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Studies on the Assimilation of Zoroastrians into Indian Society with Special Reference to Sanjan, India: A Review

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Abstract

This paper presents an overview of multidisciplinary research conducted on human skeletal remains excavated from Sanjan, located on the northern bank of the Varoli River in Umargam Taluka, Valsad District, Gujarat. The excavation, carried out during the 2002–2003 season at *Dokhama*, a Parsi funerary site dating to the 14th–15th centuries A.D., uncovered the partial remains of at least 180 individuals.The recovered skeletal material has been analyzed through a combination of bioarchaeological, ancient DNA (aDNA), and ethnographic methods. This integrated approach offers valuable insights into the biological history and cultural identity of the Parsi community in India. The research aims to trace population dynamics, health patterns, and genetic interactions between Parsis and local Indian groups.The earliest significant study, published in 2011, involved a comparative analysis of dental morphology in both ancient and modern populations. The findings indicated early signs of admixture between the migrant Parsi population and local communities. For the first time in Indian anthropological research, these results were further validated by aDNA analysis. The genetic evidence confirmed a pattern of maternal gene flow from local Indian women into the Parsi gene pool, suggesting sustained assimilation over centuries.Together, these studies contribute to a more nuanced understanding of Parsi migration, settlement, and integration in India. They demonstrate how bioarchaeology and genetics, when combined, can illuminate complex processes of cultural and biological exchange in diasporic communities.

Keywords: Zoroastrian Diaspora, Parsi Migration, Bioarchaeology, Dental Morphology, aDNA, Admixture.

Article Type: Review Article

Introduction

The interdisciplinary investigation of migratory communities offers unique insights into the complex processes of biological continuity, cultural integration, and genetic admixture. The Zoroastrian migrants from Iran to India—known as the Parsis—represent one of the most significant historical examples of such dynamics. Following the collapse of the Sasanian Empire and increasing religious pressures after the Arab conquests, this group sought refuge along the western coast of India, particularly in the region of Sanjan in present-day Gujarat. Their settlement marked the beginning of a diasporic community that maintained key elements of its religious and cultural identity in a new sociocultural context.

According to historical sources, most notably the *Qissa-i Sanjan*, composed circa 1600 CE, the initial wave of migration occurred during the early Islamic centuries, culminating in the establishment of a Zoroastrian enclave in Sanjan. Archaeological excavations at the Sanjan dokhama—conducted during the 2002–2003 field seasons—have unearthed substantial evidence of this early settlement, including human skeletal remains, ritual architecture, and culturally distinctive artefacts. These findings provide a rare opportunity for an integrated analysis employing bioarchaeological, ancient DNA (aDNA), and ethnographic methods.

The multidisciplinary research conducted on the Sanjan skeletal assemblage has revealed key patterns in the demographic, biological, and genetic

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history of the early Parsi population. These include indications of genetic continuity with Iranian populations, evidence of male-mediated migration, and, crucially, signs of maternal gene flow from local Indian groups. Such findings are further corroborated by dental morphological comparisons, osteobiographical assessments, and high-resolution genetic analyses of both ancient and modern Parsi samples.

This article presents a critical review of four major studies focused on the human remains from Sanjan, with the aim of reconstructing the patterns of integration, continuity, and transformation within the early Parsi community. In doing so, it highlights the methodological significance of combining bio-archaeological data with genomic research to better understand the historical formation of diasporic identities and the interplay of migration and assimilation over time.

Historical Background

The Parsi is one of the many communities that make up the multicultural fabric of India and consist of less than 60,000 individuals. They are Zoroastrian refugees from Iran, who fled Muslim persecution in their homeland and first landed on the coast of western India around 750 A.D. (Kamerkar and Dhunjisha 2002). It is believed that the Parsis first came to Gujarat, India on the 13th of December 715 AD (Menant 1898: 41) The only indication about the arrival of this group of migrants is contained in a book entitled "Kisseh - e Sanjan", written towards the year 1600, by a mazdien priest, called Bahman Kaikobad Sanjana, who dwelt in Naosari (Edulji 1991; Menant 1898: 41).

The Qissa chronicles the early history of the Parsees (Parsis) - the initial group of Zoroastrians who fled from Iran to India following the Arab conquest of Iran and the overthrow of the last Zoroastrian-Sassanian king of Iran, Yazdegird III in 636 CE. Qissa is an Arabic word meaning 'story', perhaps 'legend'. The name Qissa-e Sanjan means the 'Story (or Legend) of Sanjan'. Sanjan is a small town in the Indian state of Gujarat close to its border with the state of Maharashtra. The Qissa states that Parsi (Indian Zoroastrian) history in India as a community starts with the landing by the original refugees from Iran at Sanjan. It was here that they built their first fire-temple enshrining their most sacred relic, the Iranshah.

Archaeological Excavations at Sanjan

The ancient site of Sanjan (N 20º11'59.6, E 72º48'00.2) was first discovered in 2001. The ancient mound is situated about two kilometres to the north of the modern town of Sanjan on the northern bank of the Varoli River/Creek in the Umargam Taluka of Valsad District, Gujarat (Figure. 1). Medium scale excavation were carried out for three seasons, jointly by the World Zarathusti Cultural Foundation, Mumbai and Indian Archaeological Society, New Delhi, at three different locations of the site, *Sanjan bandar* (SJN-B), Sanjan kolikhadi (SJN-K) and Sanjan *dokhama* (SJN-D).

Excavations conducted over three field seasons have revealed a large number of artefacts, ceramics and structural remains belonging to the period 8th-13th centuries A.D. The preliminary reports of the 2002 and 2003 seasons have been published (Gupta *et al.* 2002, 2004). Sanjan dokhama or the Tower of Silence was the only structure found in Season III (Figure. 2). At the confluence of Kolikhadi and the Tukkar Nala, a steep mound with a circular depression at its top was found. This mound, according to local tradition, was a bhastu – a local word for a dokhama. The dokhama is a mortuary structure consisting of a large circular wall enclosing a raised platform, at the centre of which there is a dry well. This is strictly and uniquely Zoroastrian in nature. The dead body is exposed to the natural elements (devoid of garments and ornaments) on this platform and after a time, any osseous remains are swept into the central well. It is in this manner that the Parsis adhere to the Zoroastrian strictures against the pollution of the elements by the dead (Figure. 3). Thus, this structure strongly suggests of the settlement of a Parsi community. Therefore, it was decided to take up excavations at this mound since if a dokhama did in fact exist, it would be the clinching evidence of Parsi occupancy at Sanjan during the 8th to the 13th century. If so, this site would be the oldest Parsi settlement ever to be excavated.

For precise dating human bones recovered from the *dokhama* were sent to Radiocarbon Accelerator Unit, Research Laboratory for Archaeology and the History of Arts, Oxford University, Oxford, UK for AMS dating. The result gives very consistent dates confirming that the dokhama was in use in the 14th and 15th century A.D. (Mushrif-Tripathy and Walimbe 2012).



Figure. 1: *Geographical location of the archaeological site of Sanjan (After: Google Earth 15/08/2024 and modified by Author).*



Figure. 2: *Excavation at central well at dokhama, Sanjan (After: Mushrif-Tripathy and Walimbe 2012)*

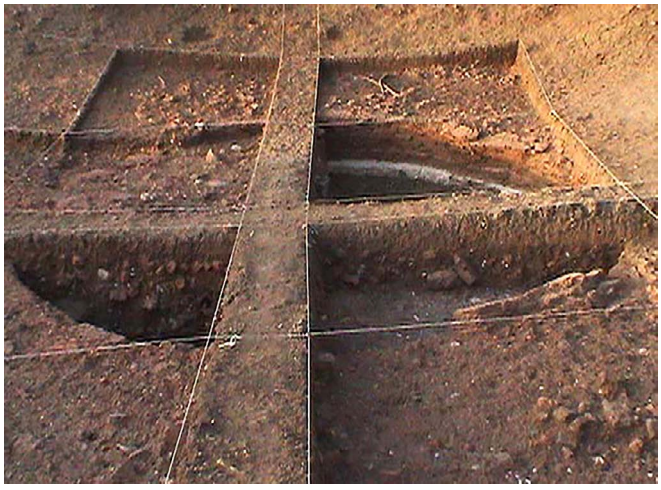


Figure. 3: *Lime plaster at well, Sanjan (After: Mushrif-Tripathy and Walimbe 2012)*

Careful excavation of the dokhama revealed the remains of at least 180 individuals in about 40% of the *bhandar*. Exact estimates were not possible on site as the bones were disarticulated and lying scattered, showing no specific arrangements or orientation. Tentative estimates were based on the fact that approximately 134 skulls or parts thereof were recovered (Figure. 4). The remains were those of a wide spectrum of age groups – newborns, children, adults and old adults. Besides human bones the *dokhama* also yielded a large number (or fragments) of glass bangles, rings of copper, silver and mixed metal, and beads of glass. Parsi women wore and continue to wear glass bangles as a symbol of their married status, as is the rings worn as a toe ornament. These traditions were borrowed from contact with autochthonous Indian groups, as the same were not extant in Iran. A tradition grew whereby women were interred upon death into the *dokhama* with their ornaments. This tradition probably discontinued only about 200 years ago. Excavations in the *bhandar* also revealed a small gold bead and a copper earring with gold caps at either end.

Methodology

The present paper summarizes the findings of the four major studies on the Sanjan skeletal remains in relationship of biological continuity in which the present author was completely involved. It is a known fact that the Parsi community practices strict endogamy. This resulted in a small inbreeding community that remained reproductively isolated from the neighboring populations. Their isolation has resulted in the continuity of their gene pool, which is rarely seen among populations. Owing to their cultural practices i.e., endogamy, there has been very little gene flow between the migrant Parsis and the native population. Therefore it was important to study continuity pattern between zorastrians. The earlier work published in 2011 (Jonnalagadda *et al* 2011) based on the morphological traits of Sanjan dental remains comparing with present Parsi population. The recent studies on aDNA (Chaubey *et al.* 2017) compaired genetic variation data on autosomal and uniparental loci (Y-chromosomal and mitochondrial DNA) of ancient Parsi DNA samples. The last publication (Kumar *et al.* 2023), explores the maternal lineage contributions during the initial settlement phase and generated full mitogenome sequences of 19 human samples from the site. All these studies have given the consistent results. In conclusion part, findings from all these four papers given in tabular form.



Figure. 4: *Lateral aspect of skull from dokhama*
(After: Mushrif-Tripathy and Walimbe 2012)

Anthropological and Dental Analysis

The anthropological study which was conducted (Mushrif-Tripathy and Walimbe 2012) becomes a base line for the further analysis to understand the affinities of these Parsai populations. The research shows the balanced sex ratio with a broad age distribution, suggesting a stable, family-based population rather than a transient or exclusively male migrant group. The infant and child mortality rates were notable, possibly reflecting environmental or nutritional stress. Craniometric comparisons show that the Sanjan population exhibits closer affinities to Iranian groups than to local Indian populations and it strongly supports the historical narrative of migration from Persia, consistent with Zoroastrian accounts of flight from religious persecution in Iran. Although, some traits does indicate minor local admixture, possibly through early assimilation with Indian populations. Thus this osteobiographic study provides biological and cultural evidence supporting the historical narrative of Zoroastrian (Parsi) migration from Iran to India. It also shows a well-established, biologically distinct, but gradually integrating community living in medieval Sanjan. The findings contribute significantly to understanding Parsi demographic history, health, and adaptation in a new environment.

Dental morphological features such as size, shape and form are genetically determined. These features show variations among different popula-

tions, which is a result of evolutionary forces such as natural selection, gene flow and genetic drift making them useful variables for assessing biological relationships and micro evolutionary trends (Scott and Turner 1997), and also estimating the relative degree of similarity among groups that have diverged from common ancestors hundreds or thousands of years ago. From the 784 permanent teeth that were excavated from the Sanjan Dokhma structure, a total of 382 teeth were examined in the study (Figure. 5). In the case of the extant Parsi sample, permanent dental casts were taken from 50 Parsi individuals (25 males and 25 females) within 15–40 years from the city of Pune (Figure.6). The individuals were selected using a snowball sampling technique (Goodman 1961) and their dental impressions were taken using Alginate powder. Positive casts were made using dental stone plaster (Dental Products of India, Mumbai) by the procedure explained by Walimbe and Kulkarni (1993). From the collected casts 292 teeth are used in this study for comparison (Jonnalagadda *et al.* 2011).



Figure.5: *Representation of dental morphology, dokhama*
(After: Mushrif-Tripathy and Walimbe 2012)



Figure. 6: *Dental cast of maxilla from modern Parsi individual*
(After: Jonnalagadda et al. 2011)

It was observed that the extant Parsis and Sanjan samples are distantly separated from each other as indicated by MMD values and trait frequencies. Extant Parsis are seen to exhibit closer affinities to contemporary Maharashtran groups. It is important to note that these results may be an effect of small size of both extant Parsi and Sanjan samples, and the low number of dental traits used for the purpose of analyses. Two-dimensional ordination identifies distant affinities between the two Parsi samples. Extant Parsis are most similar to contemporary Maharashtiran groups than South Asian and Central Asian groups. 2D plot shows distantly positioned clusters of Central Asian and Maharashtran groups. Extant Parsis are placed closer to low caste Mahars and high caste Marathas than tribal Madia Gonds. Sanjan sample like Papago Indians is distant from all other groups including extant Parsis.

Genetic Studies and aDNA Findings

Previous genetic analyses of the Parsis have focused mainly on low-resolution uni-parental markers, which have suggested their affinity with both West Eurasian and Indian populations (Qamar *et al* .2002, Quintana-Murci *et al.* 2004, Rosenberg *et al* .2006). Autosomal analysis based on microsatellites or human leukocyte antigens (HLA) have revealed their intermediate position among the populations of South Asia and the Middle East/Europe (Mohyuddin and Mehdi 2005, Rosenberg *et al.* 2006). A study of mitochondrial DNA (mtDNA) variation reported 60% of South Asia lineages among the Pakistani Parsi population, whereas the male lineages based on Y chromosome admixture estimates were almost exclusively Iranian. Based on these results, a male mediated migration followed by assimilation of local South Asia females was concluded.

The present analysis discuss the genome-wide genotyping array data from 43 and high-resolution mtDNA and Y-chromosome genotyping data from 174 Parsi samples from India and Pakistan as well as genotype of mtDNA polymorphisms from 21 ancient Parsi samples excavated from site of Sanjan (Chaubey *et al.* 2017). The inquries were made on the lines of a) whether the current Parsi people living in India and Pakistan are genetically related amongst themselves and with the present-day Iranian population; b) since Parsis diverged from Iranians just after this conquest, whether they represent the genetic strata of Iran before the Islamic con-

quest; c) to estimate the time of admixture between Parsis and their neighboring South Asian populations; d) to determine the nature of the gene flow and admixture of Parsis with their parental (Iranian) and neighboring (Gujarati and Sindhi) populations and e) is there any sex-specific admixture between South Asian and Iranian ancestries.

To comprehend the degree to which the current Parsi populations assimilated local females during their long formation history, the mtDNA haplogroup composition with ancient remains excavated in Sanjan, the initial settlement established by these migrants from Persia were compared with various populations. The combined Parsi data set was merged with a global data set from the published literature (Chaubey *et al.* 2011, Metspalu *et al.* 2011, Raghavan et al 2014). The mean allele frequency differentiation between the two Parsi (Indian and Pakistani) groups was the lowest suggesting a common stock for both the Indian and Pakistani Parsis with the closest inter population affinity with populations from their putative homeland, Iran.

The first and second principal components (PCs) plot of the population-wise mean of the eigen values showed their placement between the Pakistani and Iranian populations, indicating that the Parsis might have admixed from these two groups. Such an intermediate position of Parsis closer to Iranians than to their present geographic neighbors (Sindhi and Gujarati) suggests that the Parsis may have major ancestry from West Eurasians (Iranians) and minor ancestry with South Asians. At the same time it is seen that the present-day Iranian population exhibited a striking difference from the Parsis, mainly in carrying an additional European component and substantially lower South Asian ancestry. Furthermore, the ancestral North Indian ancestry calculated from the f4 ancestry estimate showed a substantially higher level of this ancestry among Parsis than any other South Asia population (Figure.7).

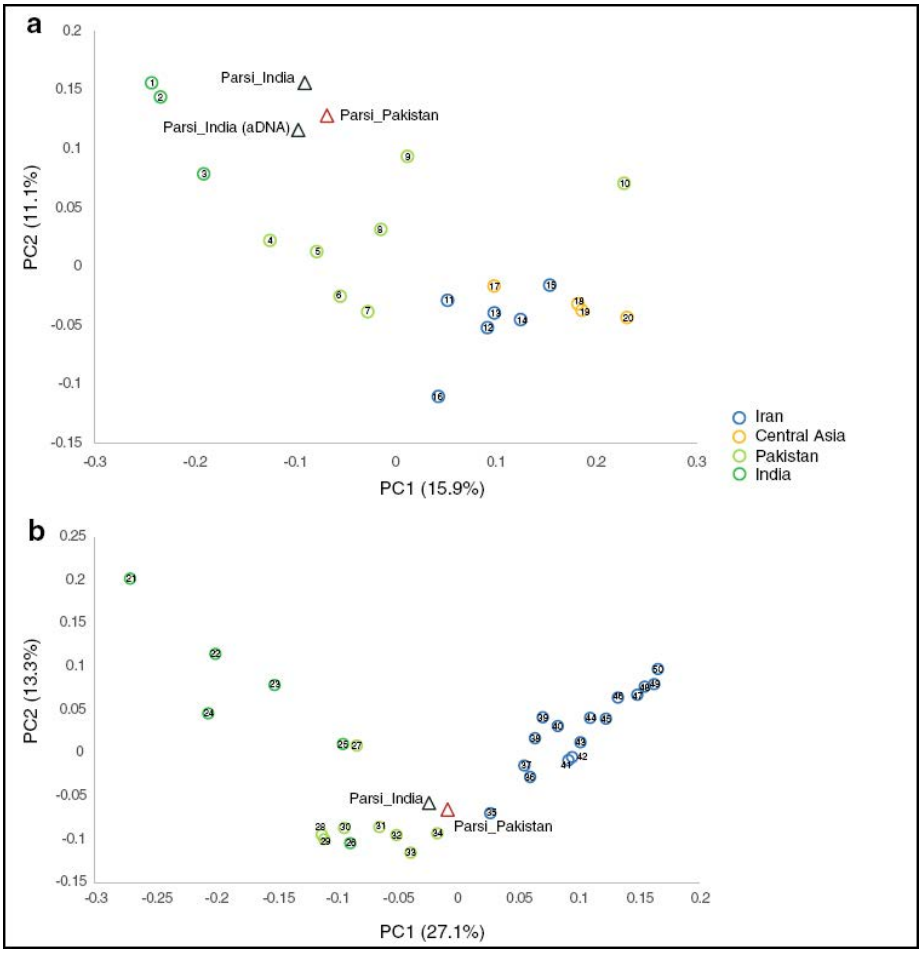


Figure. 7: *Principal component analysis using haplogroup frequencies for a mtDNA and b Y chromosome in Parsi, Iranian, Central Asian, Pakistani, and Indian populations (After: Chaubey et al. 2017)*

The formal test of admixture f3 statistics shows that for Iranians, a negative value with significant Z scores supports the hypothesis that they are descendants of a population formed by the admixture of Neolithic Iranians and populations from the Arabian Peninsula, while for Parsis this test was positive with significant Z scores. After using computed D statistics it was seen that there is a significant level of genetic affinity between Parsis and Neolithic Iranians the South Asian populations (Gujarati and Sindhi). This in further establish significant levels of gene flow with each other, as well as with both of the Parsi populations when evaluated with respect to the present-day Iranian population. This analysis aligned the Parsis closer to the Iranian axis between Pakistani and West Eurasian populations, supporting the historical interpretation of the most recent common ancestry of Parsis with the Iranians.

The computation of a maximum likelihood tree and co-ancestry matrix based on the haplotype structure of the Parsi populations shows likelihood tree split South Asian and West Eurasian populations into two distinct clusters. The fine STRUCTURE and D statistic results largely suggest unidirectional minor gene flow from South Asians to Parsis. To estimate the time of admixture between Parsis and their neighboring South Asian populations ALDER method based on linkage disequilibrium was used. The present-day Iranian vs Gujarati or Sindhi populations as their surrogate ancestors were used for this analysis. It estimated that the admixture time of Parsi groups was to be around ~40 generations (95% CI 26–50), which yields a time of 1160 years (assuming a generation time of 29 years), in good agreement with their historically recorded migration to South Asia.

To understand a details of the sex-specific South Asian and Iranian ancestries, we examined maternally inherited mtDNA and paternally inherited Y chromosome biallelic polymorphisms in a larger sample in both the Indian and Pakistani Parsi populations. Interestingly, it is observed 48% South-Asian-specific lineages (haplogroups M2, M3, M5, and R5) among the ancient Parsi samples, which could potentially be explained in two ways. First, these haplogroups might have been carried by the migration of Zoroastrian refugees from Fars (Iran), a possibility that is supported by the presence of these clades in present day Persian samples (9.9%). Second, they might have resulted from the assimilation of local females during the initial settlement. The comparison of ancient and modern samples thus identified maternal lineages that can be considered as founding (surviving or lost), as well as those that were subsequently assimilated. For mtDNA, the Parsi cluster was closer to the Indian and Pakistani cluster, whereas for the Y chromosome it aligns between the Iranian and Pakistani populations. The Y chromosomal PCA is similar to the autosomal PCA. The contrasting patterns of maternal and paternal ancestry support a largely female-biased admixture from the South Asian populations to the Parsis.

Recently the study has been published (Kumar *et al.* 2023) where the authors sequenced and analyzed the complete mitochondrial genomes (mitogenomes) of 19 archaeological samples from Sanjan. Previous genetic studies of the Parsi community—comprising autosomal, Y-chromosomal, and partial mitochondrial data—had already indicated a dual ancestry rooted in both West Eurasian (Iranian) and South Asian origins. However, maternal lineage analysis remained underexplored at high resolution (Pathak *et al.* 2019). To fill this gap, the authors generated full mitogenome sequences of ancient remains in order to clarify maternal lineage contributions during the initial settlement phase.

DNA was extracted from ancient bone samples and sequenced using high-throughput methods tailored for degraded ancient DNA. Once complete mitogenomes were assembled, the team conducted phylogenetic analyses—including Maximum Likelihood and Bayesian models—comparing the ancient samples to modern reference populations across West Eurasia and South Asia.

Key Findings

•All individuals belonged to mitochondrial haplogroup M3a1+204, a lineage primarily associated with South Asia but also identified in West Eurasia.

•Phylogenetic trees demonstrated that the ancient Parsi mitogenomes cluster alongside both South Asian and Middle Eastern individuals, revealing shared maternal ancestry between these regions.

•This haplogroup's historical presence in populations such as medieval Swat Valley (in current-day northern Pakistan) and Roopkund indicates an ancient maternal gene flow connecting broadly across geography.

•Phylogenetic network analysis confirmed shared haplotypes between the Sanjan Parsis and both modern South Asian and Middle Eastern individuals, demonstrating admixture on the maternal side.

This study marks the first ancient mitogenomic analysis of early Parsi settlers and provides high-resolution evidence of maternal admixture. The results reveal a maternal ancestry comprising both South Asian and Middle Eastern components, indicating that assimilation through marriage and integration of local women occurred from the initial migration phase. These insights deepen our understanding of Parsi demographic history and highlight the power of ancient DNA to illuminate complex migration and integration narratives.

Discussion and Comparative Synthesis

If we compare the above researches specifically discussing Sanjan and their habitant, following observation can be made (Table. 1). This indicate despite practice of strict endogamy, closeness of extant Parsis with Maharashtran groups' indicates that some admixture of Parsi populations with local groups in India might have occurred. This is supported by mtDNA study by Quintana-Murci *et al.* (2004) which was conducted among the Parsis of Pakistan. In contrast to mtDNA, Y-chromosome study (also among Parsis of Pakistan) (Qamar *et al.*2002) shows that they resemble Iranian populations rather than their neighbours in Pakistan and support the historical records of Iranian origin of Parsis. Based on the diversity of both Y-chromo-

Table. 1: *Comparison of four Key Studies on Parsi Population History*

Aspect	**Jonnalagadda *et al*. (2011)**	**Mushrif-Tripathy and Walimbe (2012)**	**Chaubey *et al*. (2017)**	**Kumar *et al.* (2023)**
Main Focus	Dental comparison of Parsi remains	Osteobiographic study of Sanjan skeletal population	Genetic history of Parsis (ancient + modern DNA)	Ancient maternal lineage (mtDNA) of Parsis
Type of Data	Dental morphology	Skeletal remains: age, sex, pathology, burial context	Autosomal, Y-DNA, and mtDNA (modern + ancient)	Ancient mtDNA from Sanjan site
Sample	Skeletal remains from Sanjan and modern Parsi dental samples	96 individuals from Sanjan	19 ancient + 300+ modern DNA samples	21 ancient mitogenomes from Sanjan
Population Affinity	Closer dental traits to Iranian groups than Indian ones	Iranian affinity with some Indian admixture; family-based settlement	Largely West Eurasian (Iranian) ancestry; post-migration Indian admixture (mainly maternal)	Predominantly West Eurasian mtDNA; limited early Indian input
Sex-specific Data	Not addressed	Adult male/female analysis;	Iranian paternal lines; Indian maternal contribution	Emphasis on maternal (female) lineages
Health & Diet	Not studied	Moderate nutritional stress; mixed diet; dental wear	Not applicable	Not applicable
Cultural Identity	Not discussed	Suggests cultural cohesion	"Like sugar in milk": cultural integration with genetic distinctiveness	Early settlers maintained distinct genetic identity
Admixture Timing	Post-migration, limited	Early contact, but minimal genetic integration	After arrival in India, gradually increasing	Little Indian admixture in earliest phase
Methodological Contribution	First dental morphometric study of Parsis	Comprehensive osteobiographic baseline	Most extensive genetic reconstruction of Parsi ancestry	First ancient mitogenomic study of Parsi women

some and mtDNA lineages, Quintana-Murci *et al.* (2004) note that a strong drift effect is unlikely. This pattern therefore supports a male mediated migration of the ancestors of the present-day Parsi population from Iran to India, where they admixed with local females, or directional mating in Gujarat between Iranian males and local women, ultimately leading to the loss of mtDNAs of Iranian origin (Quintana-Murci *et al.* 2004). Hence we contend that admixture with local populations could explain the patterns of divergence between Sanjan Parsis and extant Parsis and that of convergence between extant Parsis and Maharashtran populations.

From the recent papers also it is being emphasized that the Parsis arrived in Indian around 10 the century AD. The result of this migration led to the admixture of this population with locals mainly from maternal DNA.

Conclusion

Interdisciplinary studies on the human remains from Sanjan present a nuanced, multi-layered picture of the biological, cultural, and genetic history of the Parsi community—an immigrant group that, while maintaining core aspects of its identity, gradually assimilated into the socio-cultural and biological milieu of India. Bioarchaeological evidence, including craniometric analyses and demographic profiling, indicates early affinities with Iranian populations. However, genetic data, particularly ancient DNA and mitochondrial analyses, reveal notable maternal gene flow from local South Asian women into the Parsi gene pool.

Recent advances in genomic technologies, especially in ancient mitogenomics, compellingly demonstrate a pattern of gradual biological integration whereby male migrants from Iran intermarried with indigenous South Asian women. This process resulted in a unique blend of Iranian and South Asian ancestry within the Parsi community. This genetic pattern aligns closely with historical narratives such as the *Qissa-i Sanjan* and highlights the community's continuity with its ancestral roots alongside cultural adaptation.

Thus, despite strict endogamous practices, the Parsi population engaged in cultural and genetic exchanges with local populations from the earliest phases of settlement in India. These findings not only enhance our understanding of migration dynamics in South Asia but also offer a valuable model for studying genetic and cultural admixture in diasporic communities. Continued genomic and ethnographic research promises to shed further light on the complex processes of historical assimilation and identity formation.

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