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Genetic and Environmental Influences on General Skin Traits: Healthy Twins and Families in Korea

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Family study can provide estimates of overall genetic influences on a particular trait because family relationships provide accurate measures of average genetic sharing. However, evidence of genetic contributions to skin phenotypes is limited, which may preclude genetic studies to identify genetic variants or to understand underlying molecular biology of skin traits. This study aimed to estimate genetic and environmental contributions to selected dermatologic phenotypes, that is, to melanin index, sebum secretion, and skin humidity level in a Korean twin-family cohort. We investigated more than 2,000 individuals from 486 families, including 388 monozygotic twin pairs and 82 dizygotic twin pairs. Variance component method was used to estimate genetic influences in terms of heritability. Heritability of skin melanin index, sebum secretion, and skin humidity (arm and cheek) were estimated to be 0.44 [95% CI 0.38–0.49], 0.21 [95% CI 0.16–0.26], 0.13 [95% CI 0.07–0.18], and 0.11 [95% CI 0.06–0.16] respectively, after adjusting for confounding factors. Our findings suggest that genetics play a major role on skin melanin index, but only mild roles on sebum secretion and humidity. Sebum secretion and skin humidity are controlled predominantly by environmental factors notably on shared environments among family members. We expect that our findings add insight to determinants of common dermatologic traits, and serve as a reference for biologic studies.

■ **Keywords:** melanin index, sebum secretion, skin humidity, twins, heritability

Paying attention to one's appearance is a part of basic human behavior, with which many daily life decisions are made. Many skin traits are related to appearance, and skin color is probably one of the most distinctive traits that characterize complexion.

Skin color is affected by melanin, carotenoids, oxyhemoglobin, and hemoglobin itself or its metabolite such as bilirubin (Freedberg et al., 2003). In addition, clinical conditions, such as jaundice, flushing, anemia, and melanin level affected by sunlight play important roles in determining complexion. Many people have been very interested in skin pigmentation disorders such as melasma and vitiligo. Dermal hyperpigmentary diseases are commonly found in Asians (Kang, 2012). Genetic factors have been reported to play significant roles in skin pigmentation, with heritabilities (h^2) ranging from 0.34 to 0.90 (Byard, 1981; Clark et al., 1981; Paik et al., 2012). The importance of genetic influence on melanin index response to sunlight exposure has also been reported (Barsh, 2003).

Levels of sebum secretion and skin humidity are additional traits that influence dermatologic conditions and aesthetic characteristics. Individual variations in sebum and humidity levels may be associated with the risk of acne or eczematous skin lesions. Sebum is a secretion of liquefied fat from sebaceous glands and protects the skin surface from drying. Alterations in sebum secretion are

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associated with common dermatologic conditions, such as acne vulgaris and seborrheic dermatitis, and a sebum excretion rate correlates with the severity of acne (Bataille et al., 2012; Bataille et al., 2002; Walton et al., 1988). The heritability estimate of acne was reported as 0.81 in the UK Twin Registry. Prevalence of acne is found in 70% of adolescents in Korea (Cho et al., 2014). The study reported that family history of acne is associated with increased risk of occurrence of acne in Korea (Cho et al., 2014). Sebum excretion is considered to be under genetic control but modified by environmental factors (Walton et al., 1988). Skin humidity is maintained by the skin barrier function but influenced by exogenous factors such as climate and endogenous factors such as hormones (Pons-Guiraud, 2007). Dysregulation of skin humidity is associated with xerosis, pruritus, increased irritability, and aggravation of existing skin diseases such as atopic dermatitis, psoriasis, hand eczema, contact dermatitis, or xerotic eczema (Miyagaki & Sugaya, 2015). However, to our knowledge, it has not been reported to what extent genes are involved in the regulation of skin humidity. Inference from indirect evidence might suggest the role of genetics in skin humidity control; that is, a recent meta-analysis of genome-wide association studies found that mutation in the filaggrin gene, known to stabilize the skin barrier (Ginger et al., 2005), is associated with atopic dermatitis, in which humidity may modify the onset or severity of the disease (Paternoster et al., 2012).

Heritability, which is a proportion of additive genetic variation out of total phenotypic variation, commonly evaluates the genetic contributions to the traits. The rest of the variance is explained by shared family environment and unique environmental factors (Bataille et al., 2012). Because family relationships provide accurate measures of average genetic sharing, family studies can provide estimates of overall genetic influences on a particular trait. However, to our knowledge, evidence of genetic contributions to skin phenotypes is limited, which may preclude genetic studies to identify genetic variants or to understand underlying molecular biology of skin traits.

Family studies confer an advantage in dissecting genes and environments, and adding twins can enrich family studies. The presence of monozygotic (MZ) twins enables the discrimination of polygenic and shared environmental variances, and potentially increases the power of family-based studies (Abecasis et al., 2002; Bataille et al., 2012) In order to estimate genetic and environmental contributions to skin phenotypes and to identify associated risk factors, we measured skin melanin index, sebum secretion, and skin humidity levels by using standardized measures in a Korean twin-family cohort.

Materials and Methods

Participants

The subjects involved in this study were selected from the Korean Healthy Twin Study, which is a twin-family cohort study aimed at investigating the genetic and environmental risk factors associated with complex diseases. The study cohort consisted of same-sex twin pairs (≥30 years old) and their first-degree adult family members. Participants were recruited by mail, based on the existing nationwide twin-family register, and by advertisement. The study design for the Korean Healthy Twin study has been previously described in detail (Gombojav et al., 2013; Sung et al., 2006). The skin survey was accompanied with the general health examination, which requires fasting for 12 hours (for glucose and lipids test). A very limited amount of water is allowed but no alcohol. Epidemiologic and clinical data were recorded by qualified interviewers at two clinical centers of general hospitals at the Samsung Medical Center in Seoul, and at the Busan Paik Hospital in Busan from November 2005 to January 2011. The study protocol of the Healthy Twin Study was approved by the institutional review board (IRB) of each hospital. The declaration of Helsinki protocols was followed and participants in the Healthy Twin Study gave their written, informed consent.

We used 16 short tandem repeat markers (AmpFlSTR Identifier Kit; PerkinElmer, Norwalk, CT) to confirm the zygosity until 2009, and then a zygosity questionnaire validated for accuracy (Song et al., 2010). Family relationships were further confirmed using 1 million SNP markers (Affymetrix GeneChip version 6).

Measurements

Skin phenotypes were measured by using a C+K multi probe adapter MPA 9 and probes (Courage + Khazaka Electronic GmbH, Köln, Germany). A Mexameter® MX 18 was used to assess melanin indices (MIs), as described by the EEMCO (European Group for Efficacy Measurement on Cosmetics and Other Topical Products; Pierard, 1998). The probe type used produces light and a receiver measures light reflected by skin. The MI value is computed as the ratio of the quantity of light emitted by the probe and the amount absorbed by the skin. Skin MIs were measured at three sites, that is, a cheek, the flexor surface of the right upper arm, and the lumbar area of the back. The authors selected the back region because it is less affected by exposure to sunlight. The participants were instructed to avoid applications of facial or body cream for 1 day before coming for their health examination and survey. Measurements of sebum secretion were taken from the glabella after washing the face for 30 minutes with a standardized detergent, using a Sebumeter® SM 815, as described by the EEMCO (Pierard et al., 2000). For skin humidity, measurements were taken from two sites, on a cheek and on the flexor surface of the right upper arm. Hydration level was estimated by using a Corneometer® CM825, as described by the EEMCO (Berardesca, 1997). All skin measurements were repeated three times, and if two measurements differed

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by more than 10%, the median value of the three were used, otherwise the average was taken; room temperature was maintained at 18–23°C and a relative humidity of 40–60%.

Statistical Analysis

We explored the relationships between continuous skin phenotypic variables (melanin index, sebum, and humidity) and covariates such as, age, sex, serum creatine, medical histories (hyperthyroidism, diabetes mellitus, atopic dermatitis, and chronic hepatitis/liver cirrhosis), smoking status, and the season when measurements were taken, using Spearman correlation analysis (for continuous variables), Wilcoxon rank sum test (Mann–Whitney *U*-test for dichotomous variables), or the Kruskal–Wallis test (for categorical variables). Statistical analysis was performed by using SAS version 9.3 (SAS Institute, Cary, NC, USA). Intraclass correlation coefficients (ICC) of skin phenotypes were estimated to evaluate familial correlations between specific family pairs in the pedigree by using S.A.G.E. software, version 6.1 (http://darwin.cwru.edu/sage/). Heritabilities (h^2) of each skin phenotype were estimated by using variance components methods using the SOLAR-Eclipse software package (http://solar-eclipse-genetics.org/). For heritability analysis, rank-based inverse normal transformation was applied to sebum and humidity values with deviated non-normal distributions (Beasley et al., 2009). Estimated heritabilities of skin phenotypes were adjusted for linear and non-linear effects of age, sex, the interaction between age and sex, and other covariates found to be significant. Differences between twins and non-twins are dissected into their respective genetic distances in the analysis. Identical twins show 100% genetic correlations, whereas fraternal twins shares 50% of genetics (the same as a usual sibling). Being a same family are further considered as random effects (as shared familial environments) in the model. The best-fitting model was selected based on likelihood estimates, for different models explained by additive genetics (A), non-additive genetics (= dominant genetics, D), unmeasured shared environments (C), and unique environments (E). Shared environmental components with household effects were considered by using the ACE model (including additive genetics and unmeasured shared and unique environments in the variance component model) for each skin phenotype.

Results

Initially, 3,079 subjects from 661 families, with 531 MZ and 121 dizygotic (DZ) twins were eligible for this study, and of these, 2,089 individuals (484 families, 385 MZ/81 DZ) were included in the analyses for melanin index, 2,167 (476 families, 375 MZ/81 DZ) for sebum production, and 2,185 (486 families, 388 MZ/82 DZ) for skin humidity.

Table 1 shows the distribution of subject characteristics in relation to skin phenotypes. Subject age was significantly correlated with each skin phenotype (r = -0.214, p value < .0001 for melanin index, r = -0.061, p value = .005 for sebum, r = 0.043, p value = .044 for humidity in arms, and r = 0.066, p value = .002 for humidity in cheeks by Spearman correlation analysis). Comparing the ranks of melanin index phenotype for other covariates, they were found to differ by history of diabetes mellitus, atopic dermatitis (p values < .05 by Wilcoxon rank sum test), and smoking status (p value < .0001 by the Kruskal–Wallis test). Ranks of sebum differed by sex (p value < .0001 by Wilcoxon rank sum test), smoking status, and season (p value < .0001 by the Kruskal–Wallis test), and were significantly correlated with creatine (r = 0.244, p value < .0001 by Spearman correlation analysis). When we compared the MZ ICC for melatonin indices at different sites, ICC = 0.745 [95% CI = 0.704–0.780] at cheek, followed by the ICC = 0.705 [95% CI = 0.657–0.744] at the flexor surface of right upper arm, and ICC = 0.593 [95% CI = 0.548–0.638] at the lumbar area of the back. Comparing the ranks of arm humidity for each covariate, they were found to differ by history of atopic dermatitis (p value < .05 by Wilcoxon rank sum test), and season (p value < .0001 by the Kruskal–Wallis test). The ranks of cheek humidity differed by sex, history of hyperthyroidism (p value < .05 by Wilcoxon rank sum test), smoking status, and tested season (p value < .05 by the Kruskal–Wallis test), and were negatively correlated with creatine (r = -0.103, p value < .0001 by Spearman correlation analysis).

Supplementary Table S1 presents the association between clinical characteristics and each skin phenotype. Except for age and smoking status, melanin index did not show significant associations. For sebum secretion index and skin humidity, age, sex, seasonal variation, and medical history (chronic hepatitis/liver cirrhosis, atopic dermatitis, or hyperthyroidism) showed associations (Supplementary material is available on the Cambridge Journals Online website.).

Table 2 shows the familial correlations between possible pair of family members for each skin phenotype. Correlations between MZ twins were moderately significant with r = 0.593 for melanin index, r = 0.459 for sebum, r = 0.379 for arm humidity, and r = 0.460 for cheek humidity (all p values < .0001), and these were higher than between pairs of full siblings (r = 0.315 for melanin index, r = 0.242 for sebum, r = 0.249 for arm humidity, and r = 0.315 for cheek humidity, all p values < .0001) and that between parent–offspring pairs (r = 0.222 for melanin index, r = 0.216 for sebum, r = 0.232 for arm humidity, and r = 0.298 for cheek humidity, all p values < .0001). Spousal correlation estimates of sebum and humidity were significant with r = 0.203 for sebum (p value = .0012), r = 0.240 for arm humidity (p value = .0001), and r = 0.373 for cheek humidity (p value < .0001).

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TABLE 1

Distribution of Study Population Characteristics in Relation to the Skin Phenotypes

		Melanin index ($N = 2,089$)		Sebum ($N = 2,167$)		Arm humidity ($N = 2,185$)		Cheek humidity ($N = 2,185$)	
	N (%) or Median (IQR)[a]	*p*	*p* value[b]	Median (IQR)	*p* value	Median (IQR)	*p* value	Median (IQR)	*p* value
Age (year)	41 (34–54)	132 (102–165)	<.0001 (-.214)[c]	56 (28–99)	.005 (-.061)	39.2 (31.7–47.9)	.044 (.043)	44.9 (29.8–57.5)	.002 (.066)
Sex									
Male	1,377 (42.3)	167 (100–167)	.857	85 (47–145)	<.0001	39.0 (30.9–47.6)	.214	40.3 (27.4–53.4)	<.0001
Female	1,879 (57.7)	132 (103–164)		43 (21–78)		39.3 (32.0–48.3)		47.4 (32.6–60.4)	
Creatine	0.9 (0.8–1.0)	132 (102–165)	.226 (-.027)[c]	56 (28–99)	<.0001 (.244)	39.2 (31.7–47.9)	.854 (-.004)	44.9 (29.8–57.5)	<.0001 (-.103)
History of hyperthyroidism			.234		.006		.846		.025
Yes	50 (1.6)	153 (95–194)		30.5 (16.0–64.0)		38.7 (33.0–46.0)		54.1 (41.5–63.5)	
No	3,029 (98.4)	132 (102–165)		57 (29–99)		39.2 (31.7–48.0)		44.7 (29.8–57.4)	
History of diabetes mellitus			.0001		.903		.797		.994
Yes	201 (6.5)	121 (91–150)		62 (26–105)		39.6 (32.2–48.6)		43.3 (31.0–57.6)	
No	2,878 (93.5)	133 (103–167)		56 (28–98)		39.2 (31.7–47.9)		45.0 (29.7–57.4)	
History of atopic dermatitis			.033		.215		.011		.544
Yes	151 (4.9)	121 (92–156)		61 (33–98)		36.7 (31.2–43.5)		44.5 (34.9–56.2)	
No	2,928 (95.1)	133 (103–166)		56 (28–99)		39.4 (31.7–48.3)		44.9 (29.5–57.5)	
History of chronic hepatitis/liver cirrhosis			.132		.927		0.387		.648
Yes	121 (3.9)	128 (92–161)		56 (26.5–99.5)		40.0 (32.9–49.7)		42.5 (31.0–54.3)	
No	2,958 (96.1)	132 (102–166)		56 (28–99)		39.2 (31.7–47.9)		45.0 (29.8–57.5)	
Smoking status			<.0001		<.0001		0.556		.005
Current	603 (19.6)	146 (111–186)		71 (37–133)		39.3 (32.0–47.9)		42.9 (29.5–54.8)	
Former	417 (13.5)	128 (96–159)		78 (35–140)		39.2 (31.5–46.2)		42.9 (28.5–55.5)	
Never	2,059 (66.9)	130 (101–162)		50 (24–90)		39.2 (31.7–48.5)		46.2 (30.5–58.6)	
Season					<.0001		<.0001		<.0001
Summer	517 (21.7)			58 (28–103)		43.1 (35.1–52.2)		50.7 (30.5–62.6)	
Spring/fall	1,032 (43.3)			64 (31–119)		39.8 (31.9–48.1)		46.0 (29.5–59.6)	
Winter	835 (35.0)			49 (24–84)		36.5 (29.7–44.4)		42.0 (30.0–52.1)	

Note: [a] *N* (%) for categorical variables and Median (interquartile range) for continuous variables; [b] *p* value obtained by Wilcoxon rank sum test or Kruskal–Wallis test, as appropriate, to test the difference of the skin phenotypes between groups; [c] *p* value (correlation coefficient estimates) obtained by Spearman correlation analysis, to test the correlation between the skin phenotype and covariate.

The ADE model (including additive and dominant genetics and unique environments in the variance component model) for melanin index fitted better than the AE (including additive genetics and unique environments in the variance component model) or ACE models. For sebum and humidity phenotypes, the ACE model fitted better than the AE or ADE models; however, heritability estimates according to the ACE model tended to be lower than those of the AE or ADE models (Table 3). Heritability estimates for the AE model were $h^2 = 0.547$ ($h^2 = 0.573$ adjusted for age, sex, age^2, history of diabetes mellitus, atopic dermatitis, and smoking status) for melanin index, $h^2 = 0.457$($h^2 = 0.410$ adjusted for age, sex, age^2, age^2 × sex, history of atopic dermatitis, smoking status, and season) for sebum, $h^2 = 0.398$ ($h^2 = 0.381$ adjusted for age, histories of atopic dermatitis, and season) for arm humidity, and $h^2 = 0.474$ ($h^2 = 0.483$ adjusted for age, sex, history of hyperthyroidism, smoking status, and tested season) for check humidity (all *p* values < .0001). Heritability using the ACE model was significantly estimated as $h^2 = 0.437$ (adjusted $h^2 = 0.486$) for melanin index, $h^2 = 0.339$ (adjusted $h^2 = 0.211$) for sebum, $h^2 = 0.147$ (adjusted $h^2 = 0.125$) for arm humidity, and $h^2 = 0.109$ (adjusted $h^2 = 0.109$) for cheek humidity (all *p* values < .05). Heritability using the ADE model was $h^2 = 0.333$ (adjusted $h^2 = 0.438$) for melanin index.

Discussion

Skin phenotypes, such as melanin index, sebum, and humidity are common complex traits that are explained by genetic and environmental factors. However, only a few genetic studies have addressed these skin phenotypes. Family studies of quantitative skin phenotypes enable the dissection of individual variation in skin phenotypes into genetic and environmental contributions, comparing the similarities of traits across different genetic relationship, assuming that they share certain level of common environments. In this study based on Korean healthy twins and their family members, each skin phenotype was found to be influenced by genetic and environmental components to varying degrees. Our heritability estimation finding suggests that over 43% of variation in skin melanin index in Korean twins and their families was conferred by genetic influences. Genetic studies on skin complexion involving genetically homogenous population have reported similar or larger genetic effects; 0.34∼0.48 for Australian (Clark et al., 1981) or 0.83 for Mongolian (Paik et al., 2012). Differences in study design and analytic methods make comparisons between previous studies and ours inconclusive. The study by Clark et al. (1981) measured pigmentation on more exposed skin areas and only involved twins. Thus, the findings from this study may reflect both melanin index and response to

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TABLE 2

Familial Correlations Between Possible Pair of Family Members for Each Skin Phenotype

Skin phenotypes	MZ twins			DZ twins			Full siblings			Parent-offspring			Spouse		
	N^a	ICC[b] ± *SE* [95% CI]	*p* value	*N*	ICC ± *SE* [95% CI]	*p* value	*N*	ICC ± *SE* [95% CI]	*p* value	*N*	ICC ± *SE* [95% CI]	*p* value	*N*	ICC ± *SE* [95% CI]	*p* value
Melanin index	236	0.593 ± 0.045 [0.548–0.638]	<.0001	44	0.302 ± 0.139 [0.163–0.440]	.041	1,442	0.315 ± 0.039 [0.275–0.354]	<.0001	1,566	0.222 ±0.032 [0.190–0.255]	<.0001	222	0.033 ± 0.069 [-0.035–0.102]	.629
Sebum	227	0.459 ± 0.055 [0.404–0.514]	<.0001	45	0.368 ± 0.130 [0.238–0.498]	.010	1,428	0.242 ± 0.037 [0.205–0.279]	<.0001	1,596	0.216 ± 0.031 [0.185–0.247]	<.0001	234	0.203 ± 0.061 [0.142–0.264]	.0012
Arm humidity	241	0.379 ± 0.058 [0.321–0.437]	<.0001	46	0.370 ± 0.129 [0.241–0.499]	.009	1,498	0.249 ± 0.037 [0.212–0.286]	<.0001	1,667	0.232 ± 0.031 [0.201–0.263]	<.0001	241	0.240 ± 0.059 [0.181–0.299]	.0001
Cheek humidity	241	0.460 ± 0.053 [0.407–0.513]	<.0001	46	0.190 ± 0.144 [0.046–0.334]	.198	1,494	0.315 ± 0.039 [0.276–0.354]	<.0001	1,670	0.298 ± 0.034 [0.264–0.332]	<.0001	242	0.373 ± 0.057 [0.316–0.430]	<.0001

Note: [a]Number of pairs; [b]ICC = Intraclass correlation coefficient.

ultraviolet exposures. Additionally, involving only twins may inflate the heritability estimation, because non-additive genetic effects are not easily discriminated from the additive genetic effects.

A study in a Mongolian population that measured skin darkness on the buttocks showed a very high level of genetic contribution of 0.83 (Paik et al., 2012). However, the participants in the study were younger, with an average age of 30 years, and shared environmental effects, including other environmental factors such as smoking and medical history of atopic dermatitis, were not considered. Considering that these environmental contributions were not accounted for in the Mongolian study, differences in the heritability estimates might be smaller with our study. We believe estimates in our study are stable because we involved more subjects with diverse genetic distances, and we accounted for a range of environmental factors.

We found that the heritability of sebum or humidity was weakly attributable to genetic contributions. However, if the shared environments are not accounted, the heritability of sebum, humidity increased to 0.41, 0.38 (arm), and 0.48 (cheek). It is noteworthy because some studies, such as nuclear family studies, cannot properly address shared environmental effects among family members. When shared environments are mixed with background polygenic effects, the heritability estimation might be inflated for skin sebum secretion or skin humidity levels.

The meaning of 'shared environments' for sebum secretion or humidity cannot be specified in this study alone. Because we adjusted for associated factors in each analysis, the 'common environments' refer to other unaddressed factors independent of both genetic or covariates in this study. Nutrition or other shared lifestyle factors, as well as indoor environments, might be possible explanations.

Quantitative genetic and environmental contributions to skin melanin index, sebum secretion, or humidity level would provide insight not only to the underlying biology of the traits, but related skin disease as well. For example, excessive sebum secretion or alterations in the composition of the secretion is a risk factor of acnes vulgaris. And low level of skin humidity is associated with eczematous dermatitis or pruritus (Freedberg et al., 2003). It is not clear with this study alone, whether genetic measures of skin melanin index in general healthy population are consistent with those among the clinical cases such as vitiligo. Our findings suggest that the role of sunlight exposure to skin melatonin index might be complex and probably interactive. The skin sites with more sunlight exposure (cheek) showed higher MZ ICC than with less (lower back skin). This might suggest that there exists a moderate level of heritability for baseline skin melatonin index, but the tanning ability might have more genetic influences.

This study confers several strengths. First, our data included various familial relationships in a Korean twin-family cohort, and these enabled us to decompose

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TABLE 3

Heritability (h^2) Estimates of Skin Phenotypes

	$h^2 \pm SE$ [95% CI]					Variance component[a]					
Skin phenotypes	Crude	*p* value	-2LL	Adjusted	*p* value	A	C	D	E	-2LL[b]	Model[c]
Melanin index	0.437 ± 0.053 [0.384–0.490]	<.0001	18162.5	0.486±0.049 [0.437–0.535][d]	<.0001	0.486	0.071	—	0.442	17996.7	ACE
(flank)	0.333 ± 0.056 [0.277–0.389]		18142.8	0.438±0.056 [0.382–0.494]		0.438	—	0.179	0.383	17993.0	**ADE**[h]
	0.547 ± 0.033 [0.514–0.582]	<.0001	18171.6	0.573±0.031 [0.542–0.604]	<.0001	0.573	—	—	0.427	18003.1	AE
Sebum	0.339 ± 0.050 [0.289–0.389]	<.0001	1992.7	0.211±0.049 [0.162–0.260][e]	<.0001	0.211	0.158	—	0.632	1557.1	**ACE**[h]
(glabella)	0.439 ± 0.051 [0.388–0.490]		1944.9	0.410±0.033 [0.377–0.444]	<.0001	0.410	—	0.000	0.590	1590.2	ADE
	0.457 ± 0.035 [0.422–0.492]	<.0001	1945.2	0.410±0.033 [0.377–0.444]	<.0001	0.410	—	—	0.590	1590.2	AE
Arm humidity	0.147 ± 0.054 [0.093–0.201]	.0023	1953.8	0.125±0.055 [0.070–0.179][f]	.0088	0.125	0.188	—	0.688	1906.6	**ACE**[h]
	0.398 ± 0.032 [0.366–0.430]			0.373±0.045 [0.329–0.418]		0.373	—	0.015	0.612	1940.8	ADE
	0.398 ± 0.032 [0.366–0.430]	<.0001	1988.0	0.381±0.032 [0.349–0.413]	<.0001	0.381	—	—	0.619	1940.9	AE
Cheek humidity	0.109 ± 0.050 [0.059–0.159]	.0122	14821.8	0.109 ± 0.049 [0.060–0.158][g]	.0103	0.109	0.287	—	0.604	14700.7	**ACE**[h]
	0.443 ± 0.045 [0.398–0.488]		14907.1	0.469 ± 0.044 [0.425–0.513]		0.469	—	0.023	0.507	14794.4	ADE
	0.474 ± 0.031 [0.443–0.505]	<.0001	14908.1	0.483±0.031 [0.452–0.514]	<.0001	0.483	—	—	0.517	14794.6	AE

Note: [a]A = additive genetics, D = dominant genetics, C = unmeasured shared environments, E = unique environments in the variance component model after adjusting for covariates; [b] -2×log-likelihood for the corresponding model after adjusting for covariates; [c]ACE = additive genetics and unmeasured shared and unique environments included in the variance component model, ADE = additive and dominant genetics and unique environments included in the variance component mode, AE = additive genetics and unique environments included in the variance component model; [d]Adjusted for age, sex, age^2, histories of diabetes mellitus and atopic dermatitis, and smoking status; [e]Adjusted for age, sex, age^2, age^2 × sex, history of atopic dermatitis, smoking status, and season; [f]Adjusted for age, history of atopic dermatitis, and season; [g]Adjusted for age, sex, history of hyperthyroidism, smoking status, and season; [h]Best-fitting models shown in bold type were selected using likelihood ratio test.

genetics and environments of skin phenotypes more precisely than those from classical twin studies or conventional family studies. Second, traits were measured from relatively large number of subjects by trained staff in centralized clinics, using standardized protocols. This study reported genetic contributions to general skin phenotypes such as sebum and humidity. This study has some limitations as well. First, the nature of the skin traits may differ from the anatomical sites. Our findings may not represent the influences of genetics on other sites. Second, our findings are mainly focused on the first question of the '20 questions' about skin biology. Even though the melanocortin-1 receptor (MC1R) gene is known as one of major genes that determine skin pigmentation (Latreille et al., 2009), studies regarding which specific genetic variants are associated with skin melanin index in Asians or the environmental determinants of skin humidity will ensue. Third, the moderate genetic effects on the skin melanin index with adjustment for environments may need replications in other populations as well.

In summarizing, we estimated genetic and environmental contributions to commonly measured skin traits in a Korean twin-family cohort. Our findings suggest that level of inherited susceptibilities may differ between skin melanin index and sebum secretion or humidity level; genetics play a major role in skin melanin index but a lesser role in sebum secretion or humidity control. Sebum secretion and skin humidity are controlled predominantly by environmental factors, notably on shared environments among family members. We expect that our findings add insight to determinants of common dermatologic traits, and serve as a reference for biologic studies.

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Disclosure of Interests

None.

Supplementary Material

To view supplementary material for this article, please visit https://doi.org/10.1017/thg.2016.86.

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