

# Nonmetric Cranial Trait Expression in Pre-contact Southwest Native Americans and Modern Asians



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## Introduction

The ability to accurately estimate the ancestry of skeletonized remains is vital to forensic anthropologists. Several methods have been developed to assist in the estimation of ancestry, and one such method is through the analysis of nonmetric cranial trait expression (Bass 2005; Brues 1990; Gill 1998; Hefner 2009; Rhine 1990). However, ancestry estimation methods are not free of problems. For example, one issue that arises with ancestry estimation is that the methods used to assess ancestry were predominately developed on African and European populations (Tallman 2016). This can generally be attributed to the lack of ancestral variation within skeletal collections throughout North America. As a result, methods for estimating ancestry have not been extensively developed for minority populations. In particular, pre-contact Native Americans have traditionally served as a biological reference for identifying modern Asian individuals due to their distantly shared genetic history (Bass 2005; Brues 1990; Gill 1998; Rhine 1990). Although the techniques for assessing ancestry, sex, stature, and age in Asians have been widely accepted in forensic settings (Tallman 2016), the idea that pre-contact Native Americans can sufficiently serve as a biological reference for identifying modern Asians has never been directly tested. Therefore, the present study explores craniomorph variability between pre-contact Native Americans and modern Asian individuals (Japanese and Thai) to ascertain whether population-specific methods should be developed.

## Skeletal Samples and Methods

The Native American sample consists of **150 pre-contact individuals** (housed at the AMNH) from the American Southwest that were recovered from various archaeological sites in New Mexico, Arizona, Colorado, and Utah. Data for the Asian sample were originally collected by Tallman (2016), and includes **300 modern Japanese and Thai individuals**. The Japanese sample consists of 150 known individuals from the greater Tokyo area who died during the 1960s-1990s (Jikei University, JU). The Thai sample consists of 150 known individuals from northern Thailand who died within recent decades (Khon Kaen University, KKU).

Thirty-five cranial and mandibular nonmetric traits were scored on the Native American sample following Hefner (2009), Parr (2006), and Rhine (1990) and compared to the cranial/mandibular trait data for the modern Thai and Japanese individuals. To assess intraobserver variation, 10% (n=15) of the Native American sample were re-scored. Descriptive statistics, Pearson chi-square analyses, and binary logistic regression equations were calculated using SPSS. Intraobserver error was examined with Cohen's kappa following Landis and Koch (1977). The binary logistic regression equations were tested on **20% holdout samples** consisting of 30 Japanese (JU), 30 Thai (KKU), and 30 Southwest Native American individuals from the Macromorphoscopic Databank (Hefner 2018).

## Results

Chi-square analyses indicate that 22 traits (62.9%) differed significantly among the groups for both sexes at the  $p < 0.05$  level. Intraobserver error ranged from fair to perfect following Landis and Koch (1977). The majority of traits fell within the moderate to substantial agreement categories; however, traits such as inferior nasal aperture and suture complexity performed less reliably (fair and moderate agreement, respectively).

Binary logistic regression equations for cranial and mandibular traits (Model 1), Hefner's (2009) traits (Model 2), cranial-only traits (Model 3), and mandibular-only traits (Model 4) are presented in Tables 1 through 4 and resulted in classification accuracies of **66.4-97.7%**. Further, cross-validated correct classifications using the holdout samples are presented in Table 5 (**60.0-90.0%**). The morphological traits that contributed the most to the models include ascending ramus profile, mandibular border shape, nasal overgrowth, nasal aperture width, nasal aperture shape, postbregmatic depression, mandibular tori, and prognathism, depending on the model.

Table 1. Binary logistic regression equations using cranial and mandibular traits combined (Model 1).

| Group       | Coefficients - Model 1 |       |        |        |        |        |       |       |       |        |       |        | % Correct |      |      | Total |
|-------------|------------------------|-------|--------|--------|--------|--------|-------|-------|-------|--------|-------|--------|-----------|------|------|-------|
|             | NAS                    | INA   | NO     | ZP     | ORB    | KEEL   | PROG  | ARP   | MBS   | GAR    | CP    | CON    | NA        | J    | TH   |       |
| J vs. NA*   | -1.484                 | --    | -1.992 | -1.167 | -1.002 | -0.862 | --    | 2.897 | 2.054 | --     | --    | 2.455  | 84.7      | 88.9 | --   | 88.1  |
| TH vs. NA** | --                     | --    | -2.334 | --     | -2.178 | -1.741 | -3.08 | 2.073 | 2.344 | --     | --    | 1.967  | 94.1      | --   | 89.6 | 91.8  |
| TH vs. J*** | -0.551                 | 0.559 | --     | --     | --     | 0.76   | 1.239 | --    | --    | -0.674 | 0.777 | -0.869 | --        | 74.8 | 77.9 | 76.3  |

\*Model used 270 individuals to build equation; \*\*Model used 269 individuals to build equation; \*\*\*Model used 279 individuals to build equation; NAS = nasal aperture shape; INA = inferior nasal aperture; NO = nasal overgrowth; ZP = zygomatic projection; ORB = orbital shape; KEEL = keeling; PROG = prognathism; ARP = ascending ramus profile; MBS = mandibular border shape; GAR = gonial muscle attachment ridging; CP = chin prominence; CON = constant; NA = Native American; J = Japanese; TH = Thai

Table 2. Binary logistic regression equations using Hefner's (2009) Traits (Model 2).

| Group       | Coefficients - Model 2 |        |        |        |       |        |        |        |        |        |        |        | % Correct |      |      | Total |
|-------------|------------------------|--------|--------|--------|-------|--------|--------|--------|--------|--------|--------|--------|-----------|------|------|-------|
|             | INA                    | IOB    | NAW    | NO     | SNS   | PBD    | TPS    | MT     | ZMS    | ANS    | NBC    | CON    | NA        | J    | TH   |       |
| J vs. NA*   | --                     | -1.043 | 0.624  | -1.536 | 0.809 | 20.841 | 0.962  | --     | -0.984 | --     | --     | -0.424 | 82.8      | 71.1 | --   | 77.1  |
| TH vs. NA** | -0.349                 | --     | 2.409  | -2.589 | 0.203 | --     | 1.456  | 0.561  | -0.452 | 0.411  | -0.125 | -7.177 | 85.8      | --   | 80.2 | 83.2  |
| TH vs. J*** | 0.525                  | -0.182 | -1.084 | 0.73   | 0.299 | 1.013  | -0.162 | -0.492 | -0.983 | -0.549 | --     | 3.168  | --        | 78.1 | 67.0 | 72.8  |

\*Model used 262 individuals to build equation; \*\*Model used 250 individuals to build equation; \*\*\*Model used 243 individuals to build equation; INA = inferior nasal aperture; IOB = interorbital breadth; NAW = nasal aperture width; NO = nasal overgrowth; SNS = supranasal suture; PBD = postbregmatic depression; TPS = transverse palatine suture; MT = malar tubercle; ZMS = zygomaticomaxillary suture; ANS = anterior nasal spine; NBC = nasal bone contour; CON = constant; NA = Native American; J = Japanese; TH = Thai

Table 3. Binary logistic regression equations using cranial traits (Model 3).

| Group       | Coefficients - Model 3 |        |        |        |       |        |        |       |        |        |       |        |        |        |        | % Correct |        |      | Total |      |      |
|-------------|------------------------|--------|--------|--------|-------|--------|--------|-------|--------|--------|-------|--------|--------|--------|--------|-----------|--------|------|-------|------|------|
|             | INA                    | IOB    | NAS    | NAW    | NBC   | NBS    | NO     | SNS   | ORB    | PBD    | TPS   | KEEL   | SF     | ZP     | PROG   | DAS       | CON    | NA   |       | J    | TH   |
| J vs. NA*   | 0.127                  | -1.681 | -2.31  | 1.374  | 0.023 | -0.988 | -1.615 | 1.074 | -0.66  | 20.716 | 1.42  | -1.406 | -1.949 | -1.394 | -0.825 | 1.949     | 10.118 | 91.4 | 91.4  | --   | 91.4 |
| TH vs. NA** | -0.74                  | --     | -4.117 | 6.429  | --    | --     | -3.905 | 1.793 | -4.675 | --     | 3.252 | -4.56  | -2.721 | -3.047 | -5.596 | 6.705     | 5.414  | 97.7 | --    | 95.9 | 96.9 |
| TH vs. J*** | 0.56                   | --     | --     | -0.641 | 0.071 | --     | --     | --    | --     | 0.61   | --    | 0.847  | --     | --     | 1.11   | --        | -1.164 | --   | 70.8  | 72.7 | 71.7 |

\*Model used 244 individuals to build equation; \*\*Model used 226 individuals to build equation; \*\*\*Model used 243 individuals to build equation; INA = inferior nasal aperture; IOB = interorbital breadth; NAS = nasal aperture shape; NAW = nasal aperture width; NBS = nasal bone shape; NO = nasal overgrowth; SNS = supranasal suture; ORB = orbital shape; PBD = postbregmatic depression; TPS = transverse palatine suture; KEEL = keeling; SF = suture form; ZP = zygomatic projection; PROG = prognathism; DAS = dental arcade shape; CON = constant; NA = Native American; J = Japanese; TH = Thai

Table 4. Binary logistic regression equations using mandibular traits (Model 4).

| Group       | Coefficients - Model 4 |       |       |       |        |        |        |        |        |        |       | % Correct |         |      | Total |      |      |
|-------------|------------------------|-------|-------|-------|--------|--------|--------|--------|--------|--------|-------|-----------|---------|------|-------|------|------|
|             | MBS                    | GAR   | CS    | CP    | MRI    | GE     | AMF    | TORI   | MB     | ARS    | ARP   | NMF       | CON     | NA   |       | J    | TH   |
| J vs. NA*   | 2.171                  | 0.388 | 0.365 | 2.438 | --     | -0.513 | --     | 2.588  | --     | -1.112 | 2.768 | 1.133     | -9.765  | 87.9 | 85.6  | --   | 86.8 |
| TH vs. NA** | 1.82                   | 1.739 | 0.493 | 2.262 | 1.019  | -0.677 | 1.39   | 3.304  | -2.929 | --     | 2.741 | --        | -13.533 | 89.8 | --    | 83.8 | 87.0 |
| TH vs. J*** | --                     | -0.69 | --    | 0.518 | -1.065 | --     | -1.164 | -0.557 | --     | --     | 0.323 | 1.417     | -0.284  | --   | 75.0  | 66.4 | 70.8 |

\*Model used 288 individuals to build equation; \*\*Model used 277 individuals to build equation; \*\*\*Model used 271 individuals to build equation; MBS = mandibular border shape; GAR = gonial muscle attachment ridging; CS = chin shape; CP = chin prominence; MRI = mandibular ramus inversion; GE = gonial eversion; AMF = accessory mandibular foramen; TORI = mandibular tori; MB = mylohyoid bridging; ARS = ascending ramus shape; ARP = ascending ramus profile; NMF = number of mental foramen; CON = constant; NA = Native American; J = Japanese; TH = Thai

Table 5. Cross-Validation Results.

| Group      | n  | Model 1   | Model 2   | Model 3   | Model 4   |
|------------|----|-----------|-----------|-----------|-----------|
|            |    | % Correct | % Correct | % Correct | % Correct |
| J* vs. NA  | 30 | 83.3      | 66.7      | 83.3      | 90.0      |
| J* vs. TH  | 60 | 78.3      | 76.7      | 75.0      | 71.7      |
| TH* vs. NA | 30 | 73.3      | 60.0      | 86.7      | 66.7      |
| NA* vs. J  | 30 | --        | 73.3      | --        | --        |
| NA* vs. TH | 30 | --        | 83.3      | --        | --        |

\*test sample analyzed

## Discussion and Conclusions

Pre-contact SW Native American individuals and modern Japanese and Thai display a considerable amount of nonmetric cranial and mandibular variation. In total, 22 traits differed significantly in both sexes between the groups. The skeletal morphology of these groups differs such that they can be distinguished with a fair amount of certainty using cranial and mandibular nonmetric traits within a statistical framework, indicating that more fine-tuned ancestry estimations are possible beyond the broadly defined "Asian" classification. This discriminatory ability is due, in part, to their differing population histories.

The binary logistic regression equations that determined the top predictor variables for each group include the combined cranial and mandibular traits (Model 1), and the cranial-only traits (Model 3). Overall, these models produced total correct classification rates of 71.7 to 96.9%. Hefner's (2009) trait model (Model 2) and the mandibular trait model (Model 4) demonstrate slightly lower total correct classification rates (70.8 to 87.0%) than Models 1 and 3, and therefore have marginally reduced discriminatory power (66.4-87.9%). While the facial traits are the most discriminatory, several neurocranial and mandibular traits also perform well. In all four models, the Japanese versus Thai equations produced the lowest correct classification rates, which is not surprising, given the groups' more closely related ancestral history compared to Southwest Native Americans. The cranial and mandibular traits demonstrated intraobserver error rates that ranged from fair to perfect agreement, with most traits exhibiting moderate to substantial agreement. This ultimately indicates that the scoring systems used within the present study are sufficient at producing consistent scores from the same observer on two separate occasions.

Although the logistic regression equations presented here exhibit varying levels of discriminatory power, with some below that which is accepted within forensic contexts, they were, nonetheless, created within a statistical framework with known error and success rates. These logistic regression equations have the scientific rigor necessary in a post-Daubert era. The results demonstrate that modern Asian and pre-contact Native American individuals are not skeletally homogenous, and as such, pre-contact Native Americans do not serve as accurate biological representatives for modern Asian individuals. The traditional approach of grouping Native Americans and Asians into one broad ancestral category for ancestry estimation purposes within the forensic context is scientifically invalid, especially in the current judicial climate. Thus, the results ultimately underscore the importance of the development and continued refinement of population-specific methods for ancestry estimation.

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