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Dermatoglyphic changes during the population admixture between Kam and Han Chinese

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Abstract

Genetic studies and gene localization for human dermatoglyphs are currently ongoing. However, the inheritance modes of various genetic traits are not well understood because of the complexity of dermatoglyph genetics. The study of admixed populations can contribute to the understanding of population genetic traits of dermatoglyphs. Here, we present the dermatoglyphic characteristics of Kam and Liujia Han, and the admixed population consisting of these two parent populations.

The characteristics of the admixed population do not always fall in the same ranges as the parent population characters but do seem to be biased to Kam or Liujia parent populations, depending on sex and ethnicity of parents. The total frequencies of different fingerprint types do not differ among these populations, but several of the quantitative traits and the palm true pattern frequencies do significantly differ between admixed and parent populations. The simple arch fingerprint frequency decreases significantly in the admixed population in comparison with parent populations while both simple whorl fingerprint frequency and finger

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ridge counts increase significantly. True pattern frequency of the span area of interdigital III and IV areas on right hands and the radial-loop frequency of the right index fingers in the admixed populations are consistent with their matrilineal population. These dermatoglyphic changes may result from increased heterozygosity in the admixed population. The genetic modes of these changes may be relatively simple and will be useful for future dermatoglyph genetic studies.

摘要

人类肤纹的遗传分析和基因定位正在如火如荼地展开。但由于肤纹遗传学的复杂性，各种遗传性状的遗传模式没有被很好地了解。通过研究混合群体将会有助于理解肤纹的群体遗传性状。本文分析了侗族和汉族六甲人的肤纹参数，以及这两个族群的后代混合群体的肤纹特征。后代混合群体的肤纹特征并不完全与父母辈侗族或汉族六甲人群体特征一致，而是根据个体性别和父母的民族不同而各有所偏离。各种指纹型的总频率在各种群体中没有显著差异，但是在混合群体和父母群体之间一些掌面定量参数和掌面花纹频率有显著差异。与父母系群体相比，混合群体中指纹的简弓频率显著减少，而简斗频率以及指纹嵴数却显著增加。混合群体的右手跨越指间三区和四区真实花纹频率和右食指的桡箕频率与母系群体数据接近。这些肤纹变化可能是由后代混合群体的有关等位基因杂合性增加而引起的。这些在群体混合中有变化的肤纹参数的遗传模式可能相对简单，深入研究这些参数可能会有所突破。

Introduction

Dermatoglyphics, highly heritable (Zhang, 2007) and derived from the hypodermal neural system (Albers and Davis, 2007), is a pattern of skin ridges that enhances tactile sensation, especially prevalent in primates (Li et al., 2001). Due to the complex appearances of the dermatoglyphic traits, e.g. age-related changes, the genetic study of dermatoglyphs had steadily declined until genetic modes of inheritance for certain dermatoglyph indices were discovered recently. Finger ridge counts and frequencies of all palm patterns follow the genetic modes of major genes (Gilligan et al., 1987). The distribution of interdigital patterns has been proven to follow a multi-allelic major gene mode of inheritance (Li et al., 2003). A similar mode of inheritance has also been observed for finger ridge counts, in which significant genomic linkage has been found on chromosome 5 and 1 (Medland et al., 2007). However, no Mendelian modes of inheritance have been discovered for most dermatoglyph characteristics in pedigree studies because of either low inheritance or a too large number of contributing genes (Sengupta and Karmakar, 2004). To better study the genetic modes of dermatoglyph inheritance, it is helpful to observe and analyse the changes in dermatoglyphic traits resulting from population admixture.

Dermatoglyphic differences among geographic regions and ethnic groups are widely used in the measurement of relevant population relationships and genetic distances (Cummins and Midlo, 1976; Li et al., 2006; Vormittag et al., 1986). For example, among populations in China (Ding et al., 2001), dermatoglyphic traits are shown to be highly associated with ethnicity (Liu et al., 2004). Dermatoglyph variables are steadily inherited and change slowly in populations. However, variability of dermatoglyphics may increase during the population admixture from two parent populations largely differentiated in dermatoglyphic characters, potentially revealing unknown modes of inheritance for certain traits. Furthermore,

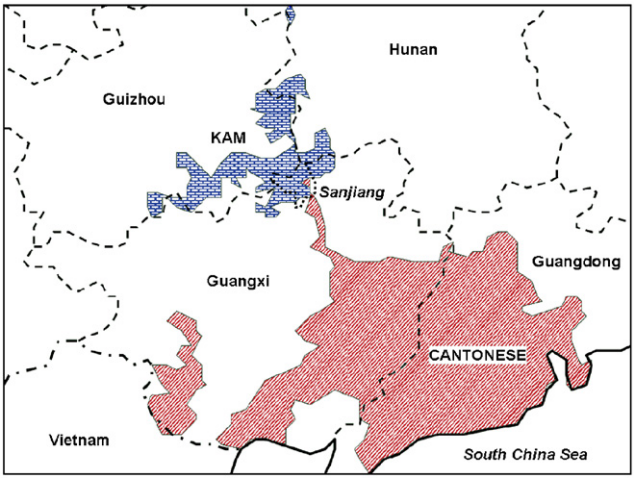

Fig. 1. Distributions of Cantonese Han and Kam and the location of Sanjiang County.

population intermarriages may counteract the multiple effects of dermatoglyphic changes in pedigree analyses, such as age, manual labor, and multi-gene effects.

In this paper, we analysed the dermatoglyphic changes in the offspring of intermarried Kam and Han populations, residing in the Sanjiang Dong Autonomous County of the Guangxi Zhuang Autonomous District in southern China (Fig. 1), studying all participants in the same age group. Kam belong to the Daic ethnic phylum, an indigenous population in South China, and have a population of approximately 2.96 million (2000 census), 192,000 of whom reside in Sanjiang County. Han Chinese in Sanjiang are comprised of 30,000 Liujia people who immigrated from northern China in recent history and speak Cantonese (Li et al., 2002). Kam differ largely from Liujia Han in many dermatoglyphic traits (Ding et al., 2001), as well as in other physical characters (Huang et al., 2008; Pang et al., 1989; Zhou et al., 2002) and genetic markers (Li et al., 2008; She et al., 2001). Y chromosome is one of the most ethnically associated genetic markers. The most frequent Y chromosome haplogroup of Kam is O2, while that of Han Chinese is O3, indicating a distinctly different genetic history of these two populations (Li et al., 2008). Intermarriages between these two groups were not culturally permitted in their history until recently (Li et al., 2002), making these populations good samples to study dermatoglyphic changes during population admixture.

Materials and methods

Population samples

Dermatoglyph samples were collected from Liujia Han, Kam and their intermarriage offspring in Sanjiang Dong Autonomous County in northern

Table 1. Ten fingers' fingerprint type frequencies of the simplex and admixed populations of Kam and Han from Sanjiang.

Father	Mother	Sex	Code	Sample size	Simple arch (As)	Tented arch (At)	Radial loop (Lr)	Ulnar Loop (Lu)	Simple whorl (Ws)	Double whorl (Wd)
Kam	Kam	Male	KKM	51	6.47	0.00	4.12	39.41	42.94	7.06
Kam	Kam	Female	KKF	51	10.98	0.39	1.57	48.43	32.16	6.47
Han	Han	Male	SSM	54	4.81	0.00	3.70	41.85	44.07	5.56
Han	Han	Female	SSF	56	7.14	0.36	3.21	52.50	33.21	3.57
Kam	Han	Male	KSM	45	2.00	0.00	3.11	50.22	36.67	8.00
Kam	Han	Female	KSF	40	4.75	0.00	2.25	39.75	48.75	4.50
Han	Kam	Male	SKM	42	2.86	0.00	2.14	47.14	43.57	4.29
Han	Kam	Female	SKF	40	1.25	0.00	3.75	36.25	48.75	10.00

Guangxi. The sample size is 379 and the size of each subpopulation is shown in Table 1. All individuals in the study are 13–16 years old, healthy, and not related to each other. The subjects are in the same age group to eliminate possible age-associated dermatoglyphic changes. The same work can be done in other age groups in the future studies. The subjects and their guardians signed consent forms in accordance with consent guidelines.

Samples were collected by taking ink impressions of fingerprints and palm prints on white anti-acid paper.

Statistical standards

Frequencies of each fingerprint pattern and total finger ridge numbers were counted. For palm print samples, frequencies of every true pattern of interdigital areas, thenar, and hypothenar, as well as palmar flexion creases, a-b interdigital ridge counts, and axial triradius angles were measured. Classification and calculation of each pattern are based on Cummins and Midlo standards (Cummins and Midlo, 1976; Li et al., 2006).

Method of analysis

Samples were divided into eight subpopulations by sex and parental ethnic groups for further analysis and comparison. SPSS13.0 was used in dendrogram clustering, principal component analysis, and paired *t*-test analysis (Liu et al., 2004).

Results

Fingerprint frequency changes during Kam–Han admixture

Fingerprints are classified into six pattern types in this study. The frequency of each fingerprint type for the sum of each individual's ten fingers is listed in Table 1. Frequencies of the ulnar loop (Lu) and simple whorl (Ws) patterns are the highest, while frequencies of the tented arch (At) are the lowest. The frequency of simple arch (As) for each simplex population is significantly higher than that of admixture groups ($\chi^2 = 39.83$, $p < 0.01$), while Ws frequency is significantly lower ($\chi^2 = 14.52$, $p < 0.01$). For other types, there are no significant differences between simplex and intermarriage populations. If fingerprint type follows a multi-gene model, the simple arch fingerprint may be produced by homozygous genotypes of different alleles on several loci. As heterozygotes will increase in an admixture population, the fact that simple arch frequency decreases significantly in admixture offspring suggests that the arch fingerprint type results from homozygous genotypes on several loci. In each population, fingerprint types have variable distributions on different fingers (Table 2). The double whorl (Wd) fingerprint, the most variable trait, has a high frequency on the left thumbs but a low frequency for the other fingers. Frequencies

Table 2. Each finger's fingerprint type frequencies of the simplex and admixed populations of Kam and Han from Sanjiang.

Subpopulations	L1[a]						R1					
	As	At	Lr	Lu	Ws	Wd	As	At	Lr	Lu	Ws	Wd
KKM	5.88	0.00	5.88	35.29	35.29	17.65	5.88	0.00	0.00	23.53	47.06	23.53
KKF	3.92	0.00	0.00	35.29	43.14	17.65	5.88	0.00	0.00	37.25	45.10	11.76
SSM	7.41	0.00	0.00	40.74	25.93	25.93	7.41	0.00	0.00	29.63	51.85	11.11
SSF	7.14	0.00	3.57	42.86	28.57	17.86	7.14	0.00	3.57	60.71	28.57	0.00
KSM	4.44	0.00	2.22	44.44	26.67	22.22	0.00	0.00	0.00	64.44	33.33	2.22
KSF	7.50	0.00	0.00	50.00	25.00	17.50	20.00	0.00	0.00	25.00	55.00	0.00
SKM	0.00	0.00	14.29	35.71	35.71	14.29	0.00	0.00	0.00	42.86	50.00	7.14
SKF	0.00	0.00	0.00	25.00	37.50	37.50	0.00	0.00	0.00	12.50	75.00	12.50
	L2						R2					
	As	At	Lr	Lu	Ws	Wd	As	At	Lr	Lu	Ws	Wd
KKM	11.76	0.00	11.76	29.41	41.18	5.88	17.65	0.00	0.00	47.06	35.29	0.00
KKF	11.76	3.92	5.88	35.29	35.29	7.84	17.65	0.00	1.96	41.18	33.33	5.88
SSM	11.11	0.00	3.70	29.63	55.56	0.00	11.11	0.00	18.52	29.63	37.04	3.70
SSF	7.14	0.00	7.14	46.43	39.29	0.00	10.71	0.00	14.29	42.86	32.14	0.00
KSM	4.44	0.00	11.11	22.22	44.44	17.78	0.00	0.00	17.78	55.56	26.67	0.00
KSF	0.00	0.00	0.00	27.50	72.50	0.00	0.00	0.00	22.50	47.50	27.50	2.50
SKM	14.29	0.00	0.00	28.57	42.86	14.29	7.14	0.00	7.14	35.71	50.00	0.00
SKF	0.00	0.00	25.00	25.00	37.50	12.50	0.00	0.00	0.00	37.50	50.00	12.50
	L3						R3					
	As	At	Lr	Lu	Ws	Wd	As	At	Lr	Lu	Ws	Wd
KKM	11.76	0.00	5.88	47.06	35.29	0.00	0.00	0.00	0.00	52.94	41.18	5.88
KKF	13.73	0.00	0.00	56.86	25.49	3.92	13.73	0.00	0.00	64.71	15.69	5.88
SSM	0.00	0.00	3.70	48.15	40.74	7.41	0.00	0.00	3.70	59.26	29.63	7.41
SSF	10.71	3.57	0.00	46.43	35.71	3.57	7.14	0.00	0.00	67.86	21.43	3.57
KSM	2.22	0.00	0.00	57.78	22.22	17.78	0.00	0.00	0.00	80.00	17.78	2.22
KSF	0.00	0.00	0.00	27.50	70.00	2.50	0.00	0.00	0.00	72.50	25.00	2.50
SKM	0.00	0.00	0.00	64.29	35.71	0.00	0.00	0.00	0.00	64.29	28.57	7.14
SKF	12.50	0.00	12.50	25.00	37.50	12.50	0.00	0.00	0.00	62.50	37.50	0.00
	L4						R4					
	As	At	Lr	Lu	Ws	Wd	As	At	Lr	Lu	Ws	Wd
KKM	5.88	0.00	0.00	17.65	64.71	11.76	0.00	0.00	0.00	41.18	58.82	0.00
KKF	11.76	0.00	0.00	37.25	43.14	7.84	7.84	0.00	1.96	45.10	45.10	0.00
SSM	0.00	0.00	0.00	29.63	70.37	0.00	0.00	0.00	7.41	25.93	66.67	0.00

Table 2. (*continued*)

Subpopulations	L1[a]						R1					
	As	At	Lr	Lu	Ws	Wd	As	At	Lr	Lu	Ws	Wd
SSF	7.14	0.00	0.00	35.71	53.57	3.57	0.00	0.00	3.57	46.43	46.43	3.57
KSM	0.00	0.00	0.00	24.44	68.89	6.67	0.00	0.00	0.00	26.67	73.33	0.00
KSF	0.00	0.00	0.00	27.50	72.50	0.00	0.00	0.00	0.00	27.50	72.50	0.00
SKM	0.00	0.00	0.00	42.86	57.14	0.00	0.00	0.00	0.00	35.71	64.29	0.00
SKF	0.00	0.00	0.00	25.00	75.00	0.00	0.00	0.00	0.00	25.00	75.00	0.00
	L5						R5					
	As	At	Lr	Lu	Ws	Wd	As	At	Lr	Lu	Ws	Wd
KKM	0.00	0.00	11.76	47.06	35.29	5.88	5.88	0.00	5.88	52.94	35.29	0.00
KKF	11.76	0.00	3.92	64.71	17.65	1.96	11.76	0.00	1.96	66.67	17.65	1.96
SSM	0.00	0.00	0.00	70.37	29.63	0.00	11.11	0.00	0.00	55.56	33.33	0.00
SSF	7.14	0.00	0.00	67.86	21.43	3.57	7.14	0.00	0.00	67.86	25.00	0.00
KSM	0.00	0.00	0.00	60.00	28.89	11.11	8.89	0.00	0.00	66.67	24.44	0.00
KSF	0.00	0.00	0.00	57.50	42.50	0.00	20.00	0.00	0.00	35.00	25.00	20.00
SKM	0.00	0.00	0.00	64.29	35.71	0.00	7.14	0.00	0.00	57.14	35.71	0.00
SKF	0.00	0.00	0.00	62.50	37.50	0.00	0.00	0.00	0.00	62.50	25.00	12.50

[a]Fingers are marked as L for left hand, R for right hand, and 1 thumb, 2 index finger, 3 middle finger, 4 ring finger, 5 little finger.

of arches (At and As) are quite low on the ring fingers and middle fingers of the right hand. There is a large difference in radial-loop (Lr) frequency between populations. The radial loop usually appears on the index fingers (Ding et al., 2001). Here, a high frequency of radial loop appears on the right index finger of simplex Han and a much lower frequency on the same finger of simplex Kam. Even among offspring of different parental intermarriages, there is a difference in radial-loop frequency for the right index finger. KSM and KSF (offspring of Kam-father and Han-mother) have almost the same radial-loop frequency on the right index finger as the Han, while the frequency of SKM and SKF (offspring of Han-father and Kam-mother) are identical to the observed frequency in Kam. This suggests that the inheritance mode of radial loop may be relatively simple, perhaps related to the sex chromosome.

Changes of dermatoglyph quantitative traits during Kam–Han admixture

Dermatoglyph genetic studies are most concerned with quantitative indices. For instance, finger ridge counts and axial triradius angles ($\angle$atd) have been shown to have notable heritability (Gilligan et al., 1985, 1987; Medland et al., 2007). Total finger ridge counts on average for Kam and Han are 122.19 and 117.95, respectively.

Table 3. Finger ridge counts of the simplex and admixed populations of Kam and Han from Sanjiang.

Subpopulations	L5	L4	L3	L2	L1	R5	R4	R3	R2	R1	Total
KKM	12.82	14.59	13.29	11.06	14.76	12.06	13.94	12.53	10.82	15.88	131.75
KKF	10.35	12.25	10.84	9.31	13.45	9.47	12.67	9.39	9.65	15.25	112.63
SSM	11.81	14.26	12.93	11.56	14.41	9.89	14.44	12.22	11.22	15.96	128.70
SSF	10.21	11.64	10.75	9.43	10.68	9.32	13.36	9.96	9.89	11.96	107.20
KSM	14.22	14.56	13.33	11.44	15.44	11.22	15.33	12.00	13.22	16.56	137.32
KSF	15.25	19.00	15.50	13.75	11.50	10.75	19.00	14.50	12.75	9.75	141.75
SKM	12.57	14.71	12.86	12.21	16.21	10.36	14.21	12.43	12.93	17.79	136.28
SKF	13.00	15.75	12.25	13.63	16.88	13.13	15.63	13.13	13.88	16.88	144.16

Table 4. Palm quantitative parameters of the simplex and admixed populations of Kam and Han from Sanjiang.

Subpopulations	Interdigital ridge number (a-bRC)		Axial triradius (∠atd)		Percent distance of palm axial triradius (tPD)	
	L	R	L	R	L	R
KKM	34.00	34.94	41.88	42.53	17.85	18.22
KKF	33.33	34.25	41.69	41.90	18.35	26.41
SSM	35.78	36.70	41.37	41.70	17.44	18.24
SSF	35.00	36.93	43.46	42.46	21.57	20.73
KSM	35.56	35.89	38.11	37.67	14.94	14.05
KSF	33.50	38.00	44.50	46.00	23.19	25.22
SKM	35.86	39.07	43.93	44.64	21.77	22.16
SKF	36.63	34.75	40.75	40.13	17.64	18.41

Intermarriage offspring have an average of 139.88, higher than the two parent populations (Table 3), suggesting a heterozygote genotype possibility for genes associated with greater finger ridge numbers.

There is no significant difference in palm quantitative characters among any groups in the study (Table 4). This consistency among these characters may be explained by similarity in the two parent populations for these specific characters. If another study is conducted in other populations with large differences in these characters, changes in the admixed populations may be found.

Changes of palm pattern frequencies during the Kam–Han admixture

True pattern frequencies, largely vary among different palm areas (Table 5), they are highest in the interdigital IV area in our samples, which has also been found in

Table 5. Palm true pattern frequencies of the simplex and admixed populations of Kam and Han from Sanjiang.

Subpopulations	Thenar (T)		Interdigital II		Interdigital III		Span area of interdigital III and IV		Interdigital IV		Hypothenar (H)	
	L	R	L	R	L	R	L	R	L	R	L	R
KKM	0.00	0.00	0.00	0.00	5.88	5.88	0.00	0.00	47.06	41.18	11.76	11.76
KKF	0.00	0.00	0.00	0.00	3.92	17.65	0.00	1.96	41.18	45.10	9.80	7.84
SSM	0.00	0.00	0.00	0.00	0.00	11.11	3.70	14.81	48.15	37.04	3.70	3.70
SSF	3.70	0.00	0.00	0.00	11.11	22.22	7.41	7.41	40.74	37.04	18.52	11.11
KSM	0.00	0.00	0.00	0.00	0.00	11.11	11.11	33.33	44.44	55.56	33.33	11.11
KSF	0.00	0.00	0.00	0.00	0.00	2.50	0.00	20.00	50.00	52.50	32.50	17.50
SKM	0.00	0.00	0.00	0.00	7.14	0.00	0.00	0.00	64.29	57.14	14.29	7.14
SKF	2.50	0.00	0.00	0.00	12.50	0.00	0.00	0.00	65.00	57.50	0.00	0.00

Table 6. Palm flexion creases type frequencies of the simplex and admixed populations of Kam and Han from Sanjiang.

Subpopulations	Normal (N)		Bridge (B)		Sydney line (Sd)		Simian line (Sm)	
	L	R	L	R	L	R	L	R
KKM	88.24	82.35	0.00	5.88	0.00	0.00	11.76	11.76
KKF	92.16	88.24	1.96	7.84	3.92	0.00	1.96	3.92
SSM	88.89	96.30	0.00	0.00	0.00	0.00	11.11	3.70
SSF	100.00	89.29	0.00	0.00	0.00	0.00	0.00	10.71
KSM	88.89	100.00	0.00	0.00	11.11	0.00	0.00	0.00
KSF	100.00	100.00	0.00	0.00	0.00	0.00	0.00	0.00
SKM	92.86	85.71	7.14	0.00	0.00	7.14	0.00	7.14
SKF	75.00	87.50	12.50	0.00	0.00	0.00	12.50	12.50

other Chinese populations. Intermarriage offspring had a similar phenotype pattern of palm pattern frequencies as their matriline parent population, which has been observed for other characteristics such as the radial-loop frequency on the right index finger. Intermarriage offspring of Kam-fathers and Han-mothers inherited a high true pattern frequency of interdigital areas III and IV, as was observed in the simplex Han populations, while offspring from Han-fathers and Kam-mothers inherited a low frequency seen in the simplex Kam population. Although there seems to be no significant correlation between the appearance of right index finger radial loop and interdigital area between III and IV true pattern frequency, these findings suggest that both traits might be related to the X chromosome.

Normal type dominates palm flexion creases and does not differ much among populations (Table 6).

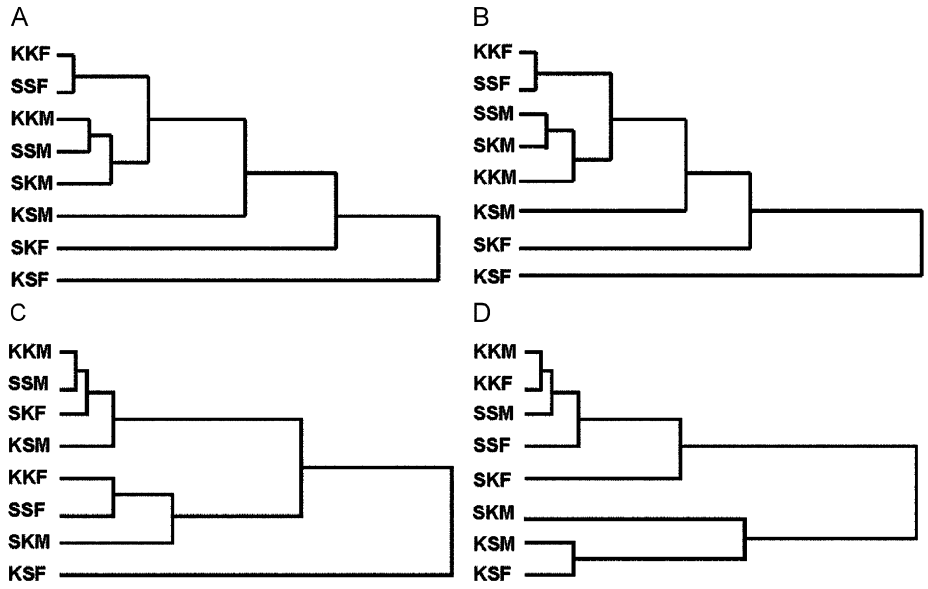

Fig. 2. Complete linkage dendrograms of the subpopulations of the simplex and admixed populations of Kam and Han from Sanjiang: (A) all dermatoglyphic traits; (B) fingerprint type frequencies; (C) quantitative traits: (D) palm pattern frequencies.

Dermatoglyph clustering analysis of Kam, Han and their intermarriage offspring

In our study, dermatoglyphs are divided into three categories as follows: frequencies of fingerprint pattern, quantitative traits, and palm pattern frequencies. Subpopulation samples are analysed and clustered at each category level, separately and at the full-scale level. Fig. 2 depicts the dendrograms of subpopulations, generated by the neighbor-joining maximum-likelihood method. For all the dendrograms except for the palm pattern, simplex subpopulations tend to cluster by sex, or rather, the same sex from simplex Han and simplex Kam populations are closer to each other than those of different sexes from the same simplex subpopulations. For example, females of two simplex populations are grouped much closer to each other than they are with males from their respective subpopulations.

In contrast, in the palm pattern frequency dendrogram, subpopulations are clustered within ethnic groups and not within sex groups; two sexes from the same population are clustered closer than the same sex from different populations. Therefore, palm pattern presents a clearer and more ethnic association than the other traits. Intermarriage offspring are on the outside branches of simplex group clusters and do not resemble the parent populations, suggesting complicated variations taking place in dermatoglyphic changes during admixture rather than a simple average.

Fig. 3 contains principal component plots of subpopulations based on different dermatoglyphic categories and all dermatoglyphic characteristics. Principal component

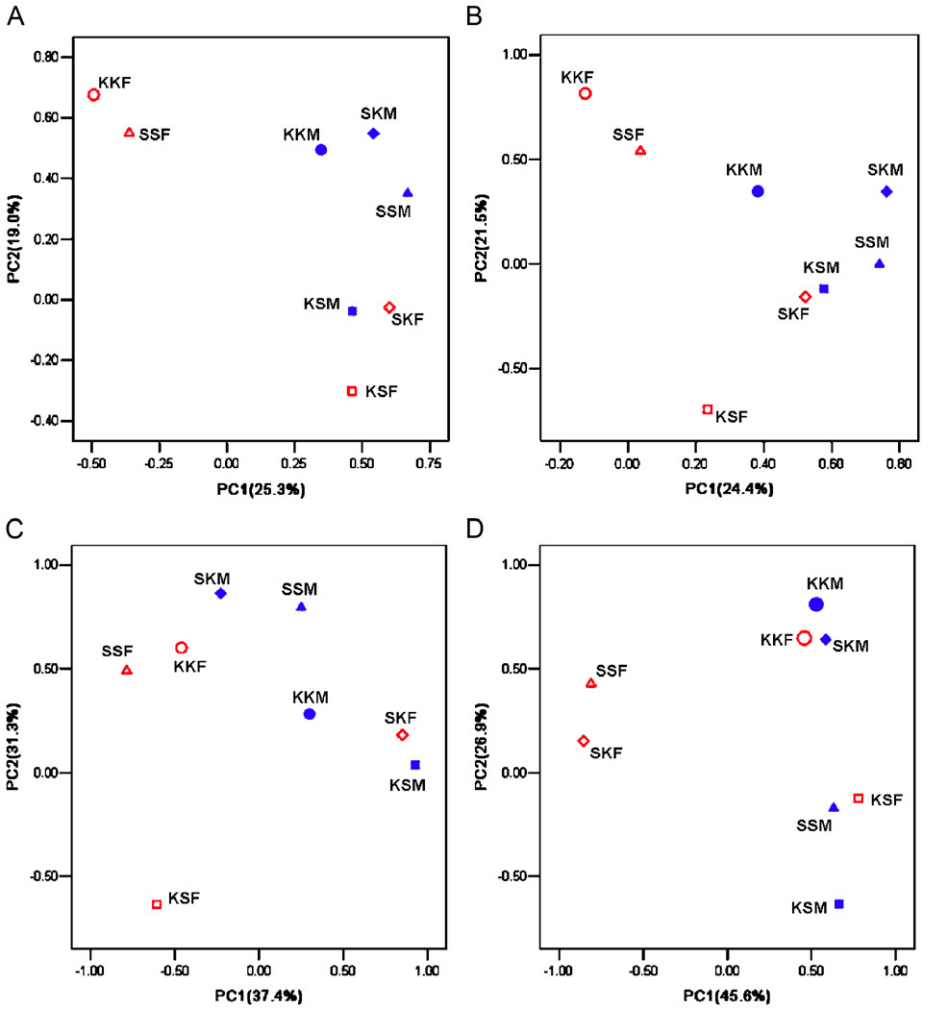

Fig. 3. Principal component plots of the simplex and admixed populations of Kam and Han from Sanjiang: (A) all dermatoglyphic traits; (B) fingerprint type frequencies; (C) quantitative traits: (D) palm pattern frequencies.

plots indicate that dermatoglyphic characters in intermarriage offspring are outside the range of simplex populations.

Significance of dermatoglyph differences among Kam, Han and their intermarriage offspring

To examine the significance of dermatoglyph differences among the subpopulations of our samples, pairwise *t*-tests were performed and the results can be found in

Table 7. Subpopulation pairwise comparison significance *t*-test of the simplex and admixed populations of Kam and Han from Sanjiang.

Pairs	All dermatoglyph	Fingerprint frequencies	Quantitative parameters	Palm pattern
KKM–KKF	0.905	1.000	0.243	0.807
SSM–SSF	0.752	1.000	0.182	0.159
KSM–KSF	0.920	1.000	0.058	0.353
SKM–SKF	0.312	1.000	0.264	0.084
KKF–SSF	0.585	1.000	0.895	0.072
KKF–KSF	0.523	1.000	0.005**	0.238
KKF–SKF	0.659	1.000	0.081	0.028*
SSF–KSF	0.641	1.000	0.001**	0.708
SSF–SKF	0.513	1.000	0.070	0.001**
KSF–SKF	0.345	1.000	0.244	0.025*
KKM–SSM	0.969	1.000	0.753	0.955
KKM–KSM	0.522	1.000	0.406	0.083
KKM–SKM	0.484	1.000	0.005**	0.313
SSM–KSM	0.429	1.000	0.447	0.050
SSM–SKM	0.428	1.000	0.001**	0.455
KSM–SKM	0.837	1.000	0.034*	0.312

*$p<0.05$, **$p<0.01$.

Table 7. There is no significant difference (at the 95% level) for fingerprint frequencies and whole-scale dermatoglyphics between any pair of subpopulations or between either sex within subpopulations. However, dermatoglyph quantitative characters of the same sex in different groups do significantly differ (at the 99.9% level) in some pairs, and significance is also observed for palm pattern frequencies for females only. The significant deviation of the characters among intermarriage offspring may result from increased heterozygosity for a few genes. As these dermatoglyphic traits are controlled by a few genes and there are different available alleles for each gene that cause variation between populations, heterozygous genotypes will be increased in the intermarriage offspring. This interpretation explains the significant differences in dermatoglyph quantitative characters and palm pattern frequencies among simplex and admixed populations.

Discussion

This study has shown genetic changes for some dermatoglyph traits as a result of intermarriage. There was a significant decrease of simple arch fingerprint frequency within the admixed population, a significant increase in finger ridge counts and simple whorl fingerprint frequency within the admixed population, and a strong relationship between matrilineal and offspring traits for both the right index finger

radial-loop frequency and the true pattern frequency of interdigital III and IV span area. These findings corroborate what has been reported in the literature about genetic modes and genomic location for dermatoglyphic characteristics. The hypothesis of bifactorial inheritance for fingerprint patterns was proposed by Grüneberg in 1928 (Zhang, 2007). He believed that the simple arch pattern is controlled by homozygous alleles on two different gene loci. However, Grüneberg only hypothesized that two alleles existed for each gene locus. In fact, there could be multiple nonsynonymous polymorphisms in one gene region, producing multi-haplotypes that weigh more than just two alleles. If there are multi-gene loci and multiple alleles at each of these loci, then gene heterozygosity within admixed populations will be more prevalent than in simplex populations. If genotype of simple arch reflects homozygosity at gene loci, the frequency will decrease among admixed populations. This prediction is exactly what is observed in this study. The increase of the simple whorl frequency may be just a ripple effect of the decrease of simple arch frequency.

Total finger ridge count is also related to heterozygous genotypes. Finger ridges are formed through regression of embryonic volar pads on fingers, and the number of ridges is largely related with the time and degree to which these pads sink (Loesch, 1983). Genetic or environmental influences during finger ridge formation are likely to affect the total finger ridge number. Contributing genes of finger ridge counts are located at 5q14.1, which include several zinc finger genes controlling gene expression (Medland et al., 2007). Different allelotypes of these genes may be associated with directions of finger ridges. Thus, heterozygosity for zinc finger genes may produce finger ridges with more directions and complex distributions and may also cause an increase in finger ridge counts.

Further analysis of the matrilineal inheritance of right index finger radial-loop and true pattern of the span area of interdigital III and IV may be revealing. Pedigree analysis has already revealed a multi-allelic major gene inheritance mode for interdigital III and IV true patterns. Analysis of whole genome linkage indicated a strong linkage signal at 7q21, near the split hand/foot malformation (ectrodactyly) type 1(SHFM1) gene (Li et al., 2003). However, genes on chromosome 7 do not follow matrilineal inheritance. There may be other related gene regions on the X chromosome that control the matrilineal inheritance in these two observed patterns. Abnormal sex chromosomes have been shown to cause dermatoglyph abnormality, especially finger ridge counts (Loesch, 1983), suggesting the existence of genes on sex chromosomes that control the formation of dermatoglyphs. The right index finger radial-loop frequency's genetic propensity deserves further analysis. It should also be noticed that the sample sizes are not large after being divided into eight subpopulations if the large variability of dermatoglyphic traits is taken into account. Samples with larger sizes and from different age groups should be collected in the future studies to confirm our conclusion.

In conclusion, through this study of dermatoglyph variation among simplex populations and intermarriage offspring, significant changes are found in the frequencies of simple arch and simple whorl fingerprints, and in finger ridge counts, which may be related to the increase of heterozygosity for relevant genes. We

postulate that radial-loop of the right index finger and the true pattern of interdigital III and IV areas are jointly affected by genes controlling the formation of finger ridges and other regulatory genes. There could be many genes associated with the formation of dermatoglyphs. However, through different analyses of pedigrees and populations, relevant genes and interactions may finally be found.

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