CHAPTER

22

A Baffling Convergence: Tooth Crown and Root Traits in Europe and New Guinea

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INTRODUCTION

All members of Homo sapiens share the same fundamental bauplan. That is why the medical community has long trained practitioners following normative standards. Only recently have doctors started paying more heed to variation in body size, gender, ethnicity, and so on when prescribing drugs and interpreting metabolic panels. In contrast to the medical arts, the roots of anthropology can be traced back to describing world and regional variation in stature, hair and eye color, hair and eye form, and nose form. These anthroposcopic variables were supplanted initially by precise measurements of the skeleton and body (osteometrics/anthropometrics) and these, in turn, were supplanted by variation in nuclear genetic markers and increasingly elaborate characterizations of the human genome (mtDNA and Y chromosome haplogroups, microsatellites, genomics, etc.).
For most measures of variation, two particular geographic groupings, Europeans and New Guineans, are diametrically opposed. The former are medium- to tall-statured and light-skinned while the latter are short-statured and dark-skinned. They differ in marked ways for hair form and color, eye color, and countless genetic variables. Not surprisingly, biodistance studies of world populations place Europe and New Guinea on the opposite branches/quadrants of dendrograms and ordinations (cf. Cavalli-Sforza et al., 1994; Nei and Roychoudhury, 1982, 1993).

Until recently, teeth played no role in worldwide biodistance studies so little attention was paid to the similarities and differences in tooth crown and root morphology between Europe and New Guinea. The presumption was that they would show a contrast in dental characteristics parallel to their differences for other biological and/or genetic variables.

In 1997, Scott and Turner analyzed world variation in dental morphology. In one analysis that involved 23 crown and root traits in 21 major regional groups (Figure 7.5, page 289), they found one major discordant result. Their dendrogram showed that most groups clustered in a manner that conformed to the analyses of genetic markers and cranial dimensions. One group, however, was out of place. Rather than clustering with Australia, Melanesia, and other Southeast Asian/Pacific populations, New Guinea clustered with Western Eurasians (Western and Northern Europe, North Africa). The authors were aware of this oddity but multiple analyses yielded the same result so they were presented as found, not as hoped for.

In a review of *The Anthropology of Modern Human Teeth* (Scott and Turner, 1997), Stodder (1998, p. 73) noted the anomalous placement of New Guinea and added that “One hopes that they fill some data gaps—New Guinea, Melanesia, Australia—so that future analyses will avoid perplexing results like the grouping of New Guinea dentition with those of Western Eurasians.” The goal of this paper is to do just that—fill some data gaps and evaluate the veracity of the bizarre linkage of New Guinea and Europe.

## A CLOSER LOOK AT THE BAFFLING CONVERGENCE

To derive the dendrogram that clustered New Guinea with Western Eurasians, the senior author had access only to samples that were composites of many smaller samples. In 2013, it became possible to access a greater variety of samples, including multiple subsamples from New Guinea, Australia, Europe, Southeast Asia, East Asia, and the Pacific. With a much larger assemblage of samples from the Christy G. Turner II database, it is now possible to reassess biodistance on a finer scale to determine if the tree linking New Guinea to Europe was an artifact of the earlier analysis.

### Traits

Eighteen crown and six root traits, scored on the basis of the Arizona State University Dental Anthropology System (ASUDAS) standards (Turner et al., 1991), were employed to reevaluate the puzzling New Guinea-European cluster. The traits are listed in Table 22.1 along with mean trait frequencies for New Guinean, Australian, European, Southeast Asian, Polynesian, and Melanesian samples. All numbers represent mean total trait frequencies unless noted by breakpoints.

### Methods

Although our primary emphasis is on biodistance, Model I Analysis of Variance was first used to compute means and standard deviations for multiple samples from each of the following regions: New Guinea,
<table>
<thead>
<tr>
<th>Trait</th>
<th>New Guinea (4-8)</th>
<th>Australia (6-15)</th>
<th>Europe (9-11)</th>
<th>SE Asia (13-18)</th>
<th>East Asia (9-15)</th>
<th>Polynesia (4-7)</th>
<th>Melanesia (4-5)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Tooth BP</td>
<td>Mean S.D.</td>
<td>Mean S.D.</td>
<td>Mean S.D.</td>
<td>Mean S.D.</td>
<td>Mean S.D.</td>
<td>Mean S.D.</td>
</tr>
<tr>
<td>Shoveling</td>
<td>UI1 3+</td>
<td>0.000 0.0000</td>
<td>0.162 0.1497</td>
<td>0.040 0.0502</td>
<td>0.421 0.2083</td>
<td>0.531 0.2596</td>
<td>0.132 0.1032</td>
</tr>
<tr>
<td>Distal accessory ridge</td>
<td>UC 2+</td>
<td>0.345 0.1920</td>
<td>0.601 0.2714</td>
<td>0.434 0.1499</td>
<td>0.623 0.2816</td>
<td>0.604 0.1568</td>
<td>0.413 0.1085</td>
</tr>
<tr>
<td>Root number</td>
<td>UM2 3</td>
<td>0.550 0.1205</td>
<td>0.811 0.0478</td>
<td>0.596 0.0328</td>
<td>0.752 0.1026</td>
<td>0.645 0.1471</td>
<td>0.475 0.0936</td>
</tr>
<tr>
<td>Lingual cusp number</td>
<td>LP2 2+</td>
<td>0.611 0.2538</td>
<td>0.745 0.1103</td>
<td>0.633 0.0800</td>
<td>0.783 0.0982</td>
<td>0.700 0.1461</td>
<td>0.836 0.0961</td>
</tr>
<tr>
<td>Cusp 6</td>
<td>LM1 1+</td>
<td>0.133 0.1723</td>
<td>0.645 0.1494</td>
<td>0.077 0.0575</td>
<td>0.369 0.1273</td>
<td>0.367 0.1279</td>
<td>0.589 0.1092</td>
</tr>
<tr>
<td>Cusp number</td>
<td>UM2 4</td>
<td>0.556 0.1517</td>
<td>0.096 0.0514</td>
<td>0.734 0.1518</td>
<td>0.311 0.1101</td>
<td>0.303 0.1696</td>
<td>0.331 0.0858</td>
</tr>
<tr>
<td>Deflecting wrinkle</td>
<td>LM1 2+</td>
<td>0.104 0.1259</td>
<td>0.388 0.1193</td>
<td>0.137 0.0667</td>
<td>0.429 0.1665</td>
<td>0.363 0.2261</td>
<td>0.289 0.2190</td>
</tr>
<tr>
<td>Tomes' root</td>
<td>LP1 1</td>
<td>0.038 0.0427</td>
<td>0.287 0.0640</td>
<td>0.108 0.0674</td>
<td>0.219 0.1118</td>
<td>0.158 0.1326</td>
<td>0.163 0.1273</td>
</tr>
<tr>
<td>Root number</td>
<td>LM1 3</td>
<td>0.000 0.0000</td>
<td>0.035 0.0315</td>
<td>0.005 0.0070</td>
<td>0.111 0.0507</td>
<td>0.197 0.1332</td>
<td>0.090 0.0723</td>
</tr>
<tr>
<td>Winging</td>
<td>UI1 1</td>
<td>0.140 0.2190</td>
<td>0.104 0.0889</td>
<td>0.016 0.1533</td>
<td>0.230 0.1357</td>
<td>0.254 0.0688</td>
<td>0.225 0.1508</td>
</tr>
<tr>
<td>Double shaving</td>
<td>UI1 2+</td>
<td>0.045 0.1167</td>
<td>0.063 0.1293</td>
<td>0.240 0.2175</td>
<td>0.284 0.2595</td>
<td>0.350 0.2426</td>
<td>0.186 0.1163</td>
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<tr>
<td>Interrupption groove</td>
<td>UI2 1+</td>
<td>0.146 0.0770</td>
<td>0.200 0.1161</td>
<td>0.379 0.0875</td>
<td>0.322 0.1296</td>
<td>0.413 0.1375</td>
<td>0.272 0.1097</td>
</tr>
<tr>
<td>Hypocone</td>
<td>UM2 0+1</td>
<td>0.049 0.0398</td>
<td>0.042 0.0605</td>
<td>0.243 0.0873</td>
<td>0.101 0.0699</td>
<td>0.146 0.0586</td>
<td>0.090 0.1014</td>
</tr>
<tr>
<td>Cusp 5</td>
<td>UM1 1+</td>
<td>0.632 0.1646</td>
<td>0.613 0.1408</td>
<td>0.152 0.0941</td>
<td>0.246 0.1220</td>
<td>0.191 0.1148</td>
<td>0.344 0.1733</td>
</tr>
<tr>
<td>Missing pegged</td>
<td>UM3 1</td>
<td>0.068 0.0233</td>
<td>0.094 0.0295</td>
<td>0.165 0.0728</td>
<td>0.213 0.2343</td>
<td>0.397 0.2317</td>
<td>0.310 0.0454</td>
</tr>
<tr>
<td>Root number</td>
<td>LC 2</td>
<td>0.004 0.0078</td>
<td>0.000 0.0000</td>
<td>0.000 0.0000</td>
<td>0.000 0.0000</td>
<td>0.000 0.0000</td>
<td>0.000 0.0000</td>
</tr>
</tbody>
</table>

Continued
Table 22.1  Mean Trait Frequencies for Seven Regional Groupings With an Emphasis on New Guinea, Australia, and Europe—Continued

<table>
<thead>
<tr>
<th></th>
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<td></td>
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<td>Mean</td>
<td>S.D.</td>
<td>Mean</td>
<td>S.D.</td>
<td>Mean</td>
<td>S.D.</td>
<td>Mean</td>
</tr>
<tr>
<td><strong>Australia</strong></td>
<td><strong>Europe</strong></td>
<td><strong>NG</strong></td>
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<td></td>
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<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Root number</td>
<td>UP1</td>
<td>2</td>
<td>0.272</td>
<td>0.0530</td>
<td>0.448</td>
<td>0.0722</td>
<td>0.479</td>
<td>0.1524</td>
<td>0.373</td>
</tr>
<tr>
<td>Groove pattern</td>
<td>LM2</td>
<td>Y</td>
<td>0.389</td>
<td>0.1453</td>
<td>0.257</td>
<td>0.0954</td>
<td>0.261</td>
<td>0.0755</td>
<td>0.310</td>
</tr>
<tr>
<td>Distal trigoid crest</td>
<td>LM1</td>
<td>1</td>
<td>0.000</td>
<td>0.0000</td>
<td>0.048</td>
<td>0.0536</td>
<td>0.038</td>
<td>0.0347</td>
<td>0.074</td>
</tr>
<tr>
<td>Protoconid</td>
<td>LM1</td>
<td>2+</td>
<td>0.049</td>
<td>0.0798</td>
<td>0.015</td>
<td>0.0211</td>
<td>0.008</td>
<td>0.0169</td>
<td>0.046</td>
</tr>
<tr>
<td>Odontomes</td>
<td>All PM</td>
<td>1+</td>
<td>0.000</td>
<td>0.0000</td>
<td>0.035</td>
<td>0.0479</td>
<td>0.016</td>
<td>0.0378</td>
<td>0.024</td>
</tr>
</tbody>
</table>

**NG = Australia = Europe**

<table>
<thead>
<tr>
<th>Trait</th>
<th>Tooth</th>
<th>BP</th>
<th>Tuberculum dentale</th>
<th>Bushman canine</th>
<th>Cambell's cup</th>
<th>Pantrylo</th>
<th>Enamel extensions</th>
<th>Cusp 7</th>
<th>Root number</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td>U12</td>
<td>2+</td>
<td>0.254</td>
<td>0.0900</td>
<td>0.309</td>
<td>0.1082</td>
<td>0.249</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2+</td>
<td>UC</td>
<td>0.020</td>
<td>0.0500</td>
<td>0.008</td>
<td>0.0125</td>
<td>0.019</td>
<td>0.0198</td>
</tr>
<tr>
<td></td>
<td></td>
<td>3+</td>
<td>UMI</td>
<td>0.370</td>
<td>0.0940</td>
<td>0.342</td>
<td>0.0897</td>
<td>0.391</td>
<td>0.1455</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1+</td>
<td>UMI</td>
<td>0.038</td>
<td>0.0420</td>
<td>0.059</td>
<td>0.0556</td>
<td>0.024</td>
<td>0.0205</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2+</td>
<td>UMI</td>
<td>0.046</td>
<td>0.0272</td>
<td>0.083</td>
<td>0.0379</td>
<td>0.035</td>
<td>0.0462</td>
</tr>
<tr>
<td></td>
<td></td>
<td>1+</td>
<td>LM1</td>
<td>0.045</td>
<td>0.0452</td>
<td>0.048</td>
<td>0.0315</td>
<td>0.040</td>
<td>0.0392</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2</td>
<td>LM2</td>
<td>0.813</td>
<td>0.0792</td>
<td>0.932</td>
<td>0.0534</td>
<td>0.741</td>
<td>0.0802</td>
</tr>
</tbody>
</table>

Numbers in parentheses next to regional grouping refer to number of samples used to compute means (which varied by trait).
Results

Australia, Europe, Southeast Asia, East Asia, Polynesia, and Melanesia. With few exceptions, the frequencies for these regions were drawn from the Christy G. Turner II database. The number of samples ranged from 4 to 17 relative to region and individual trait.

Biodistance was analyzed for three sets of data that differed in number of samples, geographic regions compared, and number of traits used. The first analysis was performed on a dataset that contained 45 samples from New Guinea, Australia, Southeast Asia, Oceania, East Asia, and Europe. This analysis used 24 nonmetric dental traits. The second analysis was performed on a more restricted set of samples from the same regions (ie, 29 samples and 24 dental traits). The third analysis expanded the geographic reach of the previous analyses with the addition of 14 South Asian samples and two Sub-Saharan African samples from Hawkey (1998) and Irish (1993). For this analysis, we analyzed 23 nonmetric dental traits in 45 samples.

Four types of quantitative analysis were performed on the three datasets using R: A Language and Environment for Statistical Computing (R Core Team, 2013). The first method was to calculate biodistance statistics for each set of samples. The first statistic used was the mean measure of divergence (MMD) developed by C.A.B. Smith (Constandse-Westermann, 1972). This was conducted in the R environment using a script developed by Softyski (2011). After the MMD values were calculated, Bray–Curtis measures of dissimilarity (Bray and Curtis, 1957) were computed. The final two measures of biodistance were the Mahalanobis (1936) and Euclidean distance functions found in the R package, ecodist (Goslee and Urban, 2007). The results for the MMD, Bray–Curtis, Mahalanobis, and Euclidean values were presented in the form of similarity/distance/dissimilarity matrices for each dataset. The Mantel test was performed in R using the ade4 package to derive correlations between each pair of matrices (Dray et al., 2007).

To create dendrograms, or trees, the hclust function in R was used to derive hierarchical clusters from each matrix generated in the first method of analysis. Trees were drawn from the clusters using the plot and as.phylo functions in R. The as.phylo function instructions are to draw clusters in the form of trees. This function is found in the APE package (Paradis et al., 2004).

RESULTS

Analysis of Variance

Table 22.1 shows the summary statistics from Model I ANOVAs for 28 crown and root traits. The analysis involved 12 regional groupings, but results are restricted to New Guinea, Australia, Europe, Southeast Asia, East Asia, Polynesia, and Melanesia. Although Asian and Pacific groupings are included in the table, our focus is on the differences and similarities between New Guinea, Australian, and European trait means (ie, NG = Eur ≠ Aus; NG = Aus ≠ Eur; Aus = Eur ≠ NG; Aus = NG = Eur).

**New Guinea ≠ Europe ≠ Australia**

For 9 of 28 variables, New Guinea and Europe show similar mean frequencies and differ significantly from Australia. For eight of nine traits, the frequencies for Australia are significantly higher. The single exception is lower second molar (LM2) cusp number. For that variable, we used the frequency of 4-cusped LM2. If we focused on the frequency of 5-cusped teeth, then all nine variables would be significantly higher in Australia. Noteworthy similarities between Europe and New Guinea include a very
low frequency of UI1 shoveling, more UM2 root simplification, and the virtual absence of 3-rooted LM1. Cusp 6 is very low in Europe and New Guinea, a contrast to not only Australia but to all other Asian and Pacific groupings. Four-cusped LM2 frequencies in New Guinea are second only to Europeans, and this is a hallmark of the Eurodont dental pattern (Scott et al., 2013).

**New Guinea ≠ Australia ≠ Europe**
Seven variables are similar in New Guinea and Australia and differ significantly from Europeans. Of note, Europeans have higher frequencies of UI2 interruption grooves, missing-pegged UM3, and 2-rooted LC (another element of the Eurodont dental pattern). In contrast to the cusp number reduction shown in the lower second molars, there is relatively little cusp reduction in the upper second molar (i.e., hypocone) of New Guineans. One hallmark of the Australian dentition, UM1 cusp 5, has an almost identical frequency in New Guinea (61.3% and 62.2%, respectively). Bilateral incisor winging, a rare trait in Europeans, is around 10–15% in New Guinea and Australia, somewhat lower than the frequency range in Asian and Pacific populations (17–25%).

**Australia ≠ Europe ≠ New Guinea**
Five variables distinguish Australia and Europe from New Guinea. Two-rooted UP1 is much lower in New Guinea while LM2 Y pattern is significantly higher. Although rare in all groups, odontomes were not observed in any New Guinea sample but attain low frequencies in Australia and Europe.

**New Guinea = Australia = Europe**
Seven traits fail to differ significantly between New Guinea, Australia, and Europe. The cusp form of Carabelli’s trait (grades 5–7) is almost identical in the three groups (34–39%). New Guineans and Australians share with Europeans a low frequency of enamel extensions, which sets them apart from Asians and Polynesians but not Melanesians. Cusp 7, an Afridont trait (Irish, 2013), is in low frequency in all groups (3–7%), except for Melanesians where it is slightly higher (11%). UI2 tuberculum dentale is likewise similar for all groups falling generally in the 20–30% range.

When the surprising dental morphological linkage between New Guinea and Europe was first noted, the opportunity to examine this result was not available. Now that multiple samples from all geographic areas can be evaluated for a full suite of dental traits, the explanation for the finding is more apparent. Initially, it was thought that the high frequency of 4-cusped LM1 and LM2 played the major role in bringing New Guinea into the Western Eurasian sphere. A trait-by-trait breakdown shows 4-cusped lower molars are only part of the equation. Australians show significantly more shoveling, 3-rooted UM2, cusp 6, deflecting wrinkle, Tomes’ root, and 3-rooted LM1 than New Guinea and Europe. Only 4-cusped LM2 is significantly more common in New Guinea and Europe but for the presence of the hypoconulid, Australia would again have the highest frequency. For all of these traits, Australia is more in line with Southeast Asia. Turner (1992) may have been correct in noting Australians as proto-Sundadont but this does not apply to New Guinea. For this group of traits, New Guinea is more in line with the simplified dentition of Europe.

**Correspondence Between Distance Values**
A Mantel test evaluated the level of correlation between the four biometric distance methods: MMDs, Bray–Curtis, Mahalanobis, and Euclidean squared distance (Table 22.2). Distance methods should produce relatively congruent results with associated high levels of correlation between pairwise values in a distance
matrix. In this instance, that was the case for MMDs, Bray–Curtis, and Euclidean distances, all of which showed correlations ranging from 0.80 to 0.95. The odd statistic out was Mahalanobis. The correlations between Mahalanobis and the other three distance measures varied between 0.20 and 0.40. For the distances based on 29 samples, the correlations between Mahalanobis and the other three distance matrices were significantly different.

### Distance Values

Space precludes the inclusion of 12 large distance matrices (three datasets × four distance statistics). As focus is on the New Guinea–European similarity, Table 22.3 presents a summary pairwise matrix based on mean MMDs between nine regional groups (including India and Africa). In addition to the individual pairwise values, mean MMDs were computed for each region. At the bottom of the table, the rank order of regions relative to the regions noted along the top horizontal axis are listed from most to least similar.

In the summary matrix, the highest mean MMD values are associated with Africa, East Asia, India, and Australia, in that order. New Guinea has the lowest average MMD value compared to other regional groups followed by Melanesia, Southeast Asia, and Polynesia. Of the nine groups, Europe is exactly in the middle. Based on the distance rankings, Europe has the smallest MMD value with New Guinea (0.063). Melanesia is also close to New Guinea (0.071), but Australia is no closer to New Guinea (0.139) than Polynesia (0.133). For Europe, its closest distance is to New Guinea even with India included in the matrix. Interestingly, Australia is closer to Melanesia (0.091) than to New Guinea (0.139) and is quite divergent from Europe (0.312).

### Dendrograms

Two tree diagrams are presented as Figs. 22.1 and 22.2. Both diagrams include 45 samples but Fig. 22.1 includes samples from Europe, Asia, and the Pacific while Fig. 22.2 includes those regions plus 14 Indian and 2 African samples.

In Fig. 22.1, the first division in the dendrogram is between East Asian groups and everyone else. These samples are representative of the highly specialized Sinodont dentition (Turner, 1990). The next major split in the tree diagram is between a top cluster that includes European and New Guinea samples and a bottom cluster that includes an Australian branch and a Southeast Asian/Pacific branch. In other words, even with multiple samples representing Europe and New Guinea, as well as other Asian and Pacific samples, Europe and New Guinea still cluster together. This is consistent with both the findings of trait-by-trait comparisons via analysis of variance and the mean MMD values shown in Table 22.3.
<table>
<thead>
<tr>
<th></th>
<th>NG</th>
<th>AUS</th>
<th>EUR</th>
<th>SEA</th>
<th>EA</th>
<th>MEL</th>
<th>POL</th>
<th>IND</th>
<th>AFR</th>
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<td>0.000</td>
<td>0.000</td>
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<td>0.325</td>
<td>0.075</td>
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<td>0.000</td>
<td>0.000</td>
<td>0.000</td>
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<tr>
<td>East Asia</td>
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<td>0.280</td>
<td>0.172</td>
<td>0.075</td>
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FIGURE 22.1
Complete linkage dendrogram based on Mean Measure of Divergence values for 45 samples from New Guinea, Australia, East Asia, Southeast Asia, Melanesia, Polynesia, and Europe.
FIGURE 22.2
Complete linkage dendrogram based on Mean Measure of Divergence values for 45 samples from New Guinea, Australia, East Asia, Southeast Asia, Melanesia, Polynesia, Europe, Africa, and India.
The inclusion of Indian and African samples in Fig. 22.2 has a significant impact on how populations cluster. For this tree, there is a major dichotomy between the top and bottom clusters that are differentiated at the highest level. Within the top cluster, East Asia separates out from other Asian and Pacific groups. A second level division within the top cluster separates New Guinea from Australia and Pacific groups. As discussed in the section comparing trait frequencies among regions, Australia is closer to Southeast Asia and Pacific populations than to New Guinea. However, in this instance, New Guinea clusters with Australia/Pacific and not Europe. In the bottom segment of this tree, there are three clusters with the two African samples splitting off first. The remaining two major clusters show the linkage between Europe (four samples) and India (14 samples).

**DISCUSSION**

Genetic studies do not agree on whether or not the populations of Australia and New Guinea were derived from a single colonizing event 40 to 60 thousand years ago or if they were a product of two independent peopling events. Many agree that Australia and New Guinea are more closely related to one another than they are to any other group in Asia or the Pacific (cf. Bowcock et al., 1994; Hudjashov et al., 2007; Ingman and Gyllensten, 2003; Roberts-Thomson et al., 1996; Serjeantson et al., 1982). Despite the commonly held assumption that Australians and New Guineans, the long-time occupants of Sahulland, are related to one another, mtDNA suggests the two groups had very different histories, possibly reflecting two separate peopling events (Redd and Stoneking, 1999). Kayser et al. (2001) found a similar distinction between Australia and Melanesia (ie, Papua New Guinea) for Y chromosome haplotypes.

With relatively few exceptions, patterns of relationships indicated by dental morphology are congruent with genetic analyses. The convergence between Europe and New Guinea in crown and root morphology remains an enigma that is not easily reconciled with nuclear genetic markers or mtDNA and Y chromosome haplogroups. Nine traits show a close similarity between Europe and New Guinea and a significant difference from Australia. In every instance, the Australian frequencies are in the direction of East and Southeast Asian and Pacific populations. In other words, New Guinea frequencies are in the direction of the more simplified European dentition with less shoveling and more simplified lower molar cusp number (more 4-cusped LM2 and lower cusp 6 frequencies). Paradoxically, New Guinea shares with Australia more complex upper molars (ie, little hypocone reduction and the world's highest frequencies of cusp 5). For roots, New Guinea does not have the 2-rooted canine most common in Europeans nor the 3-rooted LM1 most common in Asians (and >5% in Australians). In other words, for some traits, New Guinea converged toward the simplified crown pattern of Europeans while in other instances, they retained the more complex crown traits common in Australians.

There are many genetic studies of New Guinean populations, but little attention has been paid to dental variation. In a broader study of the Eastern Highlands populations of New Guinea, Robert Littlewood collected over 200 dental impressions from four villages. Following Dahlberg's (1956) traditional set of crown traits, Barksdale (1972) characterized these highland samples and made intervillage comparisons. Although done at a time before much was known of New Guinea teeth, Barksdale (1972, p. 174) concluded that "The dental morphology of the Eastern Highlands native is suggestive of the Negroid pattern, although this pattern has not been defined specifically. It is similar to the West Africa Negro, the Melanesian, and the Australian Aboriginal dentitions. The Mongoloid influence on the dentition appears to be slight." We know much more today about world populations and the similarities to Africans, Melanesians, and Australians are overstated. However, we fully concur with Barksdale on the absence of influence from East Asian Sinodont populations.
In a more recent study, Itou and Matsuno (2011) observed 17 crown traits in 117 Kasi villagers from the New Guinea highlands. They followed the ASUDAS standards employed in this study to score traits. Their results are remarkably consistent with the New Guinea frequencies reported in Table 22.1. That is, they report very low frequencies of UI1 shoveling and double shoveling, the protostyloid, deflecting wrinkle, cusp 6, and cusp 7. Also parallel to the present study, they found very high frequencies of 4-cusped LM2, LM2 Y-pattern, and UM1 cusp 5. The only notable disagreements were for Carabelli’s trait and odontomes where they found lower and higher frequencies, respectively. In a two-dimensional ordination based on MMD values, their modern New Guinea sample was compared to 13 Sinodont and 17 Sundadont groups. Although in the same quadrant of some (though not all) Sundadont groups, their sample is a distinct outlier in this broader Asian/Pacific context. Although they did not include Australian samples in their comparisons, Itou and Matsuno (2011, p. 197) note in regard to New Guinea that “They are considered to be closely related to Aboriginal Australians on the basis of genetic and archaeological studies. However, their dental characters are distinctively different than to those of Australians.”

Turner (1990, 1992) noted the differences and similarities between the Australian dentition and those of Southeast Asians and concluded that Australians exhibited a dental pattern that anticipated the Sundadont pattern of Southeast Asia. He referred to the Australian pattern as proto-Sundadont. In Table 22.1, this tendency was indicated for many traits. Australian frequencies differ from both Sinodont and Sundadont dental patterns, but the differences are quantitative rather than qualitative. The European dentition, by contrast, differs from both Asian patterns quantitatively and qualitatively. In many regards, the same could be said of New Guinea. Unlike the Australian dentition, the New Guinea dentition does not predate Sundadont.

For most studies, the 28 traits listed in Table 22.1 are sufficient to discriminate among the major populations of the world in a manner consistent with other biological evidence. The addition of more traits to this list might rectify, to some degree, the New Guinea—Europe convergence. For example, a sample of casts from living New Guinea Highlanders shows a high frequency of labial convexity, a rare trait in modern European populations (but one very common in Neanderthals and Homo heidelbergensis). It is unknown at this time if there are other traits that show a similar contrast.

Understanding New Guinea population history, impacted by numerous remote mountain valleys and highly differentiated languages, remains a unique challenge. The discovery of a relatively high frequency of Denisovan DNA only adds to the puzzle (cf. Reich et al., 2011). As for the dentition, puzzled or not, we know more than we used to. This study has provided a few answers and generated even more questions on the baffling evolution of New Guinea crown and root morphology.

CONCLUSIONS
Stimulated in part by Ann Stodder’s comment that our methods might be amiss given the linkage of New Guinea with Western Eurasian groups, a closer examination of a broader data set brings us full circle and to the same result. A few points on this finding:

• We are not suggesting Europeans and New Guineans are closely related in the sense of recent common ancestor. Their respective histories suggest a long period of geographic and reproductive isolation (perhaps as far back as 80–100 thousand years).
• Although Australia and New Guinea often cluster together in the analyses of simple genetic markers (Cavalli-Sforza et al., 1994; Nei and Roychoudhury, 1982, 1993), the linkage is not close and often
shows a very deep root (i.e., they are closer to each other than to anyone else but are still not close). The genetic distinctions between Australia and New Guinea have been summarized by Kayser (2010).

- Similarity between Europe and New Guinea may reflect convergence through simplification. The traits where the two groups show parallels are found in much lower frequencies than in Australians. This conclusion is similar to that of Itou and Matsuno (2011, p. 197), who argue that the "unique set of dental characters in Papua New Guinea was acquired by morphological reduction from the original Australian type of dental characters and by admixture with South Asian and Pacific peoples." Although it is difficult to evaluate the role of admixture in the development of the distinct New Guinea dental pattern, we concur that the highland populations have evolved a more simplified dentition than their Australian, Southeast Asian, and Pacific neighbors.

Acknowledgments

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Endnote

1. Within this text teeth are abbreviated in the following manner: U = upper, L = lower, I = incisor, C = canine, M = molar; and number indicates position in the tooth row.

References


Biological Distance Analysis
Forensic and Bioarchaeological Perspectives

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