loadings for shoveling and median lingual ridge development on UI2 and full expression of the hypocone on UM1 and UM2. Lowest loadings occur for shoveling and median lingual ridge development on UI1, the presence of the metaconule on UM1 and UM2, and presence of the Y-groove on LM1. Therefore, high scorers along the second component will feature dentitions marked by a high ratio of shoveling and median lingual ridge development on UI2 relative to UI1, by maxillary molars marked by frequent retention of the full hypocone but which lack both Carabelli's trait (UM1) and the metaconule, and by LM1s that are marked by relatively frequent absence of the Y-groove. Low scorers along the second component will feature dentitions marked by relatively low levels of shoveling and median lingual ridge development on UI2, by maxillary molars that exhibit frequent reduction of the hypocone, and by relatively high frequencies of the Y-groove on LM1.

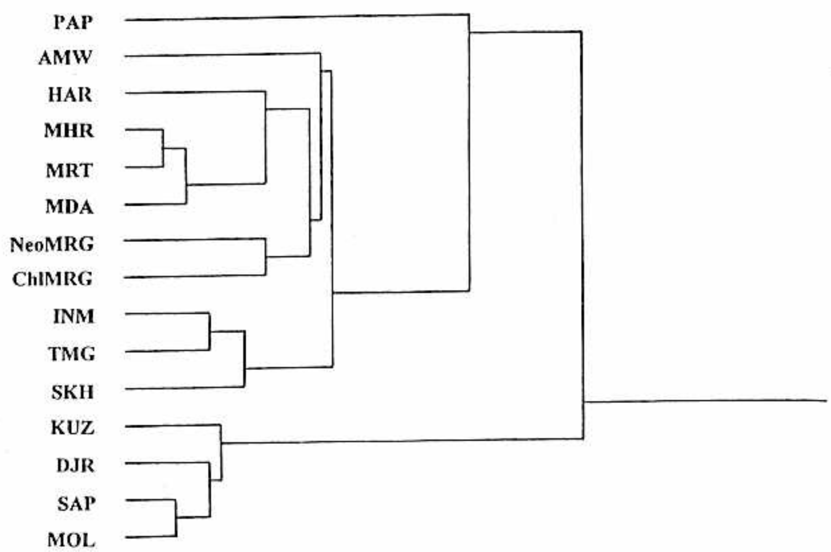

Figure 8. Two-dimensional ordination of multidimensionally scaled standardized MMD values - comparison two.

The third principal component accounts for 11.6% of the total variance. The third component receives relatively high loadings for medial lingual ridge development on the maxillary incisors, retention of the full hypocone on UM2, Carabelli's trait on UM1, presence of the metaconule on UM2, and retention of the hypoconulid on LM1. Conversely, the third component receives relatively low loadings for shoveling on the maxillary incisors, retention of the hypoconulid on LM2, and the presence of the entoconulid on the mandibular molars. Therefore, high scorers

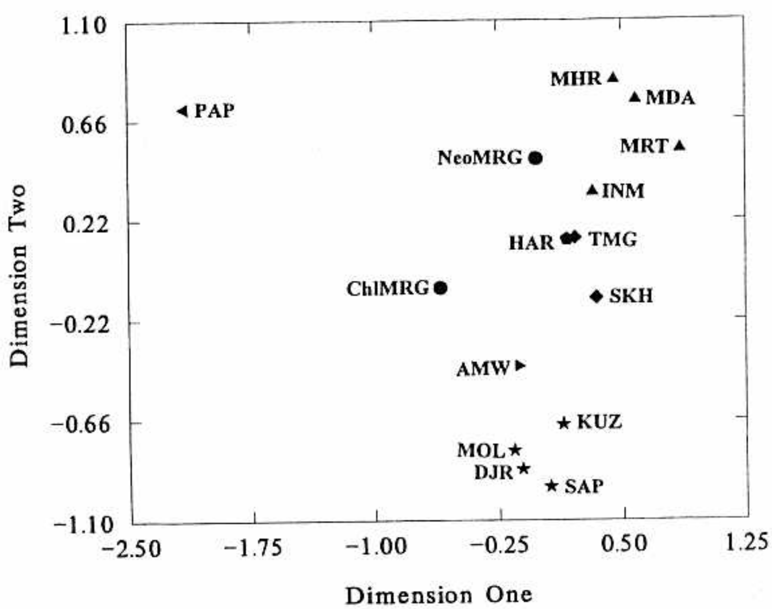

Figure 9. Cluster analysis of arcsine transformed trait frequencies - comparison two.

along component three will possess dentitions that tend to feature frequent presence of medial lingual ridge development but no shoveling on the maxillary incisors, a full hypoconulid and Carabelli's trait on UM1, UM2s which possess the metaconule coupled with UM1s which do not, mandibular molars marked by frequent presence of the hypoconulid on LM1 but by frequent absence of this cusp on LM2, and by mandibular molars which feature the entoconulid. Low scorers along component three will feature dentitions marked by high levels of shoveling but which lack median lingual ridge development, by mandibular molars which feature relatively frequent loss of the hypoconulid on LM1 but retain this cusp relatively often on LM2, as well as by mandibular molars which frequently possess the entoconulid.

Ordination of group scores for the first two principal components is provided in Figure 12. This ordination provides general support for the patterns of affinity depicted by two-dimensional ordination of multidimensionally scaled standardized MMD values (Fig. 9). Once again, the Papago are positively distinguished as the most divergent of the samples included in this analysis. Central Asians too, are identified as a unique group, possessing closer affinities to one another than to

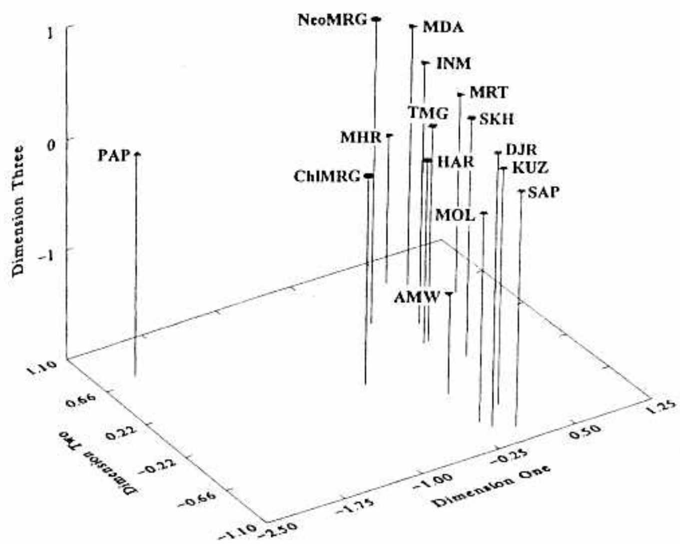

Figure 10. Two-dimensional ordination of group principal component scores - comparison two.

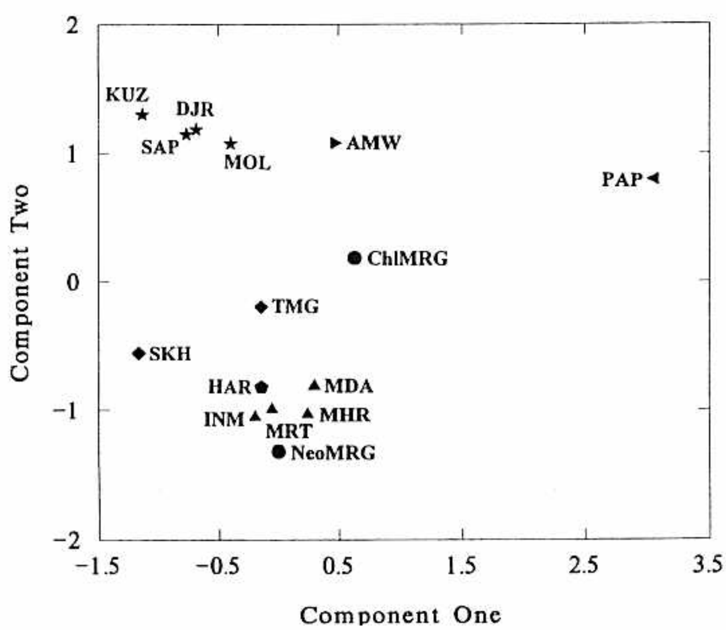

Figure 11. Two-dimensional ordination of group principal component scores - comparison two.

any other samples. American whites also appear to occupy an isolated position, only slightly closer to central Asians than to south Asians.

Although somewhat at odds with Fig. 9, but in agreement with results obtained by Hemphill *et al.* (this volume), ordination of the first two components suggests that of the south Asian samples, it is the latest of the Indus Valley samples (Sarai Khola and Timargarha) that bear closest similarities with central Asians. In agreement with the pattern of affinities depicted in Fig. 9, this ordination also suggests that the chalcolithic inhabitants of Mehrgarh occupy a rather isolated position. Affinities among remaining south Asians is quite similar, but not identical to those depicted in Figure 9. This ordination suggests that it is the Marathas that possess closest similarities to Inamgaon, with the Madia Gonds and Mahars more distantly removed. In fact, this ordination suggests that the Marathas are closer to both Inamgaon and Harappa, than to either of the other two samples of contemporary Maharashtrans. The neolithic occupants of Mehrgarh are dramatically separated from the later chalcolithic occupants of this site and share nearly equally close affinities to Inamgaon, Marathas and Mahars.

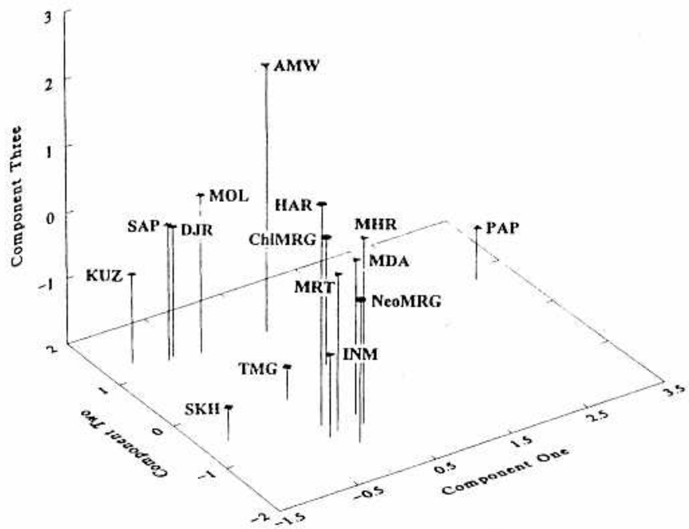

Figure 12. Three-dimensional ordination of multidimensionally scaled standardized MMD values - comparison two.

Addition of the third component, like addition of the third dimension to MMD analysis, provides further resolution to the pattern of phenetic affinities among samples (Fig. 12). Once again, the Papago are clearly recognized as the most divergent sample included in this analysis. Addition of the third component also serves to emphasize the isolation of American whites from both central Asians and south Asians. The third component serves to emphasize the distant similarity between chalcolithic Mehrgarh and Harappa, while highlighting the strong differences between these two samples and the two post-Harappan samples from the Indus Valley (Timargarha, Sarai Khola). The third component also serves to illustrate the general similarity among all contemporary Maharashtran samples, but somewhat surprisingly, this component also emphasizes that these samples tend to possess greater affinities to the sample from neolithic Mehrgarh than to Inamgaon. Once again, it is the high-status Marathas that possess the closest affinities to Inamgaon, while the low-status Mahars are the most distant. Addition of the third component underscores the intermediate position of Inamgaon between neolithic Mehrgarh on the one hand and the latest Indus Valley samples, especially Timargarha, on the other.

DISCUSSION

The first goal of this research was to test the efficacy of dental morphology variation for consistent patterning of human variation at different levels of magnitude of biological separation. Overall, the results of our analysis are very encouraging. With the sole exception of the dendrogram produced by cluster analysis in the second comparison (Fig. 8), all other analyses consistently identify Papago Indians as the phenotypically most distant group of the six samples considered. Certainly, this is what we should expect given other examinations of worldwide human variation (Hemphill 1991; Harris and Rathbun 1991; Cavalli-Sforza 1974). It is also reassuring that cluster analysis (Fig. 3) and multidimensional scaling of standardized MMD values (Figs. 4 and 5) also suggests that American whites tend to be more similar to south Asian samples than are the Papago. This too, reflects the findings of other researchers from other lines of biologic data (Hemphill 1991; Wainscoat *et al.* 1986; Long *et al.* 1986; Nei and Roychoudhury 1982; Cavalli-Sforza *et al.* 1988).

While this finding that use of multidimensionally scaled standardized MMD values and principal components analysis of arcsine transformed trait frequencies can be used to assess patterns of human variation across populations believed to be separated from one another on a macroscale is an important finding in and of itself, there is a second, and perhaps potentially more important ramification of these results. It has long been maintained by Brace and others that changes in subsistence and food preparation techniques exert a profound effect on the dental structures. Perhaps the most dramatic effect of this change in technocultural sophistication is a reduction in tooth size. This has led Brace and others (Brace 1962, 1978, 1980; Brace and Nagai 1982; Brace *et al.* 1986; Calcagno 1986; Calcagno and Gibson 1988) to suggest that because of such "evolutionary" tooth size reduction, odontometric variation will be of little utility for assessment of patterns of phenetic association among human groups (for another view see Harris and Bailit 1987; Harris and Rathbun 1991; Hemphill 1991; Hemphill and Lukacs in press; Hemphill *et al.* 1992; Lukacs and Hemphill 1993).

This trend towards diminutation of teeth among human populations that have been exposed to agricultural products and more sophisticated food preparation techniques, has also led to the suggestion that the increase in the consumption of greater amounts of sticky carbohydrates that accompanies agricultural production will lead to a simplification of crown morphology (Anderson and Popovich 1977; Calcagno and Gibson 1988; Grainger *et al.* 1966; Greene 1972; Mayhall 1972, 1977; Paynter and Grainger 1961, 1962). If this assertion is true, the pattern of expected affinities should place neolithic Mehrgarh, the Papago, and the contemporary tribal sample from Maharashtra (Madia Gonds) together as representing

Table 8. Mean Measure of Divergence Analysis- Comparison Two

	INM	MHR	MDA	MRT	PAP	AMW	SKH	TMG	NeoMRG	ChlMRG	HAR	SAP	DJR	KUZ
MHR	0.0278 **1.8692**													
MDA	0.0085 **0.5624**	0.0191 **4.5097**												
MRT	0.0051 **0.3483**	0.0016 **0.4192**	0.0053 **1.2910**											
PAP	0.4149 **26.7595**	0.3888 **83.8550**	0.3683 **74.8038**	0.4087 **90.4480**										
AMW	0.1896 **8.2756**	0.1085 **7.9445**	0.1616 **11.6298**	0.1323 **9.7494**	0.4620 **32.2701**									
SKH	-0.0130 **-0.3077**	0.0963 **3.0213**	0.0584 **1.8153**	0.0411 **1.2948**	0.6668 **20.5264**	0.1966 **4.9144**								
TMG	-0.0042 **-1.3452**	0.0100 **0.3455**	0.0058 **0.1991**	-0.0087 **-0.3041**	0.4093 **13.9363**	0.1419 **3.9685**	-0.0765 **-1.3647**							
NeoMRG	-0.0042 **-0.1835**	0.0836 **6.8389**	0.0363 **2.8986**	0.0566 **4.6765**	0.3483 **27.0001**	0.2545 **12.1493**	0.0984 **2.4522**	0.0446 **1.2155**						
ChlMRG	0.1162 **4.1075**	0.1035 **5.8849**	0.1042 **5.8276**	0.1066 **6.1004**	0.2389 **13.0849**	0.0960 **3.7319**	0.1482 **3.2800**	0.0813 **1.9600**	0.0612 **2.3775**					
HAR	0.0391 **1.1953**	0.0255 **1.1369**	0.0488 **2.1523**	0.0150 **0.6734**	0.4595 **19.9895**	0.0765 **2.5668**	0.0257 **0.5132**	-0.0014 **-0.0292**	0.0636 **2.0739**	0.0502 **1.4055**				
SAP	0.1463 **5.7116**	0.1957 **13.0860**	0.1633 **10.7207**	0.1708 **11.5077**	0.5511 **35.4735**	0.1192 **5.1676**	0.0385 **0.900**	0.0710 **31.7811**	0.2068 **8.9408**	0.0646 **2.2909**	0.0899 **2.7023**			
DJR	0.1266 **4.8237**	0.2276 **14.4873**	0.1521 **9.5112**	0.1850 **11.8572**	0.5424 **33.2718**	0.1751 **7.3339**	0.0576 **1.3242**	0.0833 **2.0692**	0.1674 **6.9962**	0.1020 **3.5114**	0.1393 **4.0914**	-0.0437 **-1.6303**		
KUZ	0.1186 **3.5401**	0.2209 **9.6757**	0.1662 **7.1904**	0.1664 **7.3281**	0.5740 **24.4807**	0.1476 **4.7725**	-0.0149 **-0.2956**	0.0408 **0.8666**	0.1778 **5.7522**	0.1008 **2.7870**	0.0759 **1.8693**	-0.05332 **-1.582**	-0.0442 **-1.2811**	
MOL	0.1144 **4.9052**	0.1512 **12.1040**	0.1348 **10.5505**	0.1398 **11.2992**	0.4570 **34.8308**	0.0832 **3.9771**	0.0616 **1.5295**	0.0427 **1.1471**	0.1525 **7.3644**	0.0209 **0.8035**	0.0487 **1.5845**	-0.0514 **-2.1848**	-0.0263 **-1.0856**	-0.0328 **-1.0461**

relatively recent converts to agricultural production. Chalcolithic Mehrgarh, and perhaps the central Asian samples, should exhibit progressive separation from the Papago, the neolithic inhabitants of Mehrgarh and the Madia Gonds. Harappans, as the product of several millennia of exposure to agricultural production and sophisticated food preparation techniques should represent the next stage of separation and should be closely associated with the late Bronze Age samples from Inamgaon, Timargarha, and Sarai Khola. Finally, the two caste samples from Maharashtra (low-status Mahars, high-status Marathas) and American whites should group together at the opposite extreme of variation from the Papago, neolithic Mehrgarh, and the Madia Gonds.

The results of our analysis suggest that while indeed such crown simplification may occur, this simplification is insufficient to obscure patterns of phenetic association among samples. Not only can samples from different technocultural subsistence strategies be successfully compared, but contrasts between prehistoric and contemporary populations still yield meaningful and consistent patterns of phenetic association. Regardless of statistical technique employed, none of these studies indicates a consistent relationship between subsistence strategy and phenetic relatedness.

While the results of our analysis indicate that there is no pervasive environmental factor compromising the efficacy of dental morphology variation for comparing samples with very different technocultural and dietary histories, nor does there appear to be a threshold of biological separation above which dental morphology is rendered incapable of yielded reasonable and consistent results, our findings suggest a methodological caveat to be considered in further comparisons. Overall, results from the first comparison were highly mixed and suggested that resolution of phenetic affinities among Maharashtran samples could not be accomplished. Taken together, our analyses yielded four different patterns of relationships among Maharashtrans. Two-dimensional ordination of multidimensionally scaled MMD values (Fig. 4) suggested that the tribal Madia Gonds share closest phenetic affinities with the prehistoric sample from Inamgaon. This pattern was somewhat tempered when the third dimension was added (Fig. 5), for in this latter ordination, Inamgaon appeared to exhibit equally close affinities to the tribal Madia Gonds as to the high caste Marathas. Two-dimensional ordination of group component scores (Fig. 6) suggested that it was the Maratha which represented most proximate contemporary group to Inamgaon, while tribal Madia Gonds were depicted as most divergent. Both three dimensional ordination of group component scores (Fig. 7) and cluster analysis (Fig. 3) suggested that none of the living Maharashtrans included in this analysis share any close affinities with the prehistoric sample from Inamgaon.

This failure to consistently resolve the patterning of phenetic affinities among Maharashtrans is likely a consequence of mixing vastly different levels of biological separation in a single comparison. These multivariate methods, in attempting to reduce the total inter-sample variation to the smallest number of linear vectors of variation, are being dominated by the great separations that differentiate Papago Indians and American whites, not only from one another, but from the four Maharashtran samples. Thus, those finer level distinctions which

Table 9. Principal Component Loadings - Comparison Two.

Variable	Component One	Component Two	Component Three
ShovI1	0.884	-0.223	-0.082
ShovI2	0.632	0.368	-0.325
MlrI1	0.566	-0.469	0.509
MlrI2	0.354	0.581	0.559
HypoM1	0.136	0.709	0.482
HypoM2	-0.228	0.874	0.168
CaraM1	0.716	-0.180	0.360
MtclM1	0.129	-0.702	-0.053
MtclM2	0.034	-0.721	0.262
YgrvM1	0.393	-0.472	0.225
YgrvM2	-0.299	0.075	-0.048
CspnM1	0.709	0.043	0.475
CspnM2	0.836	0.047	-0.446
C6M1	0.835	0.198	-0.287
C6M2	0.674	0.106	-0.482
C7M1	0.869	0.067	0.105
C7M2	0.650	0.330	-0.137
Eigenvalue	6.004	3.448	1.969
Percent of Variance	35.317	20.284	11.583
Total Variance		67.184	

serve to differentiate among more closely related samples, such as our four samples from Maharashtra, tend to be swamped out. The result is dramatic fluctuation in the patterning of phenetic affinities among closely related groups (in this case the Maharashtran samples), for those parameters which provide the strongest separations of the entire sample, do not serve as well to encompass the patterns of variation among more closely related groups.

To obviate this problem with the magnitude of biological differentiation, we conducted a second analysis in which data from nine prehistoric samples from south Asia and central Asia were incorporated into the matrix used in the first comparison. Overall, results from this second analysis are more consistent and make sense in light of our previous analyses of biological differentiation among prehistoric south and central Asians (Hemphill *et al.* this volume, 1991; Lukacs and Hemphill 1991, 1992; Hemphill and Lukacs 1993). What is especially reassuring about these results is that apart from cluster analysis, they not only consistently separate the Papago and American whites from all other samples, but they also yield fairly consistent patterns of phenetic affinity among Maharashtrans regardless of statistical technique employed.

These results suggest that multivariate statistical analyses of dental morphology variation may be used to examine patterns of phenetic affinity among strongly separated populations and closely related samples only if other samples, with biological affinities intermediate in magnitude are also considered. While a residual effect on fine-scale phenetic separations, caused by large differences between groups, remains, this "warping" effect affects the three statistical techniques to differing degrees. Cluster analysis appears to be a poor indicator of phenetic of phenetic affinity as the number of samples increases. Principal components analysis works well to separate samples that are either closely or moderately affiliated, but tends to obscure fine-scale separations when groups that are separated by very large phenetic distances are also included[1]. Overall, multidimensionally scaled standardized MMD values appear to yield to most robust results when comparisons are made at different magnitudes of phenetic separation.

The second goal of this research was to assess patterns of phenetic relatedness among Maharashtrans in light of current hypotheses surrounding the nature of human variation among the castes and tribes of India. As stated in the introduction above, these hypotheses lead to two different expectations. If the hypothesis is true that the fundamental division in the modern Indian gene pool occurs between Hindu caste groups versus non-Hindu castes (Balakrishnan 1978; Malhotra 1978), then low-status Mahars and high-status Marathas should be biologically more similar to one another and to the prehistoric sample from Inamgaon, than any of these samples are to the non-caste, tribal Madia Gonds. If, however the Mahars do represent the autochthonous inhabitants of Maharashtra, then they should exhibit closer

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[1] This is quite clear from the results obtained from the second comparison. While the patterning of phenetic relationships among prehistoric south Asian and central Asian samples remained highly consistent between the current study and a previous study which included only prehistoric samples (Hemphill *et al.* this volume) when assessed with multidimensionally scaled standardized MMD values, principal components analysis caused some alteration of these relationships. Examination of principal component loadings and trait frequencies possessed by Papago Indians and American whites suggested that the strong separation of these two samples from one another and from all central and south Asian samples has a pervasive influence one components one and three, forcing all differences between these Asian samples to be accommodated by the second principal component.

affinities to the prehistoric sample from Inamgaon than either the high-status Marathas, or the non-caste, tribal Madia Gonds.

Regardless of whether multidimensionally scaled MMD values (Figs. 9 and 10) or group principal component scores are employed (Figs. 11 and 12), both two- and three-dimensional ordination of data included in our second comparison consistently identify the high-status Marathas as possessing the closest affinities to the prehistoric sample from Inamgaon. By contrast, with the sole exception of two-dimensional ordination of principal component scores (Fig. 11) all of these ordinations also consistently identify low-status Mahars as the most distant of the three contemporary Maharashtran groups from Inamgaon. These results call into question the Mahars claim to be the autochthonous inhabitants of Maharashtra.

The third goal of this research was to contrast dental morphology data derived from contemporary populations with that obtained from prehistoric samples to discern patterns in the peopling of the subcontinent and intergroup interaction in south Asia. Our earlier research consistently indicated that the biological history of the Indus Valley, located in the extreme northwestern region of south Asia, was not one of uninterrupted biological continuity (Hemphill *et al.* 1991; Hemphill and Lukacs 1993; Lukacs and Hemphill 1991). To the contrary, there appears to have been a sharp discontinuity between 6000-4500 B.C., and this discontinuity is signalled by the strong phenetic differences exhibited by the neolithic and chalcolithic samples from Mehrgarh. While the chalcolithic inhabitants of this site appear to be distantly aligned with the later Harappan occupation of the Indus Valley (2300-1700 B.C.), the neolithic inhabitants of Mehrgarh exhibit closer phenetic affinities to the late Bronze Age sample from Inamgaon (1600-700 B.C.) than to any later Indus Valley samples. Based upon examinations of glottochronology (Gardner 1980), recent attempts at deciphering the Indus script (Fairservis 1983; Parpola 1984, 1986), the presence of isolated Dravidian-speaking peoples in Baluchistan (Brahui), and identification of Dravidian inclusions in the *Rg Veda*, the oldest written texts of south Asia (Fairservis and Southworth 1989), we speculated that the neolithic inhabitants of Mehrgarh may have been Austro-Asiatic speaking incipient agriculturalists, the descendants of whom were displaced by the appearance of new Dravidian speaking populations from the west at some point during the fifth millennium B.C. The close phenetic affinities between neolithic Mehrgarh and Inamgaon, despite a difference of 5000 years and a distance of 1600 km led us to suggest that these Austro-Asiatic speaking incipient agricultural populations may have retracted to the southeast, into northwestern peninsular India during the period of development and expansion of the Harappan Civilization.

Our previous studies suggested that a second biological discontinuity occurred in the history of the Indus Valley after the collapse of the Harappan Civilization around 1700 B.C. This second discontinuity is signalled by the phenetic separation between Harappans and the chalcolithic occupants of Mehrgarh on the one hand, from the post-Harappan northern Indus Valley samples of Timargarha (1400-850 B.C.) and Sarai Khola (200-100 B.C.) on the other. As we clearly outlined in our previous investigations, the nature of this second biological discontinuity throughout the history of the Indus Valley appears to be fundamentally different from the first. While the phenetic separation between the neolithic and the chalcolithic occupants of Mehrgarh is sharp and profound, that which separates Harappans from the post-Harappan occupants of the Indus Valley is less profound and chronologically progressive. This led us to suggest that while the biological discontinuity between neolithic and chalcolithic occupations of Mehrgarh appears to be a case of population replacement, that which separates Harappans from Timargarha and Sarai Khola appears to be a classic example of low-level progressive gene flow over time. One of the sources that has been posited for this gene flow has been central Asia (Parpola 1988, 1993; Piggott 1950; Wheeler 1968). The results of this study and that of others (Hemphill *et al.* this volume, Christensen and Hemphill 1995) suggests that a central Asian source does appear to be supported by several lines of biologic data.

Apart from cluster analysis, the results obtained from two- and three-dimensional ordination of multidimensionally scaled standardized MMD values (Figs. 9 and 10) and group principal component scores (Figs. 11 and 12) support these earlier findings. That is, neolithic Mehrgarh and chalcolithic Mehrgarh are widely separated and exhibit essentially no phenetic affinities to one another. Chalcolithic Mehrgarh and Harappa exhibit a distant relationship to one another, while Sarai Khola is strongly separated from these two earlier Indus Valley samples. The relationship between Harappa and the post-Harappan sample from Timargarha differs between MMD analysis and principal components analysis. The former suggests that Timargarha occupies a phenetic position very close to Harappa, while principal components analysis indicates a much stronger separation. Nevertheless, both analyses agree that Timargarha serves as an intermediary, linking Harappa on the one hand and the latest Indus Valley sample, Sarai Khola on the other. Finally, both MMD analysis and principal components analysis indicate that central Asians and south Asians are strongly separated from one another. However, it is also clear that the south Asian site with closest affinities to central Asians is Sarai Khola.

While these results serve to further support findings made in earlier papers, the inclusion of contemporary groups from Maharashtra permits this current investigation offer to two unique contributions to these issues. First, is to allow for further investigation of the connection between neolithic Mehrgarh and Inamgaon. Second, incorporation of living samples with prehistoric samples permits us to address the later stages of population history not possible to deal with in prior analyses.

Two- and three-dimensional ordination of multidimensionally scaled MMD values and principal component scores consistently associate neolithic Mehrgarh and Inamgaon with one another and with the three groups of contemporary Maharashtrans. Similarly, three-dimensional ordination of these analyses also indicate that Inamgaon shares closest affinities with the high-status Marathas, while the low-status Mahars exhibit the least affinity to this prehistoric sample. By contrast, the Madia Gonds appear to share the closest affinities of the three living groups to the neolithic sample from Mehrgarh.

Interpretation of these results for the population history of Maharashtra begins with the finding that the fundamental association between Inamgaon and neolithic Mehrgarh is robust. This may indicate that the people recovered from Jorwe levels at Inamgaon may represent, at least in a broad sense, the descendants from neolithic Mehrgarh. Yet, the phenetic position of Inamgaon is intriguing, for not only does this prehistoric sample exhibit affinities to the much earlier sample from neolithic Mehrgarh (6000 B.C.), but it also occupies an intermediate phenetic position between neolithic Mehrgarh and Timargarha, and to a lesser extent, Harappa and Sarai Khola. This may indicate that the late Jorwe occupants of Inamgaon may represent the effects of a genetic substrate similar to that possessed by neolithic Mehrgarh, but one that was also exposed to later gene flow from the Indus Valley. Indeed, there does appear to be some archaeological evidence (Allchin and Allchin 1982) of contact between the Indus Valley and western Maharashtra during and after the Harappan Civilization by way of the Saurashtran Peninsula during the preceding Malwa period. The Madia Gonds are clearly different from both Inamgaon and from the high-status Marathas. The indication of a closer connection between this tribal group and neolithic Mehrgarh than with Inamgaon may offer additional evidence that the occupants of neolithic Mehrgarh may in fact represent the older, indigenous Indian gene pool common among central and south Indian tribals today and which separates them strongly from caste Hindu populations (Balakrishnan 1978; Malhotra 1978; Walter 1983). The Mahars, nevertheless, remain an enigma. They clearly do not appear to represent the lineal descendants of the only prehistoric population from Maharashtra for which dental morphology data is currently available in any reasonable sample size. This, of course, does not rule out the Mahars claim as autochthons, but the results of our examination provide no support for their claim either. Thus, the role of the Mahars in the population history of Maharashtra remains unresolved and will have to await further studies which can encompass additional samples of prehistoric and contemporary Maharashtrans.

CONCLUSIONS

Frequencies of 17 dental morphology traits among three contemporary social groups of Maharashtra have been contrasted with other samples in two phases of comparison. In the first comparison, these groups were compared with a prehistoric sample from Maharashtra (Inamgaon), and with living Papago Indians and American whites. Contingency chi-square analysis indicated that 15 of these tooth-trait combinations differed significantly across all six samples. Analysis of inter-populational variation successfully identified Papago Indians and American whites as strongly separated from one another and from all Maharashtran samples. However, patterns of affinity among Maharashtran samples remained unclear.

In the second comparison, dental morphology data from nine additional prehistoric samples from central and south Asia were considered. Contingency chi-square analysis indicated that 16 of 17 tooth-trait combinations differed significantly across all 15 samples. Analysis of inter-population variation continued to provide a strong separation between Papago Indians and American whites from all central and south Asian samples. Variation among prehistoric samples provided additional evidence to support the pattern of relationships among prehistoric south Asians and central Asians identified in previous analyses. Addition of contemporary Maharashtran groups confirms the association between neolithic Mehrgarh and Inamgaon, but also emphasizes the intermediate position of this latter sample between the much earlier sample from neolithic Mehrgarh and later samples obtained from Harappa, Timargarha and Sarai Khola. Closest affinities between contemporary Maharashtrans and Inamgaon are found with the high-status Marathas. The non-caste, tribal Madia Gonds share a unique similarity with the neolithic sample from Mehrgarh. The low-status Mahars tend to be most the divergent from Inamgaon and their role in the population history of Maharashtra remains unclear.

The results of this study suggest that dental morphology variation is not substantially affected by progressive gracilization of the tooth crown corresponding with the technocultural transition to agricultural production and the adoption of sophisticated food preparation techniques. This study also indicates that there is no threshold of biological distance above which dental morphology variation fails to provide consistent and reasonable patterns of phenetic affinity. However, when samples of greatly differing degrees of biological distance are considered together, patterns of affinity among closely related samples will be distorted by large scale differences. Inclusion of additional samples of intermediate biological distance greatly obviates this problem, but various statistical procedures are differentially distorted by large-scale macrodifferences. Cluster analysis is most affected, followed by principal components analysis. Multidimensionally scaled standardized mean measure of divergence values appear to yield the most consistent results across different levels of biological separation.

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