.

## 12.9 Future Empirical Testing: General Strategy

The next stage in MCT development should move from conceptual synthesis to **independent empirical evaluation**.

Future research should not begin by assuming that MCT is correct. Instead, studies should test whether its propositions accurately predict relationships among documented genealogy, reproductive history, and molecular evidence.

A staged research programme is proposed.

### 12.10 Phase I: Validation of the Bangladesh Family Pedigree

The most immediate empirical study could revisit the Bangladesh family used in the original theory.

The first objective should be documentary rather than molecular.

The study should:

- reconstruct the complete multigenerational pedigree;
- verify mother-offspring relationships using available records;
- reconcile the numerical discrepancy in the original female-line counts;
- identify all surviving female-line branches;
- distinguish male-mediated genealogical branches;
- record reproductive histories; and
- establish the degree of documentary certainty for every proposed link.

Each link could then be coded:

[
L_i=(GC,\ GeC,\ MGC)
]

although MGC would initially remain untested.

This first phase would evaluate P2, P3, and P7 without requiring genomic analysis.

### 12.11 Phase II: mtDNA Testing of the Bangladesh Family

After pedigree verification and appropriate ethical approval, molecular testing could evaluate the maternal genetic component.

Participants should be selected from:

- multiple uninterrupted female-line branches;
- male descendants of the focal maternal ancestor;
- children of male descendants;
- and, where feasible, individuals from independent female branches.

The central prediction is:

> ***Individuals connected through uninterrupted biological female-line descent should show mitochondrial relationships compatible with the reconstructed pedigree.***

By contrast, children whose only genealogical connection to the focal woman occurs through an intervening male should not ordinarily carry her transmitted mtDNA lineage.

A simplified sampling design could be:

[
F70
\rightarrow
D_1
\rightarrow
GD_1
\rightarrow
GGD_1
]

versus:

[
F70
\rightarrow
S_1
\rightarrow
C_{S1}.
]

This comparison would provide a direct empirical test of the Transmission-Relatedness Distinction.

### 12.12 Molecular Methods for Future Testing

Depending on resources, future research could use several levels of molecular analysis.

A minimum approach could involve complete mitochondrial genome sequencing rather than relying solely on broad haplogroup classification.

The analysis should consider:

- mtDNA sequence similarity;
- haplogroup and sub-haplogroup assignment;
- private variants;
- heteroplasmy;
- mutation differences;
- potential nuclear mitochondrial sequences;
- and laboratory contamination.

Where maternal relationships are recent, autosomal genotyping or sequencing could also help corroborate biological relationships independently of mtDNA.

The most rigorous design would therefore use:

$$
\boxed{
\text{documentary pedigree}
+
\text{autosomal relationship testing}
+
\text{mtDNA sequencing}
}
$$

rather than mtDNA alone.

### 12.13 Phase III: Multi-Family Replication

Testing one extended family would remain insufficient to establish broad theoretical utility.

A second empirical stage should recruit multiple multigenerational families from different regions and social backgrounds.

A multi-family study could examine:

- whether MCT coding can be applied consistently;
- whether documented maternal pathways correspond to mitochondrial evidence;
- how frequently pedigree uncertainty occurs;
- how male-mediated branches differ molecularly from direct female-line branches;
- and whether the three-domain model improves pedigree interpretation.

A larger design could include:

[
n=20-50
]

extended families initially, followed by larger cohorts if feasibility is demonstrated.

The unit of analysis should remain the **maternal link** rather than merely the individual participant.

### 12.14 Phase IV: Cross-Population Validation

If MCT performs consistently within family studies, a subsequent phase should test whether the framework remains useful across culturally and genetically diverse populations.

Potential populations could include communities with:

- detailed civil registration;
- historically documented genealogies;
- matrilineal social organization;

- patrilineal social organization;
- high geographic mobility;
- or relatively stable multigenerational residence.

This would test whether maternal continuity is a biological framework independent of culturally variable systems of kinship.

Importantly:

[
\text{matrilineal social organization}
\neq
\text{biological maternal continuity}.
]

Cross-cultural research would help prevent conflation of the two.

### 12.15 Phase V: Testing Assisted-Reproduction Boundary Conditions

Another empirical programme should specifically examine assisted reproductive cases.

Potential groups could include:

- conventional conception;
- oocyte donation;
- gestational surrogacy;
- embryo donation;
- and mitochondrial replacement procedures where applicable.

Such studies could determine whether MCT successfully distinguishes gestational, genetic, and genealogical relationships.

This phase is especially important for evaluating P5.

For example, the prediction would be:

[
\text{gestational carrier}
\Rightarrow GC
]

but not necessarily:

[
\text{gestational carrier}
\Rightarrow MGC.
]

Similarly, an oocyte donor may contribute maternal genetic continuity without gestational continuity.

### 12.16 Phase VI: Clinical Mitochondrial-Disease Applications

MCT could also be tested in families affected by mitochondrial disease.

Existing clinical pedigrees already contain maternal inheritance patterns that may be appropriate for evaluating whether the MCT layered model improves conceptual clarity.

A future study could compare standard pedigree interpretation with an MCT-coded pedigree in families carrying pathogenic mtDNA variants.

Potential outcomes might include:

- accuracy of inheritance interpretation;
- understanding of transmission risk;
- identification of male-mediated transmission termination;
- communication clarity in genetic counselling;
- and patient understanding of maternal inheritance.

Such work would test whether MCT has practical biomedical value beyond theoretical integration.

## 12.17 Phase VII: Genealogy-Genomics Integration

A larger methodological goal would be the development of an integrated **Maternal Continuity Database** in which each documented maternal link is associated with evidence type.

For example:

| Maternal link | Birth record | Reproductive history | Autosomal support | mtDNA support | Confidence |
|---|---|---|---|---|---|
| A → B | Yes | Yes | Yes | Yes | High |
| B → C | Yes | Yes | Yes | Compatible | High |
| C → D | Family history only | Partial | Not tested | Compatible | Moderate |
| D → E | Historical inference | Unknown | Not available | Haplogroup-level only | Low |

This would operationalize the Maternal Continuity Convergence Principle.

A future validated model might assign quantitative weights to evidence sources, although such scores should be developed empirically rather than imposed theoretically.

## 12.18 Developing a Maternal Continuity Confidence Index

If sufficient empirical data become available, researchers could explore a **Maternal Continuity Confidence Index (MCCI)**.

Conceptually:

$$
MCCI=f(GC,GeC,MGC,Q)
$$

where:

- (GC) = gestational evidence;

- (GeC) = genealogical evidence;
- (MGC) = maternal genetic evidence; and
- (Q) = quality and independence of evidence.

For example:

$$
MCCI=w_1GC+w_2GeC+w_3MGC
$$

could eventually be evaluated statistically.

However, no numerical weights are proposed in the present study because the necessary validation data do not yet exist. The equation should therefore be regarded only as a **future methodological possibility**.

### 12.19 Phase VIII: Ancient DNA and Historical Maternal Lineages

A more ambitious research programme could extend MCT into historically documented populations with ancient DNA.

Where archaeological individuals have both genetic data and historically reconstructable descendants or populations, investigators could compare:

$$
\text{historical genealogy}
$$

with:

$$
\text{ancient mtDNA}
$$

and:

$$
\text{modern maternal-line variation}.
$$

Such work would provide a bridge between family-level and population-level maternal continuity.

However, ancient DNA sampling remains sparse and cannot reconstruct every intervening mother-offspring relationship. Its role should therefore remain corroborative rather than complete.

## 12.20 Phase IX: Population-Level Simulation

Computational modelling could test the long-term implications of the Serial Maternal-Link Principle.

Simulation parameters might include:

- female reproductive rates;
- sex ratios;
- mortality;
- migration;
- population size;
- lineage extinction;
- mtDNA mutation rates;
- population bottlenecks;
- and assortative mating.

Researchers could then examine how many maternal transmission pathways survive after hundreds or thousands of generations.

This would help connect the Bangladesh family model to coalescent population genetics.

A simulation could test:

[
N_{maternal\ lines}(t)
]

as a function of demographic processes over time.

Such work could clarify how a large population with many female ancestors can eventually contain relatively few surviving direct mtDNA lineages without implying that the other women ceased to be genealogical ancestors.

### 12.21 Testing the Evidence Convergence Principle

P6-the Maternal Continuity Convergence Principle-deserves a dedicated empirical test.

Researchers could compare pedigree reconstruction accuracy under three conditions:

**Model A:** documentary genealogy alone;

**Model B:** genetic evidence alone;

**Model C:** integrated documentary + reproductive + molecular evidence.

If Model C produces more accurate or reliable maternal pathway reconstruction, this would support the theoretical utility of evidence convergence.

This could be evaluated using blinded pedigree reconstruction in families whose biological relationships are already independently established.

### 12.22 Falsification-Oriented Research

Future studies should deliberately seek evidence that could **challenge MCT**, rather than only confirm it.

Examples include:

- documented female-line genealogies inconsistent with mtDNA relationships;
- reproducible paternal mtDNA transmission;
- cases where the three-domain structure fails to classify reproductive relationships;
- evidence that serial maternal linkage provides no explanatory advantage;
- and data showing that MCT terminology reduces rather than improves clinical or genealogical clarity.

This approach is essential because MCT should remain:

[
\text{testable}

\rightarrow
\text{modifiable}
\rightarrow
\text{potentially falsifiable}.
]

A theory that cannot be challenged empirically would have limited scientific utility.

### 12.23 Recommended Research Design for the First Empirical Study

The most realistic initial empirical project arising from this paper would be a **multigenerational family-based observational study**.

A possible design is:

**Study population:** 5-10 extended Bangladeshi families with at least four documented generations.

**Participants:** selected female-line descendants, male descendants, and children of male descendants.

**Data sources:** civil registration, birth documentation, structured reproductive histories, pedigree interviews, autosomal DNA where required, and complete mtDNA sequencing.

**Primary outcome:** concordance between documented uninterrupted female-line descent and mitochondrial genetic relationships.

**Secondary outcomes:** pedigree accuracy, lineage branching, male-mediated mtDNA termination, heteroplasmy patterns, and evidence convergence.

**Primary hypothesis:**

[
H_1:
]

Documented uninterrupted biological female-line descendants will demonstrate mtDNA relationships compatible with the reconstructed maternal genealogy.

**Null hypothesis:**

[
H_0:
]

There will be no systematic concordance between independently documented female-line genealogy and mitochondrial relationships beyond that expected from population background.

Such a design would transform MCT from a predominantly conceptual theory into an empirically testable research programme.

### 12.24 Statistical Approaches for Future Empirical Studies

Depending on the design, future studies could employ:

- pedigree concordance analysis;
- sequence-distance analysis;
- haplotype comparison;
- likelihood-based kinship estimation;
- Bayesian pedigree reconstruction;
- phylogenetic analysis;
- sensitivity and specificity analysis;
- inter-rater reliability for genealogical coding;
- and mixed-effects modelling in multi-family studies.

For molecular sequence data, phylogenetic relationships should be interpreted alongside population frequencies to avoid overestimating the evidentiary value of shared common haplogroups.

Statistical analysis should therefore test **specific MCT propositions**, rather than merely describe mitochondrial similarity.

### 12.25 Ethical Priorities for Future Research

Future empirical testing would require careful ethical governance.

Particular concerns include:

- informed consent;
- familial privacy;

- unexpected parentage;
- disclosure of mitochondrial disease risk;
- genomic data security;
- participation of relatives;
- incidental findings;
- withdrawal from family-based studies;
- and culturally sensitive communication.

Because genomic information about one individual can reveal information about biological relatives, consent procedures should recognize the **relational nature of genetic data**.

For Bangladesh-based research, local institutional ethical approval and compliance with applicable data-protection and biomedical research requirements would be necessary before biological samples are collected.

### 12.26 Future Theoretical Development

MCT should also continue to evolve conceptually.

Future theoretical work should examine:

- whether *maternal continuity* remains the most precise terminology;
- whether gestational continuity requires subcategories;
- how mitochondrial replacement technologies affect the genetic domain;
- whether epigenetic inheritance should constitute a fourth biological dimension;
- how maternal microchimerism might relate to embodied continuity;
- and whether the framework can be extended without becoming overly broad.

These possibilities should not be incorporated into the core theory until empirical evidence demonstrates that they add explanatory value.

## 12.27 Potential Extension to Epigenetic and Developmental Continuity

One possible future extension concerns epigenetic and developmental programming.

Maternal physiology and intrauterine exposure can influence fetal development and potentially affect later-life health. However, the mechanisms, persistence, and transgenerational interpretation of such effects are complex.

Therefore, a future version might examine:

$$
[
\text{Gestational continuity}
\rightarrow
\text{developmental biological effects}
]
$$

without equating such effects with mtDNA inheritance.

At present, epigenetic continuity should remain a **candidate extension**, not a core MCT domain.

## 12.28 Potential Extension to Maternal Microchimerism

Maternal-fetal cell exchange during pregnancy also raises intriguing questions concerning biological persistence after birth. Small populations of maternal cells can persist in offspring, and fetal cells can persist in mothers.

This phenomenon may eventually provide another empirical perspective on embodied intergenerational connection.

However, microchimerism is mechanistically different from genealogy and mtDNA inheritance. It should therefore be investigated independently before being incorporated into MCT.

Its relevance illustrates an important principle of theory development:

***New biological observations should expand MCT only when their relationship to maternal continuity can be defined and empirically tested.***

## 12.29 Long-Term Research Programme

The future development of MCT can therefore be organized as a progressive research programme:

$$
\boxed{
\begin{array}{c}
\textbf{Stage 1}\\
\text{Pedigree verification}\\
\downarrow\\
\textbf{Stage 2}\\
\text{Family mtDNA testing}\\
\downarrow\\
\textbf{Stage 3}\\
\text{Multi-family replication}\\
\downarrow\\
\textbf{Stage 4}\\
\text{Cross-population validation}\\
\downarrow\\
\textbf{Stage 5}\\
\text{Assisted-reproduction testing}\\
\downarrow\\
\textbf{Stage 6}\\
\text{Clinical mitochondrial applications}\\
\downarrow\\
\textbf{Stage 7}\\
\text{Genealogy-genomics integration}\\
\downarrow\\
\textbf{Stage 8}\\
\text{Ancient DNA and population modelling}
\end{array}
}
$$

This staged approach would allow the theory to develop in proportion to the strength of empirical evidence.

### 12.30 Overall Implications

The principal implication of MCT is therefore not that maternal continuity provides a new replacement explanation for human origins. Rather, it provides a framework for examining a **specific, recurring and biologically identifiable dimension of intergenerational descent**.

Its biomedical significance lies in clarifying the distinctions among:

$$
\boxed{
\text{gestation}
\neq
\text{genealogy}
\neq
\text{maternal genetic inheritance}
}
$$

while demonstrating that these domains can nevertheless converge in particular maternal pathways.

Its genealogical significance lies in distinguishing total family descent from direct female-line transmission.

Its population-genetic significance lies in providing a conceptual bridge between recent documented maternal relationships and deep maternal-line coalescence.

Its theoretical significance lies in transforming an original observation about maternal birth connection into a programme of **testable propositions rather than an unbounded claim about prehistoric ancestry**.

Accordingly, the future of Maternal Continuity Theory should depend on empirical performance. If independently reconstructed pedigrees, reproductive histories, and molecular evidence repeatedly converge in the

manner predicted by the framework, MCT would gain support as an interdisciplinary model of maternal intergenerational continuity. If they do not, the propositions should be revised or rejected accordingly.

The most important next step is therefore not further expansion of the theory but **empirical testing of its central predictions**.

## 13. Conclusion

Maternal Continuity Theory (MCT) was developed in this study to provide an interdisciplinary framework for examining a distinct maternal dimension of human intergenerational continuity. The theory emerged from the original observation that every gestated human individual has a direct prenatal relationship with the person who carried the pregnancy and that this relationship can, in principle, be positioned within successive generations. The earlier formulation emphasized the umbilicus as a visible marker of maternal connection and extended this reasoning toward broader maternal ancestry. The present study preserves that theoretical insight while substantially refining its scientific interpretation.

The revised MCT distinguishes three related but non-equivalent domains: **gestational continuity, genealogical continuity, and maternal genetic continuity**. Gestational continuity refers to the embodied maternal-fetal relationship established during pregnancy. Genealogical continuity refers to reconstructable mother-offspring relationships across generations. Maternal genetic continuity refers principally to predominantly maternal mitochondrial DNA transmission. These dimensions may converge in conventional biological reproduction, but they must remain analytically separate because evidence for one form of continuity does not automatically establish the others.

A central contribution of the theory is the **Serial Maternal-Link Principle**, which conceptualizes successive pregnancies along a female-line pathway as a sequence of discrete but genealogically connected reproductive relationships.

Thus:

$$
F_0 \rightarrow F_1 \rightarrow F_2 \rightarrow F_3 \rightarrow \cdots \rightarrow F_n
$$

does not represent one continuous anatomical connection. Rather, it represents serial recurrence of a maternal-offspring relationship across generations. This distinction transforms the original notion of maternal connection into a more defensible relational and genealogical concept.

The Bangladesh family example illustrates how this framework can operate at the family level. The original genealogy included a focal woman, five daughters, surviving sons, and multiple later descendants. Under the revised model, descendants through sons are not regarded as biologically disconnected from the focal woman. They remain genealogical descendants and may retain nuclear genetic ancestry, while the focal woman's direct mtDNA transmission pathway ordinarily does not continue through those male descendants. This distinction between **transmission and relatedness** is one of the most important refinements introduced by MCT.

The theory is also compatible with contemporary evolutionary and population-genetic evidence. MCT does not replace evolutionary theory, nor does it reduce human ancestry to maternal descent. Instead, it operates at a different explanatory level, linking the biology of individual gestation with family genealogy and maternal-line molecular inheritance. Human ancestry remains biparental, reticulate, and population-based, while mtDNA represents only one specific pathway within this wider ancestry network.

Accordingly, the population-genetic concept of a mitochondrial most recent common ancestor should not be interpreted as evidence for a unique biological first woman. Although the original article recognized the relevance of maternal mtDNA ancestry, the revised theory explicitly distinguishes maternal-line coalescence from species origin. A mitochondrial common ancestor was not necessarily the first female *Homo sapiens*, the only woman alive at the time, or the sole female genealogical ancestor of living humans.

The Qur'anic component contributes a comparative theological perspective rather than an alternative source of biomedical evidence. Qur'anic references to gestation, the womb, reproduction, generations, kinship, and shared human origin are conceptually relevant to MCT, but they do not independently establish placental physiology, mitochondrial inheritance, or population-genetic ancestry. Maintaining this epistemological distinction allows the theory to retain its interdisciplinary scope without conflating theological interpretation with empirical validation.

The present study also identifies clear boundaries to the theory. MCT cannot presently reconstruct an uninterrupted named maternal genealogy from living humans into deep prehistory, establish the identity of a first human woman, or demonstrate universal ancestry from one illustrative family. The umbilicus has limited evidentiary scope, genealogical relationships are not identical to detectable genetic inheritance, and mitochondrial continuity does not represent total ancestry. These limitations are therefore integral to the theory rather than secondary qualifications.

Importantly, MCT is structured as a **provisional and falsifiable framework**. Its strongest future test would involve independently reconstructed multigenerational pedigrees combined with reproductive histories and complete mtDNA sequencing. If uninterrupted biological female-line pedigrees consistently correspond with predicted mitochondrial relationships, the Maternal Continuity Convergence Principle would gain empirical support. If systematic discrepancies remain after technical, genealogical, and reproductive explanations are excluded, the relevant propositions would require revision.

The theory therefore moves the discussion from an unrestricted claim about maternal origin toward a staged evidentiary model:

$$
\boxed{
\text{Gestational Relationship}
\rightarrow
\text{Serial Maternal Link}
\rightarrow
\text{Genealogical Reconstruction}
\rightarrow
\text{Maternal Genetic Corroboration}
\rightarrow
\text{Population-Level Inference}
}
$$

Each stage requires evidence appropriate to its own explanatory level.

In conclusion, Maternal Continuity Theory proposes that human intergenerational descent contains a scientifically identifiable maternal dimension that can be examined across embodied, genealogical, and genetic domains. Its originality lies not in discovering pregnancy, genealogy, or mitochondrial inheritance separately, but in integrating them within one conceptual structure while explicitly distinguishing their mechanisms and evidentiary limits. The theory is therefore best understood as an interdisciplinary model of **maternal relational continuity across generations**, embedded within rather than opposed to contemporary reproductive medicine, genetics, genealogy, population science, and evolutionary biology.

Its ultimate scientific value will depend not on the conceptual attractiveness of the theory but on whether future empirical studies can test its propositions, reproduce its predicted relationships, and demonstrate that the integrated framework provides explanatory value beyond the disciplines from which its components are derived.

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