Population history of northern Vietnamese inferred from nonmetric cranial trait variation

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Abstract In this study, nine nonmetric cranial traits were recorded for ancient human remains excavated at early prehistoric (the late Pleistocene, early Holocene, and Pre-Pottery Neolithic) and late prehistoric (the Neolithic and early Iron age) archeological sites in northern Vietnam. The comparative samples consist of prehistoric and early historic crania from the lower Yangtze River basin, together with recent cranial series from Vietnam, Thailand, South China, and Australia. The results, based mainly on the measure of divergence, are as follows: (1) the early prehistoric northern Vietnam group is distinct from the subsequent inhabitants of northern Vietnam and neighboring populations; (2) the cranial series of northern Vietnam and the surrounding region from the late prehistoric to recent times through early historic period exhibit relative homogeneity, suggesting population continuity; (3) the recent Han Chinese from southern China, one of the possible representatives of East Asians, are relatively distant from all groups from the prehistoric age onwards; and (4) a clear separation of Aboriginal Australians from all the comparative samples, including the early prehistoric northern Vietnamese, is evident. These findings suggest partial support for the two opposing hypotheses, i.e. the two-layer model and the regional-continuity model, for the population history of Southeast Asians, at least, in the northern Vietnamese region. This may be further compatible with the recent hypothesis for modern human dispersals: an earlier out-of-Africa expansion of Australians than other contemporary Eurasians including Southeast Asians.

Key words: two-layer model, regional-continuity model, prehistoric northern Vietnam, East/Southeast Asia, Australia

Introduction

With respect to the peopling of Southeast Asia, early researchers frequently described morphological features akin to Australian Aborigines or Melanesians for a majority of the skeletal remains recovered from the pre-ceramic period, despite the fragmentary nature of remains and the lack of a clear chronological framework (e.g. Evans, 1918; Duckworth, 1934; Mijsberg, 1940; Trevor and Brothwell, 1962; Jacob, 1967). These early observations fostered the hypothesis that Southeast Asia was initially colonized at least 50000 years ago (the first layer) by anatomically modern humans (sometimes referred to as Australo-Melanesians), who later exchanged genetic material with

new immigrants (the second layer) from East Asia (the region mainly corresponding to present China), leading the formation of present-day Southeast Asians (Callenfels, 1936; Mijsberg, 1940; von Koenigswald, 1952; Coon, 1962; Jacob, 1967, 1975; Brace et al., 1991). This hypothesis, known as the two-layer model, has now received some support from more recent and extensive studies based on new skeletal discoveries (Matsumura and Zuraina, 1999; Matsumura and Hudson, 2005; Matsumura and Pookajorn, 2005; Matsumura, 2006, 2011a, b; Bulbeck et al., 2007; Matsumura et al., 2008a, b). These recent researches, which refine the context of two-layer model, clearly demonstrate that the late Pleistocene and early Holocene colonists of Southeast Asia, represented by Hoabinhian foragers, were descendants of the first occupants of late Pleistocene Sunda-land, who shared ancestors with present-day Australian Aboriginal and Melanesian populations, but never with majority of present-day Southeast Asians.

Despite the long history of the two-layer hypothesis, a number of scholars have critiqued it. A major controversial hypothesis is the regional-continuity or local-evolution

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model that declares modern Southeast Asians to be the result of long-standing genetic continuity without any significant influx of gene flow from outside the region. This scenario is, for instance, supported by ‘Sundadont/Sinodont’ dental studies (Turner, 1989, 1990, 1992), and multivariate cranial metric analyses by Hanihara (1994, 2006) and Pietrusewsky (2006, 2008, 2010). Further, this hypothesis has received support from genetic research, suggesting that Southeast Asia was a major geographic source of East Asian populations, within which the origins of all inhabitants of Southeast and East Asia were derived from a single primary source colonizing the region (e.g. Capelli et al., 2001; The HUGO Pan-Asian SNP Consortium, 2009).

On the other hand, the two-layer hypothesis has been supported by historical, linguistic, and archeological data, in which the expansions of the language families represented by Austronesian and Austroasiatic, for instance, were driven in association with the dispersal of rice-farming peoples during the Neolithic and early Metal (Bronze and Iron) ages (Higham, 1998, 2001; Bellwood and Renfrew, 2003; Diamond and Bellwood, 2003; Bellwood, 2005; Sagart, 2008). Both linguistic and archeological data suggest that southern China and Taiwan were the ultimate sources of these language and food production dispersals, with archeological evidence for the origins of Neolithic farming societies in the Yangtze basin during the early Holocene (Bellwood, 2005; Lu, 2006).

Bioanthropological evidence, supporting the agricultural-driven demographic expansion from southern China some time during the Neolithic, has come from recent excavations in mainland Southeast Asia, the most representative being from the Man Bac, a 3600–4000-year-old Neolithic cemetery site in northern Vietnam. In terms of local cultural chronologies, the material culture of Man Bac, located on the southern edge of the Red River delta, displays many similarities with the Phung Nguyen culture (4000–3500 years BP), which generally showed evidence for rice cultivation and flourished along the upper reaches of the Red River Delta (Hiep and Phung, 2004). One of the most important skeletal findings at Man Bac is the demonstration of significant morphological discontinuity with the Hoabinhian and mid Holocene pre-Neolithic pottery using cultures (PNPC), represented by the Da But series (see Oxenham and Matsumura, 2011), that exhibit Australo-Melanesian features with respect to quantitative (metric) craniodental morphology (Matsumura et al., 2008b, 2011a; Matsumura, 2011a, b). The close affinity of the majority of Man Bac individuals

with later Iron Age Dong Son and Chinese Neolithic samples from the Yangtze River region suggests that the Neolithic was the turning point in terms of the microevolutionary history of this region. The skeletal sequence at Man Bac, demonstrating an initial appearance of immigrants in northern Vietnam, clearly illustrates the two-layer model in the context of local and regional populations in debates over the demographic expansion associated with the spread of agriculture.

In order to further test and/or refine this model of major population change in Vietnam in terms of a range of comparative approaches to skeletal morphology, the present study analyzed the qualitative (nonmetric) cranial morphology of the Man Bac sample. Cranial nonmetric traits have been widely accepted to be effective for reconstructing population histories, not only within limited geographic regions but also globally (Dodo and Ishida, 1990; Ossenberger, 1994; Dodo and Kawakubo, 2002; Hanihara et al., 2003; Dodo and Sawada, 2010). The occurrences of cranial nonmetric traits were compared between the temporally disparate skeletal sequences discussed above for the Hoabinhian, Pre-Pottery Neolithic (PPNC, essentially Da But series), Neolithic Man Bac, and Metal period assemblages available for study in northern Vietnam, to test the validity of two-layer hypothesis as a model for understanding the population history of Southeast Asia.

Materials and Methods

The prehistoric series from northern Vietnam used in the present study are given in Table 1. The early prehistoric northern Vietnamese (EPNV) samples comprise the late Pleistocene Son Vi, early Holocene Hoabinhian and Bac Son, and Pre-Pottery Neolithic Culture (PPNC) Da But cranial series, totaling 67 individuals. The late prehistoric northern Vietnamese (LPNV) series includes the Neolithic Man Bac and the early Iron Age samples from Dong Son, totaling 73 individuals.

The present study is concerned with nonmetric cranial variation. The prehistoric series listed in Table 1 were examined by Y.D.

The prehistoric and early historic comparative samples consist of cranial series from the Weidun site and those from several sites attributed to the Eastern Zhou and the Western Han periods located in the lower reaches of the Yangtze River. The two early Yangtze series were reported by Wakebe (2002). The Weidun site is considered to belong to the early

Table 1. Cranial series of prehistoric northern Vietnam

Culture	Site	Date (years BP)	No. of crania	Collection
Early Prehistoric Northern Vietnamese (EPNV)				
Son Vi	Mai Da Dieu	20000–12000	1	Institute of Archaeology, Hanoi
Hoabinhian	Hang Chou, Mai Da Nuoc, Mai Da Dieu, Dong Can	15000–8000	4	Institute of Archaeology, Hanoi
Bac Son	Lang Cuom, Pho Binh Gia, Cau Giat	10000–6000	18	Musée de l’Homme, Paris
Da But	Con Co Ngua	6000–5000	44	Institute of Archaeology, Hanoi
Late Prehistoric Northern Vietnamese (LPNV)				
Phung Nguyen	Man Bac	4000–3600	33	Institute of Archaeology, Hanoi
Dong Son	Minh Duc, Vinh Quang, Quy Chu, Nui Nap	3000–1700	40	Institute of Archaeology, Hanoi

rice-cultivating (7000–5200 years BP) Majiabang Culture (Zou and Li, 2002). Skeletal remains excavated from the Weidun site are, however, assigned to c. 5000 years BP (Chen and Huang, 1995).

In addition to the prehistoric and early historic samples described above, this study includes four recent cranial series from Vietnam, Thailand, South China, and Australia. With the exception of the Thai sample examined by Y.D., all data were recorded by T.H. Relevant summary information on the nature of the samples is given in Table 2.

In the present study the following nine nonmetric traits, for which more than 20 sides of crania were observable in the prehistoric northern Vietnamese sample, were used because these traits are commonly used by other observers and have relatively low inter-observer errors (Ishida and Dodo, 1990): metopism (MET); supraorbital foramen (SOF); ossicle at lambda (OL); parietal notch bone (PNB); hypoglossal canal bridging (HGCB); ovale-spinosum open (OSO); medial palatine canal (MPC); transverse zygomatic suture vestige (TZS); and mylohyoid groove bridging (MHB). The scoring procedures for each trait are described in Dodo (1974) and Dodo and Ishida (1990). All the traits used were dichotomized into categories of present or absent.

In this study, sexes were pooled and separate records and counts were kept for the bilateral traits in order to maximize the sample size even when only one side was observable. Fisher's exact probability test was used to identify the significance of differences in trait occurrence between the samples compared. Tests were conducted using the software package HALBAU-5 for Windows (Gendaisugakusha).

The biological distance between every pair of samples was defined as follows:

Measure of divergence (MD)

$$= \sum_{j=1}^r [(\theta_{1j} - \theta_{2j})^2 / (1/4n_{1j} + 1/4n_{2j})]$$

where $\theta = \sin^{-1} \sqrt{p}$ in radian, n is the sample size, and r is the number of traits. When frequencies are zero, we performed Bartlett's adjustment, replacing a zero proportion by $1/4n$ (Snedecor and Cochran, 1980). This formula was originally developed by Fisher (1949) for testing the sexual dimorphism in recombination fraction of allelic locus of house mice. Yamaguchi (1967) applied the measure of divergence (MD) to estimate biological distance based on the frequencies of nonmetric cranial traits.

It is well known that Smith's mean measure of divergence (MMD) provides one of the best estimates of biological divergence among samples for nonmetric morphological traits (Sjøvold, 1977). In the case of small sample size, however, the MMD distance, or a corrected MMD, which is calculated by subtracting the variance of the differences ($1/n_{1j} + 1/n_{2j}$) from the raw one, often yields a negative value. In the present study, some negative values of MMDs were obtained. On the other hand, the advantage of the use of MD includes: (1) negative values are not calculated; and (2) a test of significance can be performed since they distribute as a χ^2 -statistic with r degrees of freedom (Rao, 1952). Moreover, Pearson's correlation coefficients between distance coefficients of MMDs and MDs based on 25 population

Table 2. Brief information of the recent cranial series used for comparison*

Sample name	Brief information
Vietnam	Hanoi, Da Nang, and other cities (Musée de l'Homme, Paris)
Thailand	Anatomical collection housed in Siriraj Hospital, Mahidol University mainly from Bangkok
South China	Shanghai, Canton, Hong Kong, and other cities from southern China: Han Chinese from South of Cheng Yangtze River (Natural History Museum, London; Musée de l'Homme, Paris; American Museum of Natural History, New York)
Australia	Mainly from coastal regions of New South Wales (Australian Museum, Sydney; Natural History Museum, London; Cambridge University, Cambridge; American Museum of Natural History, New York; National Museum of Natural History, Washington DC; Musée de l'Homme, Paris)

* For references, see Ishida and Dodo (1997) and Hanihara and Ishida (2001a, b, c, d).

samples (300 pairs of samples in total) are 0.936. This suggests the usefulness of MD for estimating similarities/dissimilarities among samples with relatively small sample sizes.

To visualize the patterning of intergroup relationships, principal coordinate (PCO) analysis developed by Gower (1966) was applied to the obtained MD matrix. Calculations for MD and PCO were processed using a N88-BASIC program coded by Y.D. and Tanaka et al. (1984), respectively. These N88-BASIC programs were modified for a Windows system using BASIC/98 ver. 5 (Dennougumi).

Results

The frequencies of nine nonmetric cranial traits and number of individuals or sides scored for the early and late prehistoric northern Vietnamese samples together with the six comparative series are provided in Table 3. The metopism occurs much less in the Australian cranial series. The ossicle at lambda, ovale-spinosum open, and mylohyoid groove bridging are not observable in the early prehistoric northern Vietnamese sample. The early prehistoric northern Vietnamese and Australian samples have lower frequencies of the supraorbital foramen than six other samples. The parietal notch bone is observed with relatively high frequency in the late prehistoric northern Vietnamese, Zhou/Han, and southern Chinese samples. The frequencies of the hypoglossal canal bridging are relatively high in the early prehistoric northern Vietnamese and Zhou/Han cranial series. The frequencies of the transverse zygomatic suture vestige are generally low in all the cranial samples examined here as compared to those in many of the Northeast Asian groups (Ishida, 1995).

Table 4 presents the results of tests for the difference in trait frequencies between the early and late prehistoric northern Vietnamese samples. The Fisher's exact probability test emphasizes the observation that the frequency of the supraorbital foramen in the late prehistoric northern Vietnamese sample is significantly higher than in the early prehistoric northern Vietnamese sample ($P < 0.01$).

Table 3. Comparison of side-incidences of nonmetric traits among the eight cranial series from Vietnam, South China, Thailand, and Australia

Trait	EPNV		LPNV		Weidun ¹		Zhou/Han ¹		Vietnam		Thailand		South China		Australia	
	<i>n</i>	<i>P</i>	<i>n</i>	<i>P</i>	<i>n</i>	<i>P</i>	<i>n</i>	<i>P</i>	<i>n</i>	<i>P</i>	<i>n</i>	<i>P</i>	<i>n</i>	<i>P</i>	<i>n</i>	<i>P</i>
MET	59	0.051	65	0.062	38	0.053	32	0.031	36	0.056	131	0.023	100	0.090	182	0.005
SOF	99	0.192	100	0.370	69	0.406	52	0.519	72	0.306	262	0.424	198	0.404	358	0.120
OL	40	0.006*	52	0.058	22	0.045	23	0.217	36	0.111	119	0.092	93	0.247	138	0.174
PNB	31	0.097	76	0.184	43	0.070	42	0.214	70	0.157	250	0.116	184	0.299	266	0.117
HGCB	38	0.132	73	0.082	45	0.044	44	0.136	70	0.043	260	0.077	190	0.068	332	0.048
OSO	29	0.009*	65	0.046	44	0.023	46	0.022	72	0.042	262	0.019	184	0.033	272	0.033
MPC	51	0.020	95	0.021	74	0.041	50	0.060	70	0.071	262	0.027	196	0.041	340	0.038
TZS	43	0.023	65	0.015	37	0.081	42	0.006*	62	0.004*	250	0.048	184	0.049	266	0.015
MHB	51	0.005*	105	0.048	81	0.099	44	0.023	46	0.087	236	0.047	92	0.054	232	0.103

¹ Wakebe (2002); * Zero proportion is counted as 1/4*n* (Bartlett's adjustment).

Table 4. Fisher's exact probability test for the difference in trait frequencies between the early prehistoric northern Vietnamese (EPNV) and late prehistoric northern Vietnamese (LPNV)

Trait	EPNV			LPNV			<i>P</i>
	<i>n</i>	+	%	<i>n</i>	+	%	
MET	59	3	5.1	65	4	6.2	1.0000
SOF	99	19	19.2	100	37	37.0	0.0071
OL	40	0	0.0	52	3	5.8	0.2547
PNB	31	3	9.7	76	14	18.4	0.3842
HGCB	38	5	13.2	73	6	8.2	0.5062
OSO	29	0	0.0	65	3	4.6	0.5500
MPC	51	1	2.0	95	2	2.1	1.0000
TZS	43	1	2.3	65	1	1.5	1.0000
MHB	51	0	0.0	105	5	4.8	0.1734

The results of MD statistic applied to the nine nonmetric cranial traits for the eight samples are set out in Table 5. Interpopulation relationships between the early and late prehistoric northern Vietnamese samples and the recent Vietnamese sample, based on the distance matrix shown in Table 5, are illustrated in Figure 1. The distances between the early prehistoric northern Vietnamese sample and the late prehistoric northern Vietnamese as well as the recent Vietnamese sample are significant ($P < 0.05$). On the other hand, dissimilarity between the late prehistoric northern Vietnamese and recent Vietnamese samples is statistically not significant. Such findings suggest that the early prehistoric northern Vietnamese sample is distinct from the subsequent inhabitants in this region.

Figure 2 is a two-dimensional expression resulting from PCO analysis of MD values among seven East/Southeast

Asian samples. The insignificant MD values between every pair of samples from late prehistoric northern Vietnamese, Weidun, recent Vietnamese, and recent Thai (Table 5) indicate that these groups form a relatively tight cluster. On the other hand, the clear separation of the early prehistoric northern Vietnamese sample from all other samples is indicated. These findings, together with the significant MD values between the early prehistoric northern Vietnamese sample and other samples as shown in Table 5, suggests that the early prehistoric northern Vietnamese group appears to be an outlier relative to the late prehistoric and the subsequent inhabitants in Vietnam.

The MD value between the Zhou/Han and Weidun samples is statistically significant. However, the MD values between the Zhou/Han sample and the late prehistoric northern Vietnamese, recent Vietnamese, Thai, and South Chinese series are not statistically significant. In Figure 2, the Zhou/Han sample is situated at an intermediate position between the late prehistoric northern Vietnamese and recent South Chinese samples. The recent South Chinese are the most peripherally positioned sample, separating from the late prehistoric northern Vietnamese, Weidun, and recent Vietnamese series. Except for the Zhou/Han sample, the distance measured by MD between the recent South Chinese and all other samples is statistically significant.

It is often emphasized that the late Pleistocene and early Holocene inhabitants of Southeast Asia were ancestral to modern Australian and Melanesian lineages (Bellwood, 1997; Matsumura et al., 2001; Matsumura, 2006). Taking such a hypothesis into account, the PCO analysis was applied to the MD matrix shown in Table 5, including the Australian sample. Figure 3 shows the first two principal

Table 5. MD matrix among the eight cranial series from Vietnam and the surrounding regions

	EPNV	LPNV	Weidun	Zhou/Han	Vietnam	Thailand	S China	Australia
EPNV		16.98	22.46	31.04	20.29	31.90	51.77	38.56
LPNV	16.98		9.79	10.93	6.45	8.73	18.14	47.22
Weidun	22.46	9.79		18.31	10.19	6.63	23.04	37.87
Zhou/Han	31.04	10.93	18.31		13.24	12.76	11.21	50.13
Vietnam	20.29	6.45	10.19	13.24		15.72	18.89	20.29
Thailand	31.90	8.73	6.63	12.76	15.72		39.19	96.44
South China	51.77	18.14	23.04	11.21	18.89	39.19		103.62
Australia	38.56	47.22	37.87	50.13	20.29	96.44	103.62	

Italic indicates $P > 0.05$.

Figure 1. Triangle indicating the MDs among the early prehistoric northern Vietnamese (EPNV), late prehistoric northern Vietnamese (LPNV), and recent Vietnamese. Closed squares, prehistoric; closed circle, recent.

coordinates, accounting for 77.4% of the total variance. The early prehistoric northern Vietnamese sample is slightly closer to the Australian sample than the late prehistoric northern Vietnamese sample. However, a clear separation between the Australian and the early prehistoric northern Vietnamese samples is evident. The MD value between the

two samples is significant at the 1% level. These findings suggest that the early prehistoric inhabitants in northern Vietnam, c. 12000–5000 years BP, do not necessarily share the same lineage leading to present-day Australians as far as cranial nonmetric characteristics are concerned.

Discussion

The degree to which morphological characteristics reflect population history or adaptive changes in subsistence behaviors, including environmental factors, has been the focus of much heated debate (Roseman, 2004; Betti et al., 2009; Hubbe et al., 2009; Relethford, 2010). Ossenberg (1994) and Hanihara et al. (2003) demonstrated that nonmetric cranial variation, when considered as a whole, varies across regions and periods in a manner matching neutral expectations. Such findings may allow us to fruitfully discuss a plausible population history for northern Vietnam.

The issue of the origin and movement of Southeast Asians

Figure 2. The 1st and 2nd principal coordinates based on the MD matrix among the seven cranial series from Vietnam and the neighboring regions. Closed squares, prehistoric; closed triangle, early historic; closed circles, recent; EPNV, early prehistoric northern Vietnamese; LPNV, late prehistoric northern Vietnamese.

Figure 3. The 1st and 2nd principal coordinates based on the MD matrix among the eight cranial series from Vietnam, South China, Thailand, and Australia. Closed squares, prehistoric; closed triangle, early historic; closed circles, recent; EPNV, early prehistoric northern Vietnamese; LPNV, late prehistoric northern Vietnamese.

has been one of the most controversial areas in archeology and anthropology for many years (e.g. Turner, 1990; Bellwood, 1997; Shi et al., 2005; The HUGO Pan-Asian SNP Consortium, 2009). The recent fossil record and archeological analyses ostensibly favor a complete or nearly complete replacement model (Bellwood, 1997; Matsumura et al., 2001, 2008a, b, 2011a, b; Matsumura and Hudson, 2005; Matsumura, 2006, 2011a, b). This model, the two-layer and replacement model, assumes that the indigenous inhabitants of Southeast Asia trace their phenotypic and genetic ancestry to an Australian-like lineage. Subsequently, a wave of migrants from somewhere in what is now southern China displaced and absorbed the majority of indigenous populations at some point around 5000–4000 years BP (Matsumura, 2006, 2011a, b; Matsumura et al., 2011a, b; Oxenham and Matsumura, 2011).

Here we discuss the extent to which such a general and global Southeast Asian population history model is applicable to northern Vietnam. In this context we examine the two-layer model by dividing it into two hypothesis: (1) the indigenous inhabitants of northern Vietnam were displaced by the expansion of more northerly distributed populations as a result of demographic growth related to agricultural development from around the middle Holocene; and (2) the aboriginal populations in the area of northern Vietnam represent the ancestral lineages that eventually led to present-day Australians.

Regarding the first hypothesis, a close affinity between the late prehistoric northern Vietnamese and recent Vietnamese, together with the distinctiveness of early prehistoric northern Vietnamese, as shown in Figure 1 and Figure 2, appears to fit the two-layer model emphasized by Matsumura (2006, 2011a, b) and Matsumura et al. (2008a, b, 2011a, b). The result shown in Figure 2, moreover, suggests that migrants from an outside source, for example Weidun and Zhou/Han populations from the lower Yangtze, had a strong influence on the pattern of morphological variation of the late prehistoric and subsequent northern Vietnamese.

Figure 2 and Figure 3 show the distinctiveness of the southern Chinese (one of the representatives of a major East Asian population—recent Han Chinese) from Southeast Asians. This finding may be inconsistent with the recent hypothesis for the Southeast Asian origin of East/Northeast Asians mainly supported by genetic studies (Shi et al., 2005; The HUGO Pan-Asian SNP Consortium, 2009). Future discussions of the prehistoric peopling of eastern Asia should deal with the issue of the dissimilarity of Southeast Asians and East/Northeast Asians.

Figure 3 shows what happens when the Australian sample is added to a series of Southeast Asian groups. While the interpopulation relationships shown in Figure 2 are retained for the most part, the early indigenous inhabitants of northern Vietnam, c. 12000–5000 years BP, do not necessarily share morphological characteristics with the recent Australian population. This indicates that the early Holocene inhabitants of the northern Vietnamese region were not the lineages leading to the present-day Australians, negating the second hypothesis of the model.

In contrast to the two-layer or replacement model, the regional-continuity or local-evolution model, in which

present Southeast Asians have evolved in Southeast Asia from earlier late Pleistocene peoples adapted to the tropical rainforest, rather than experiencing significant gene flow into Southeast Asia from an outside source (mainly southern China), is espoused by several scholars (Bulbeck, 1982; Turner, 1990; Hanihara, 1994, 2006; Pietrusewsky, 2006, 2008, 2010; Lertrit et al., 2008). The results shown in Figure 3 and Table 5 may support the local-evolution hypothesis at least in the region of northern Vietnam during and after the mid-Holocene periods.

These findings lead us to propose a modified version of the two-layer model as well as local-evolution model for the formation of present-day Southeast Asian physical characteristics, as far as northern Vietnam is concerned at least. How can the nonmetric cranial traits of the early prehistoric northern Vietnamese be interpreted and explained in a modern human evolutionary context?

Recent genetic and morphological studies indicate that an important factor behind the unique physical makeup of contemporary Southeast Asians may be attributed more or less to multiple gene flows from the west in the distant past (Lahr, 1996; Underhill et al., 2001; Hanihara, 2006). In other words, the Australian lineages may have been descendants of an earlier human dispersal into Southeast Asia, populations which may not have contributed to the rise of late Pleistocene and the subsequent Southeast Asians (Rasmussen et al., 2011). Another possible explanation may be a scenario of a morphological differentiation of modern humans in and after the terminal Pleistocene (Brown, 1996; Harvati, 2009; Hubbe et al., 2011). Harvati (2009) and Hubbe et al. (2011) suggest that the geographic differentiation of modern human morphology, including modernization and gracilization, is a relatively late phenomenon that occurred after the initial settlement of major geographic regions of the world. However, it still remains to be determined whether or not such morphological differentiation in fact occurred in vast areas of Southeast Asia including northern Vietnam. A higher mutation or drift rate, based mainly on small population size, may be also an undeniable possibility (Relethford, 1996; Powell and Neves, 1999). Since the present study only examined the relationship between the prehistoric northern Vietnamese and neighboring populations with relatively small sample sizes, such speculations are tentative and preliminary.

The results of the present study do not provide a clear choice between the two-layer hypothesis and local-evolution hypothesis for the formation of present-day Southeast Asian physical characteristics. As Lahr (1996) emphasizes, information on a greater temporal and spatial scale is essential for understanding the process of differentiation not only on a worldwide scale but also regional or local scales.

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