

***Garbhopaghatakara Bhavas* (Factors Affecting Fetal Development) and Epigenetics: An Integrated Ayurvedic Molecular Review**

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Abstract

Background: Congenital malformations affect 35% of live births globally. Ayurveda describes harmful prenatal factors, called *Garbhopaghatakara Bhavas*, which include maternal diet, lifestyle, and psychological influences that compromise fetal development. Epigenetics has revealed that environmental exposure during gestation can alter gene expression through DNA methylation, histone modifications, and non-coding- RNAs. This review examines whether *Garbhopaghatakara Bhavas* can induce adverse epigenetic modifications. **Methods:** Narrative synthesis of classical Ayurvedic texts (Charaka Samhita and Sushruta Samhita) and peer-reviewed- modern literature from PubMed and Scopus (1990-2025). **Results:** The six *Shadgarbhakara Bhavas*– *Matrija* (maternal), *Pitrija* (paternal), *Rasaja* (nutritional), *Satmyaja* (constitutional/environmental adaptability), *Atmaja* (soul/consciousness), and *Sattvaja* (psychological essence) collectively determine the offspring's phenotype. Deviations in modifiable factors (*Rasaja*, *Satmyaja*, and *Sattvaja*) constitute *Garbhopaghatakara Bhavas*. Modern evidence shows that maternal nutritional imbalances, chronic stress, and exposure to environmental toxins induce persistent DNA methylation changes, histone modifications, and miRNA dysregulation. Ayurvedic preventive strategies, *Garbhini Paricharya* (antenatal regimen) and *Garbha Samskara* (Ayurvedic prenatal care and developmental nurturing), directly target these epigenetic pathways. **Conclusion:** *Garbhopaghatakara Bhavas* represent a prescient epigenetic framework. The convergence of Ayurvedic prenatal wisdom with molecular epigenetics offers a compelling basis for integrative preventive healthcare, although rigorous translational validation is required.

Keywords: Ayurveda, Maternal diet and lifestyle, Epigenetics, Prenatal programming, *Garbhopaghatakara*, *Garbha Samskara*

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1. Introduction

Congenital malformations and developmental disorders affect approximately 35% of all births globally, contributing to 20-30% of infant mortality [1]. Despite advances in prenatal diagnostics, the incidence of this condition has not substantially declined. Ayurveda, the traditional Indian medical system, has long emphasized preventive measures before conception to ensure a healthy child. Central to this framework is the concept of six procreative

factors (*Shad garbhakara Bhavas*): *Matrija* (maternal), *Pitrija* (paternal), *Rasaja* (nutritional), *Satmyaja* (constitutional/environmental adaptability), *Atmaja* (soul/consciousness), and *Sattvaja* (psychological essence) [2]. A harmonious combination of these factors is essential for healthy progeny.

Within this schema, deviations in modifiable factors (*Rasaja*, *Satmyaja*, and *Sattvaja*) during gestation

constitute *Garbhopaghatakara Bhava* factors that “harm or destroy the fetus or its development” [3,4]. These include specific dietary incompatibilities (*Viruddha Ahara*), lifestyle excesses (*Ativyayama*, *Divaswapna*), psychological disturbances (*Krodha*, *Shoka*, *Bhaya*), and traumatic injuries (*abhighata*). Concurrently, the field of epigenetics has revealed that environmental exposures during critical developmental windows induce heritable changes in gene expression without altering the DNA sequence, a process known as developmental programming [5,6]. The prenatal

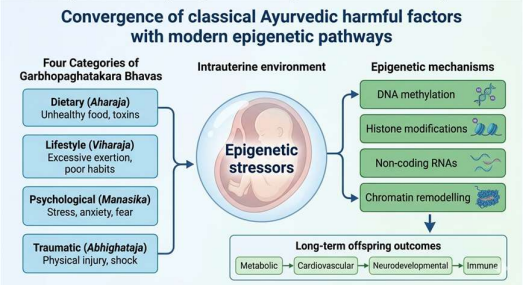


Figure 1: Conceptual convergence of Garbhopaghatakara Bhavas with modern epigenetic pathways

2. Methods

This narrative review was conducted by searching the PubMed and Scopus databases for peer-reviewed- articles published between 1990 and 2025 using the keywords “epigenetics,” “prenatal programming,” “maternal stress,” “maternal nutrition DNA methylation,” “Ayurveda antenatal,” “Garbhopaghatakara,” and “Garbha Samskara.” Classical Ayurvedic texts (Charaka Samhita, Sushruta Samhita, and Ashtanga Hridaya) were consulted in Sanskrit with standard English translations. Only human studies and high-quality-animal studies that directly informed human mechanisms were included. No citation is provided in this Methods section, as per the author’s instruction.

Table 1: Classification of Garbhopaghatakara Bhavas

Cate gory	Specific Factors	Example from classical texts
Diet ary (Aha raja)	Viruddha Ahara (incompatible foods), Ruksha (dry), Atiushna (excessively hot), Atishita (excessively cold), Atilavana (excessivel y salty)	Consump tion of mutually contradic tory foods causing A ma (meta bolic toxins) and fetal distress

period is a uniquely sensitive window during which epigenetic marks are established and can influence long-term- health outcomes.

This review synthesizes classical Ayurvedic concepts of *Garbhopaghatakara Bhavas* with contemporary epigenetic science, examining whether these harmful prenatal factors can be understood as inducers of adverse epigenetic modifications. This study also explored whether Ayurvedic antenatal interventions offer a systematic approach to preventing such modifications and promoting healthy fetal programming.

Garbhopaghatakara Bhavas and epigenetic mechanisms

3. Conceptual Framework: Garbhopaghatakara Bhavas in Ayurveda

3.1 Definition and origin

Garbhopaghatakara Bhava is derived from *garbha* (embryo/fetus), *upaghata* (injury/har m), and *kara* (causing). These factors are systematically enumerated in *Garbhini Paricharya* (antenatal care protocols) across the major Samhitas [3,4]. Approximately 10%-20% of all pregnancies end in miscarriage, with 75% occurring before the 16th week. Traditional texts attribute many of these to inadvertent exposure to contraindicated factors [3].

3.2 Classification of Garbhopaghatakara Bhavas

Based on classical literature, *Garbhopaghatakara Bhavas* are categorized into four groups [3,4,7] as mentioned in Table 1:

Lifes tyle (Vih araja a)	Divaswapna (day sleep), Ativyayama (excessive exercise), Ativyavaya (excessive intercourse), Vega Dharana (suppression of natural urges)	Prolonge d standing or heavy lifting leading to Garbh asrava (t hreatened miscarria ge)
Psyc holog ical (Ma nasi ka)	Krodha (anger), Shoka (grief), Bhaya (fear), Irshya (jealousy), Chinta (anxiety)	Maternal bereavement affecting fetal neurodev elopment

Traumatic (Ab)	<i>Patana</i> (falls), <i>Tada</i> (blows), <i>Peedana</i> (compression)	Abdominal trauma in late
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high ataja)		pregnancy
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3.3 The *Shadgarbhakara Bhavas* as an epigenetic template

The six procreative factors, *Matrija*, *Pitrija*, *Rasaja*, *Satmyaja*, *Atmaja* and *Sattvaja*, collectively determine the offspring phenotype [2]. While *Matrija* (maternal), *Pitrija* (paternal) and *Atmaja* (soul/consciousness) are considered immutable at the individual level, *Rasaja* (nutritional), *Satmyaja* (constitutional/environmental adaptability), and *Sattvaja* (psychological essence) are modifiable through lifestyle, diet, and mental cultivation [2,7]. The Ayurvedic concepts of *Beeja*, *Beejabhaga*, and *Beejabhagavayava* progressively subtler genetic units demonstrate an understanding of hereditary transmission analogous to the chromosomal, genic, and subgenic levels [8]. Deviations in these modifiable factors constitute the core of *Garbhopaghatakara Bhava*.

This tripartite distinction between the immutable core and modifiable epigenetic influences aligns with the modern understanding that while the germline genome is fixed at conception, the epigenome remains highly plastic, especially during gestation and early postnatal life [5,6].

4. Epigenetic Mechanisms of Developmental Programming

4.1 Fundamentals of epigenetics

Epigenetics refers to the molecular processes that regulate gene expression without altering the DNA sequence. The principal mechanisms are as follows:

1. DNA methylation involves the addition of methyl groups to cytosine residues in CpG islands, which typically represses transcription. Methyl groups are derived from dietary methyl donors (folate, choline, methionine, and vitamin B12) via one-carbon- metabolism [9].
2. Histone tail modifications, including acetylation, methylation, phosphorylation, and ubiquitination, alter chromatin structure and gene accessibility [10].
3. Non-coding- RNAs, microRNAs (miRNAs), and long non-coding- RNAs (lncRNAs) regulate gene expression post-transcriptionally-. Sperm-derived-ncRNAs- have been implicated in transgenerational inheritance [11].

These mechanisms enable the environment to “write” the genome, establishing transcriptional programs that can persist for decades or across generations [12].

4.2 Epigenetic programming during critical windows

The prenatal period is a developmental “critical window” of heightened epigenetic sensitivity to

environmental exposures. During embryogenesis and fetal growth, the epigenome undergoes waves of reprogramming and erasure of parental imprints, followed by the establishment of new tissue-specific- methylation patterns. Nutritional insufficiency, hormonal imbalances, or toxicant exposure during these windows can perturb normal programming [5,13], leading to:

- Metabolic syndrome (altered *PPARγ*, *GLUT4*, *leptin* methylation) [14]
- Cardiovascular disease (methylation changes in *eNOS*, *ACE*)
- Neurodevelopmental disorders (altered *BDNF*, *GABA* receptor methylation) [15]
- Immune dysregulation (altered *FOXP3*, cytokine gene methylation)

4.3 Transgenerational inheritance

In some cases, environmentally induced epigenetic changes can be transmitted across generations, an observation that aligns with Ayurvedic recognition of *Beeja-Beejabhaga-*

Beejabhagavayava transmitting constitutional vulnerabilities [8]. Animal models provide strong evidence for transgenerational epigenetic inheritance, and preliminary human data suggest that ancestral stress, poor nutrition, and toxicant exposure may affect the health of future generations [12,16]. However, true transgenerational effects (beyond F2) in humans remain debatable, with most studies showing intergenerational rather than multigenerational transmission [11].

5. Convergence: *Garbhopaghatakara Bhavas* as Epigenetic Stressors

5.1 Maternal nutrition as an epigenetic modifier

The most extensively documented epigenetic influence in humans is prenatal nutrition (PN). The Dutch Hunger Winter cohort (1944-1945) demonstrated that periconceptional famine induced persistent DNA methylation changes at the *IGF2* locus, associated with increased metabolic and cardiovascular disease risk six decades later [17]. Subsequent systematic reviews have confirmed that maternal undernutrition or overnutrition of protein, fat, fructose, and methyl group- donor nutrients alters offspring DNA methylation patterns, contributing to obesity, insulin resistance, and dyslipidemia [13,14].

Ayurveda’s *Masanumasika Pathya* (monthly dietary regimen) provides a structured nutritional plan for pregnant women. Classical texts prescribe *Ghrita* (clarified butter), milk, honey, and specific herbs to nourish the fetal *Dhatu*s as they are formed sequentially [18,19]. These foods contain bioactive polyphenols, butyrate, and methyl donors

(folate, choline, and vitamin B12), which influence DNA methylation and histone acetylation. Thus, Ayurvedic dietary prescriptions can be reinterpreted as systematic interventions that support optimal epigenetic programming [20].

5.2 Maternal stress and mental state (Sattvaja Bhava)

Sattvaja Bhava the quality of maternal consciousness and mental state is a modifiable factor with profound fetal impact. Classical texts warn that *Krodha* (anger), *Shoka* (grief), *Bhaya* (fear), and *Chinta* (anxiety) during pregnancy constitute *Garbhopaghatakara Bhavas* [4,7].

Modern studies confirm that maternal psychological distress activates the maternal-placental-fetal HPA axis, elevating cortisol levels that cross the placenta and alter fetal brain development. A systematic review of 25 studies found that prenatal stress, including perceived stress, anxiety, and depression, is associated with offspring DNA methylation changes, particularly at *NR3C1* (glucocorticoid receptor) and *BDNF* [21]. A large meta-analysis of 5,496 mother-child pairs identified differential methylation at CpG sites in *ALKBH3*, *APTX*, *MyD88*, and *UHRF1* genes implicated in neurodegeneration, immune function, global methylation regulation, and schizophrenia risk [22]. Increased *NR3C1* promoter methylation reduces hippocampal glucocorticoid receptor expression, impairing the negative feedback of the stress response [15,23].

Table 2: Specific *Garbhopaghatakara* factors and their epigenetic correlates

Classical <i>Garbhopaghatakara</i> Factor	Proposed Epigenetic Mechanism	Representative Modern Evidence
<i>Viruddha Ahara</i> (incompatible diet)	DNA methylation changes at metabolic genes (<i>MC4R</i> , <i>POMC</i>)	High-fat/sucrose diets alter <i>MC4R</i> and <i>POMC</i> methylation, increasing obesity risk [14]
<i>Krodha</i> (anger)	<i>NR3C1</i> (glucocorticoid receptor) promoter hypermethylation	Prenatal stress increases <i>NR3C1</i> methylation, impairing HPA axis feedback [21,23]

6. Ayurvedic Interventions as Epigenetic Therapeutics

6.1 *Garbhini Paricharya*

The comprehensive Ayurvedic antenatal protocol *Garbhini Paricharya* includes: monthwise diet (*Masanumasika Pathya*), daily and seasonal routines (*Dinacharya* and *Ritucharya*), psychological support (*Sattvavajaya Chikitsa*), herbal formulations (e.g., *Kasherukadi*

Conversely, positive maternal mental cultivation of *Sattva* (clarity and harmony) may induce beneficial epigenetic changes. Pilot studies on meditation suggest effects on DNA methylation of inflammation-related genes and telomere length, supporting the Ayurvedic emphasis on maternal emotional well-being- [24].

5.3 Lifestyle factors (*Viharaja*)

Ayurveda categorizes numerous lifestyle factors as *Garbhopaghatakara* as described in Table 2 such as : *Divaswapna* (day sleep), *Ativyayama* (excessive exercise), *Ativyavaya* (excessive intercourse), and *Vega Dharana* (suppression of natural urges) [3,4]. While some operate through mechanical pathways (e.g., uterine irritability), others act through epigenetic mechanisms. For example, excessive exercise induces oxidative stress, which can alter DNA methylation patterns at the promoters of metabolic genes [25].

Environmental toxins (heavy metals, endocrine disruptors, and air pollution) are recognized as epigenetic toxicants that induce DNA methylation changes at imprinted genes, alter histone modification patterns, and dysregulate miRNA expression [26]. Ayurveda's emphasis on a clean, calm, and pure environment for pregnant women, free from noise, conflict, and physical contaminants, represents an intuitive form of exposure prevention that aligns with environmental epigenetics.

<i>Ativyayama</i> (excessive exercise)	Oxidative stress-induced <i>PGC-1α</i> methylation	Extreme maternal exercise associated with intrauterine growth restriction in animal models [25]
<i>Abhighata</i> (trauma)	Inflammatory cytokine gene (<i>IL-6</i> , <i>TNF-α</i>) hypomethylation	Placental trauma upregulates pro-inflammatory epigenetic programmes [27]
<i>Chinta</i> (anxiety)	<i>BDNF</i> and <i>SLC6A4</i> methylation changes	Maternal anxiety associated with altered <i>BDNF</i> methylation in cord blood [21,22]

Yoga, Atibala), and explicit contraindications (*Garbhopaghatakara Bhavas*) [18,19,28]. This systematic program aims to shape the intrauterine environment for optimal fetal programming.

6.2 *Garbha Samskara* as epigenetic programming
Garbha Samskara the “refinement” of the fetus is a uniquely Ayurvedic approach to positive prenatal programming. It includes preconception preparation (*Garbhadana Samskara*), antenatal cultivation

(reading uplifting literature, listening to harmonious music, engaging in creative activities, and maintaining a positive emotional state), and postnatal reinforcement (breastfeeding, infant massage, and early childhood nurturing) [20,29]. Several authors have proposed *Garbha Samskara* as a structured form of epigenetic programming that may mitigate adverse modifications induced by *Garbhopaghatakara* exposure [20,29]. Although direct experimental evidence is lacking, this proposal is mechanistically plausible, given the known effects of maternal sensory and emotional experiences on fetal neurodevelopment.

6.3 *Garbhashthapaka Dravyas*

Classical texts enumerate *Garbhashthapaka Dravyas* (pregnancy-stabilizing- substances) herbs and formulations that counteract the effects of *Garbhopaghatakara Bhavas*. Common examples include *Atibala* (*Abutilon indicum*), *Kashmaryadi Ghrita*, and *Madhukadi Dravya*. A randomised controlled trial of *Kashmaryadi Ghrita* in women with recurrent pregnancy loss showed a significant reduction in abortion rates (RR = 0.42, 95% CI 0.220.80) [30]. These herbs possess antioxidant, anti-inflammatory-, and uterine-relaxant- properties that may protect against oxidative stress-induced-epigenetic damage, although direct epigenetic studies are not yet available.

7. Discussion

The conceptual alignment between *Garbhopaghatakara Bhavas* and epigenetic developmental programming is substantial [2,5,6]. Both frameworks assert that the prenatal environment, encompassing maternal diet, lifestyle, psychological state, and physical exposures, leaves a durable molecular imprint on the developing organism, shaping health and disease susceptibility throughout life [3,4,13]. Classical Ayurvedic scholars, through systematic clinical observation over millennia, identified a core set of harmful prenatal factors that modern molecular science is now validating through the lens of DNA methylation, histone modification, and non-coding-RNA regulation [7,17,22].

Several specific convergences deserve emphasis in this study. First, the Ayurvedic distinction between immutable factors (*Matrija*, *Pitrija*, *Atmaja*) and modifiable factors (*Rasaja*, *Satmyaja*, *Sattvaja*) mirrors the modern separation of germline genetics from epigenetic plasticity [2,8]. This suggests that classical authors understood that while the basic blueprint (genome) is fixed, the execution of that blueprint can be influenced by the environment, a remarkable insight predating epigenetics by two millennia. Second, the monthly dietary regimen (*Masanumasika Pathya*) anticipates the concept of critical developmental windows [5,18,19]. Each month of pregnancy corresponds to the formation of specific fetal tissues (*Dhatus*), and the prescribed foods provide nutrients that are known to act as

methyl donors or histone modifiers when those tissues are being patterned [9,14]. Third, the emphasis on the maternal mental state (*Sattvaja Bhava*) as a *Garbhopaghatakara* factor is strongly supported by the growing literature on prenatal stress and offspring DNA methylation [21,22,23]. However, this integration also reveals significant gaps. No direct human study has measured epigenetic marks in the offspring of mothers who adhered to or violated *Garbhopaghatakara* guidelines [20]. The heterogeneous nature of classical sources and the different Samhitas offer varying lists, complicating standardization for research purposes [7]. Most mechanistic evidence has been derived from animal models or observational human studies with residual confounding (e.g., socioeconomic status and maternal education) [11,12]. Adherence to Ayurvedic guidelines is often correlated with better overall health behaviors and higher social support, making it difficult to isolate the specific effect of avoiding *Garbhopaghatakara Bhavas* [28].

Despite these limitations, the framework has several practical implications. For integrative antenatal care, Ayurvedic guidelines can complement standard obstetric care by providing a culturally grounded and mechanistically plausible set of recommendations for optimizing fetal programming [19,20]. For public health in resource-limited-settings, the systematic and practical nature of *Garbhopaghatakara* guidelines renders them suitable for community-level- health education [3,4]. For future research, the priority should be prospective cohort studies that collect detailed data on *Garbhopaghatakara* exposure during pregnancy and measure epigenetic outcomes in cord blood and the placenta [21,22]. Randomized controlled trials of structured *Garbha Samskara* interventions versus standard antenatal care would provide the highest level of evidence [20,29,30].

8. Conclusion

Garbhopaghatakara Bhavas represent a prescient epigenetic framework for developmental programming. The intrauterine environment shaped by maternal diet, lifestyle, psychological state, and physical exposures leaves durable molecular imprints on offspring through DNA methylation, histone modifications, and non-coding RNAs. Classical Ayurvedic scholars identified harmful prenatal factors that modern epigenetics has now validated. Ayurvedic antenatal protocols, including *Garbhini Paricharya* and *Garbha Samskara*, offer systematic and culturally grounded interventions that may promote optimal epigenetic programming. The convergence of ancient wisdom and contemporary molecular science provides a compelling basis for integrative preventive healthcare. Rigorous translational research prospective cohorts and randomized trials are

required to transform this conceptual alignment into evidence-based- practice.

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Conflict of Interest

The authors declare no competing interests.

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