An Indonesian Component in the Yayoi?: the Evidence of Biological Anthropology

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Abstract  Recent research on the possible external origins of the new developments in technology, society, culture and civilisation that took place in Yayoi Japan has concluded that there was substantial migration from East Asia, specifically Korea. This paper presents evidence from dental, cranial and DNA studies which suggests that there was another group, from island Southeast Asia (present-day Indonesia), in the Yayoi population.

Keywords:  Population history, Yayoi Japan, Indonesia, dental and cranial studies, DNA.

In earlier papers (Kumar, 1992 and 1996) it was suggested on the basis of evidence from rice genetics, mythology, and linguistics that there may have been an Indonesian influence on early Japan. The period considered most likely for this influence was that of the Yayoi. This paper surveys the evidence of dental and cranial studies, and presents new evidence based on the investigation of DNA.

1.1 Dental studies

One of the traditional methods used for making gross classifications of macrogeographical variation in Asia has been the study of dental form. The most frequently cited large-scale distinction is that drawn by Turner between a northern group labelled Sinodonts and a southern group called Sundadonts. It is not uncommon to encounter categorical statements that the Japanese are Sinodonts and the Indonesians Sundadonts. However, if one examines the data behind these categories a rather less black-and-white picture emerges. Such an examination of the data is given below.

Method

Obviously, it would be desirable for the purposes of this paper to have a comprehensive study of Yayoi teeth. However, Turner deals only briefly with a very small series of Yayoi teeth (Turner, 1992: 103). Trait sample size range for Yayoi is given as 3-9, compared to 33-124 for South China, 92-319 for Hong Kong, 200-522 for Japan, 89-154 for North China/Mongolia, and 117-338 for Jomon. These teeth led Turner to conclude
that the origin of the Yayoi Japanese could have been in South China: see his Figure 2, which shows Yayoi and South China as well separated from Japan, North China-Mongolia and Hong Kong. It is striking that though Turner sees the Yayoi as the migration that brought the Sinodonts to Japan, the way the Yayoi sample clusters with South China rather than with North China/Mongolia/Japan forces him to characterise the Yayoi as a rather "southern" group. In the absence of a full study of Yayoi teeth, particular attention should be paid, in the following analysis of Turner's data, to the characteristics of South Chinese teeth, to which the Yayoi sample is said to be closest.

Data for dental traits was taken from Turner (1987) (analyzing 28 traits) and Turner (1990) (analyzing 8 out of the original 28 traits). The following populations were sampled in these two papers:

Turner (1987): NE Siberia, Amur, Lake Baikal, North China/Mongolia, Recent Japan, South China, Jomon, Early Southeast Asia, Recent Southeast Asia, Recent Indomalaysia, and Early Malay Archipelago.

Turner (1990): NE Siberia, Amur, Buriat, Lake Baikal, Mongol 3, Urga and Mongol 2, South China, Japan, Japan recent, Japan Kamakura, Japan Kanto, Japan Hiogo, Malay/Java, Early Malay Archipelago, Leang Cadang, and Borneo.

The approach taken was similar to that used in Turner (1990), simply graphing the frequencies of each trait in sequential order. A search was made for traits which differentiate between North Chinese/Mongolians and Southeast Asians.

Results

- It transpired that 15 traits did not produce a recognisable spectrum differentiating between Southeast Asia and North Asia. Therefore these 15 traits were not studied further.

- The remaining 13 traits were: 4 Cusp LM2; Deflecting Wrinkle LM1; Protostylid LM1; Tome's Root LP1; 3 Root LM1; 1 Root LM2; Carabelli Trait UM1; Enamel Extension UM1; 1 Root UP1; 3 Root UM2; Peg/Reduced/Congenitally Absent UM3; Shoveling UI1; and Double Shoveling UI1. The traits 4 Cusp LM2, Deflecting Wrinkle LM1, 3 Root LM1, Enamel Extension UM1, 1 Root UP1, Peg/Reduced/Congenitally Absent UM3, Shoveling UI1, and Double Shoveling UI1 correspond to the 8 traits selected by Turner in his 1990 study, showing significant differences between Sinodonts and Sundadonts.

- The spectrum produced in each of these 15 traits and the position of the Japanese on it is analysed below.

- 4 Cusp LM2. This is a trait more common in Southeast Asians than North Asians. Japan and South China are both seen to group with the North Asians.

- Deflecting Wrinkle LM1. This trait is found in higher frequencies in the North Asians. Japan and South China both show intermediate frequencies, grouping mainly with Southeast Asians.

- Protostylid LM1. With some exceptions (Early Southeast Asia, Amur), this trait is highest in North Asians. Japan groups clearly with the Southeast Asians, while South China
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- Tome's Root LP1. This is clearly more common in Southeast Asians than North Asians. South China has the highest frequency, grouping with the Southeast Asians, whereas Japan groups with the North Asians.

- 3 Root LM1. A trait more common in North Asians than Southeast Asians. Japan groups with the North Asians, South China with the Southeast Asians.

- 1 Root LM2. This is a trait more common in North Asians (with the unexpected exception of NE Siberia) than in Southeast Asians. Japan and South China both group with recent Southeast Asia and Early Malay Archipelago in having intermediate frequencies.

- Carabelli Trait UM1. A trait more common in Southeast Asians, with the exception of Early Malay Archipelago. Japan is intermediate between the two groups, and (again unexpectedly) South China groups with the North Asians.

- Enamel Extension UM1. This trait is higher in North Asians. Japan and South China both have very high frequencies, and thus group with the North Asians.

- 1 Root UP1. This trait is higher in North Asians. Turner (1987) shows Japan and South China grouping with recent Southeast Asia in being intermediate between the two categories. Turner (1990) shows the Leang Cadang Indonesian group and Japan Kanto to group with the North Asians, and Anyang China as intermediate between Japan and South China.

- 3 Root UM2. This trait is found in higher frequencies among the Southeast Asians, though not in the Jomon. Japan and South China clearly group with the Southeast Asians.

- Peg/Reduced/Congenitally Absent UM3. The spectrum between Southeast Asians and North Asians is not so clearly defined here. However if this is considered as a more “North Asian” trait, we can say that Japan groups with the North Asians, and South China, Lake Baikal and NE Siberia group with the Southeast Asians — a result which does not accord with what we would expect from the expected distribution of populations into Sinodont and Sundadont.

- Shoveling UI1. A trait more common in North Asians. Japan and South China both group with North Asians.


Discussion and conclusions

- The graphing of Double Shovelling U11 frequencies from Turner (1990) and Turner (1987) produced somewhat different results, so both results are considered separately in the following.

- What is important for our purposes is that, looking at the position of recent Japanese in regard to these 13 traits, or 14 cases, we find that in 6 cases they grouped with the
Southeast Asians, in 2 cases they were intermediate between the 2 groups, and in 6 cases they grouped with the North Asians.

- With respect to the South Chinese, in 7 cases they grouped with the Southeast Asians, in 2 cases they were intermediate between the 2 groups, and in 5 cases they grouped with the North Asians.

These results can be used to get away from the rigid classification of Japanese and South Chinese as “Sinodonts”. It can be seen that the recent Japanese are at a halfway point between North Asians and Southeast Asians (see also Manabe and others 1992). The South Chinese are in fact more like Southeast Asians than like North Asians, which confirms the opinion of Turner (1987).

Turner (1992) pointed out that Yayoi teeth were very similar to those of South China. We can infer from this that the Yayoi were also more similar to Southeast Asians than North Asians, and may have originated in a Southeast Asian population. The position of the modern Japanese further strengthens this hypothesis, as their intermediate position suggests the presence of a considerable Southeast Asian influence.

1.2 Cranial studies

Here I shall simply note the results of the more important studies, craniometric and cranioscopic.

In craniometric studies, Brace and others’ 1991 study classified the Yayoi as belonging to the Southeast Asian part of the Asian cluster (Brace and others 1991, Figure 4), and his 1990 study revealed that according to the tooth size/cranial volume index the Yayoi had exactly the same reading as Borneo (Brace and others 1991, Figure 7). In another craniometric study, Pietrusewsky (1992a: 47) noted that Borneo, Vietnam, Sulu, Java and Sulawesi (in that order, and ahead of both the Chinese and Mongolian populations) were closest to Japan. His dendrogram (Pietrusewsky 1992a: 42) indicates that Japan occupies a peripheral branch of the Southeast Asian sub-grouping, joining just ahead of Thailand, Bachuc and the southern Moluccas. Pietrusewsky concluded that “Previous researchers have noticed similarities between Japanese and East Asian groups. The results of this study only partially support this view. Although the modern Japanese are part of the East Asian cluster containing Chinese, Mongolians, and Southeast Asians, they align more closely with several mainland and island Southeast Asian samples than they do with Chinese or Mongolians.” These findings are confirmed in Pietrusewsky 1992b, which, in connection with Brace’s Sinodont/Sundadont distinction, concluded that affinities between Chinese, Japanese, and Mongolians were not as marked as previous researchers had demonstrated (Pietrusewsky 1992b: 553). However, in a later study (Pietrusewsky 1994) which now included Korean specimens, Pietrusewsky found that the Japanese series, from Yayoi to modern times, and Korea formed one branch, to which Ainu and Jomon were marginally related.

Hanihara (1986) concluded that the physical characteristics of present-day Japanese strongly indicated that migrations took place over a long period of time and from both the
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north and the south. Later, Dodo and Ishida’s (1993, 1990) cranioscopic studies also make
the point that the Yayoi period may be a phase when a number of different populations
were competing with each other for their gene dispersion.

Kozintsev’s cranioscopic studies (Kozintsev 1990 and 1992) found that the Yayoi aligned
very closely with Indonesians. He remarks that compared to the populations of northern
and central Asia, modern Japanese as well as Chinese are considerably less Mongoloid.
The proto-Japanese of Yayoi and Kofun periods at first sight appear to be more
Mongoloid than modern Japanese. But examining each trait separately we see that only in
Occipital Index (O1) do the Yayoi and Kofun people deviate towards the Siberians, the
number of observations being very small here. In most other diagnostic traits the shift is
towards the Jomon group (Kozintsev 1990: 251).

An examination of Kozintsev’s raw data, Figure 2, based on supraorbital foramen (SOF)
and hypoglossal canal bridging, shows the Yayoi very close to Indonesians, and Figure 1,
based on transverse zygomatic suture posterior trace (TZST) and infraorbital pattern type
II (IOP 11), also shows the Yayoi closer to Indonesians than to Chinese.

After concluding that massive immigration in the Yayoi period suddenly introduced a
new Mongoloid element, Kozintsev then goes on to statistically test a number of different
northern and southern Mongoloid groups to determine which group hypothesized as
these immigrants would have produced the best “fit” with later Japanese population
history. He concludes that the “Chinese model” is best. However, his method actually
seems biased against the Indonesian model, because of the similarity between some Jomon
and Southeast-Asian characteristics. If the Japanese were the descendants of an admixture
between Indonesian and Jomon peoples then Indonesia would not be the component to
cause maximal differentiation between the groups in Japan.

Kozintsev’s preferred model (Kozintsev 1990: 263) also creates another problem: the
resultant increase in MJi from the Yayoi period to the modern period is too small to
correspond to the documented population increase over this time. In other words, using the
so-called “best” model, there was not enough change towards the Mongolian characteristics
for the amount of population increase. This may suggest that the actual Mongolian influence
was something less “different” to the Jomon population. Kozintsev’s explanation is that
already during the Yayoi age the major part of the aboriginal population of West Japan
mixed with the immigrants, shifted to agriculture and began to progressively outnumber
those aboriginal groups which did not mix. An alternative possibility is that instead of this
hypothetical mixed group an Indonesian population may have been involved.

It is significant that all Kozintsev’s northern models produce better results with the
Kofun group than with the Yayoi groups while for the Chinese and Indonesian models
the opposite is true. This suggests the scenario that the Yayoi were a southern group and
that there was subsequently north Asian (Korean) immigration into Japan in the Kofun
period.

The cranial studies therefore confirm the findings of the dental studies in indicating
a southern affinity for the Yayoi. Taken together, these morphological studies reveal
significant support for the idea of a southern and most likely Indonesian group among the Yayoi.

**The evidence of DNA**

1. Constructing a dendogram based on 85 at 24 polymorphic loci

   The main constraint to constructing the dendrogram was the availability of compatible genetic data for different populations. The nuclear DNA data used in this study were obtained from Roychoudhury and Nei (1988). They consisted of 85 alleles at 24 polymorphic loci, including gene frequencies for enzymes (ACP1, ADA, AK1, ALDH2, ESD, G6PD, GPI, GPT1, PGM1, PGD), proteins (GCsub, HPA, TF), blood groups (SE, ABO, DI, FY, KEL, JK, LU, MNS, P, RH) and a DNA polymorphism (PI). Gene frequency data were obtained for groups representing 10 populations: Ainu, Caucasian, Indonesian, Japanese, Korean, Negroid, North Chinese, Melanesian, Southeast Asian (Thai and Vietnamese) and South Chinese. I believe this data set is more extensive than any yet published at least in English, in terms of both the number of polymorphic loci and the number of populations used. Data was not available for the Okinawans or any other representatives of the Ryukyu Island populations. Gene frequency data representing histocompatibility and immunoglobulin systems were not used as they were not available for all populations. Gene frequency data from mitochondrial DNA (mtDNA) was not used either, despite being extensively and systematically studied, as data of this type is subject to significantly different and larger sampling errors than frequency data from nuclear DNA. However, findings from mtDNA data are discussed below.

   To investigate genetic affinities of the Japanese with other Asian populations, genetic distances were calculated using Roger’s (1972) genetic distance. These were used to construct a dendrogram (Figure 1) by UPGMA clustering (Sneath and Sokal 1973). The relationships between the three broad lineages, Mongoloid, Caucasian and Negroid are also indicated.

   The dendrogram of Figure 1 indicates two main clusters for East Asian populations. The first includes the South Chinese, Southeast Asians and Indonesians. The second consists of the Japanese and Koreans. The close relationship between the latter two populations has also been demonstrated by other investigators who use genetic data (Cavalli-Sforza and others 1988; Harihara and others 1988; Saha and Tay 1992). The North Chinese fall between these two clusters, but align more closely with Southeast Asian populations as opposed to the Koreans.

   However, it should be stressed that such dendrograms indicate only the present situation, and not historical developments. They are based on the averaging-out of the data for each population group and of course very different components and time sequences can produce a similar average. Secondly, though the clustering of the Japanese and Koreans is marked given the relatively large distance between them and other populations, there is much more doubt about the order of branching of the various Chinese populations, the Ainu, and the Indonesians. This is because of the very small genetic distances involved.
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for example only about 1 for the Ainu, less for the North Chinese, (vide the closeness of the branching). It may be the case, therefore, that extra data would lead to revisions in the overall order of branching of the Mongoloid populations. So while the Japanese-Korean affinity is clear, the data is much less useful for separating out other Asian populations one of which might have less marked affinities with the Japanese.

2. Mitochondrial DNA: a study of d-loop sequences

A study of d-loop sequences might be expected to provide comparative material at a more detailed level than the nuclear DNA examined above. Such an investigation has been carried out, using data from relevant populations available in the public domain (Betty and others 1996; Handt and others 1997; Horai and others 1990 and 1996; Kolman and others 1996; Lum and others 1994; Redd and others 1995; Sykes and others 1995; Torroni and others 1993, and Vigilant and others 1991). These data comprise a total of 226 Japanese sequences, 69 Indonesian, 71 Korean, 40 Chinese, 103 Mongolian, 105 Taiwanese and 37 Philippine. The relationships between the d-loop sequences have been evaluated using a neighbour-joining tree constructed using Saitou and Nei's (1987) method.

Figure 1 Dendrogram showing the genetic affinities and distances of the Japanese and Ainu with respect to six other Asian populations.
Results

This tree produced a number of groupings, analysed below (j213 = Japanese sequence no. 213 of the sample; sites are indicated within brackets).

Across most human groups there are six sites that do not give very reliable information for inferring the genealogy of this region of sequence. This is because the same change has occurred in more than one lineage at those sites, which can be deduced from the fact that the phylogenetic information at these sites is incompatible with the information at the majority of other sites. These sites are 16000 + 129, 189, 223, 278, 311, 362. Any groupings that are based on identity at these sites are therefore not reliable.

Some of the groupings depended entirely on these sites. These were:

korea69/indo18
indo31/j213
indo33/j157/j147
indo46/j26/j122/j182
indo36/indo37/j136/j153/j221

These groupings may not be real because of the possibility of recurrent mutation at the unreliable sites leading to identity by state but not by descent.

Several other groupings were based on one other site in addition to these sites. These groupings include:

indo14/korea2 (16217)
indo62/indo63/indo69/j52/j80 (16266)
indo57/phil36/j46/j113 (298)
indo7/j200 (217)
j86/indo10/indo11(217)

These are more likely to be real groupings, but one site is still not a reliable basis for making an inference.

There are two other groupings that are based on two sites other than the unreliable ones. These are:

indo68/j134/j214 (243, 325)
j226/indo15/indo16/indo24/indo25/korea69 (136, 217)

It seems very likely that these groupings reflect identity by descent and therefore a sharing of lineages between Japan (and in one case also Korea) and Indonesia that are not present in the the other populations in the region sampled, such as Mongolian, Chinese and Taiwanese. This would suggest some movement of people between these two regions (Indonesia and Japan/Korea). The data does not show the direction of the migration, and
further work could be done to try to establish this. For instance, if the frequently-shared site 217 were more common in one of the populations and less in the other(s), this would suggest that the source of the migration was the population where this site was more common.

The results are compatible with the theory of some Indonesian migration, and indeed represent quite a positive result given the possibility that such a migration might have been predominantly male. In this case the maternal inheritance of mitochondrial DNA would have weakened the reflection of their genetic legacy in the modern Japanese population. The sharing of some sites between Indonesians, Japanese and Koreans to the exclusion of other Asian populations raises the possibility that some Indonesians may have gone to Korea. Such a scenario which cuts across present national boundaries is not inherently impossible but does complicate the picture and the analysis of the data. The fact that none of these sites are shared by the Taiwan group means that this shared Indonesian and Japanese genetic inheritance cannot go back to the earlier period of the original Austronesian expansion out of Taiwan.

**Conclusion and suggestions for further research**

The material surveyed here provides enough indications from a number of different areas to suggest that Turner’s “dual origin” hypothesis (“Sundadont” Jomon population + “Sinodont” Yayoi population) should be replaced by a “triple origin” hypothesis: that the present day Japanese population is the result of a three-way mixture consisting of the Jomon population plus two different groups of immigrants in the Yayoi period, one of which is of Indonesian origin. (This may also be the reason why Pietrusewsky’s studies of Yayoi affinities have produced conflicting results.) Indeed, this scenario has been foreshadowed by Dodo and Ishida’s (1990) comment that the Yayoi period may be a phase when a number of different populations were competing with each other for their gene dispersion. This possibility should receive further investigation — *which should focus on the Yayoi population itself*. This paper has had to use mostly data on the modern Japanese population, which is clearly unsatisfactory.

Further linguistic research is in progress, following up Kumar’s (1996) preliminary investigations, and this has produced promising indications of a possible non-genetic relationship between a Western-Malayo-Polynesian language and Japanese.

Finally, archaeological research is another area that would repay further investigation. There are strong typological resemblances between Yayoi artefacts and their Indonesian counterparts. Pottery and metalwork, especially blades and bells, spring to mind. At the moment, however, archaeological work on Indonesia is insufficiently advanced for us to be able to say whether or not these typological resemblances are due to a historical connection.
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