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EVALUTATING MORPHOSCOPIC TRAIT FREQUENCIES OF  
SOUTHEAST ASIANS AND PACIFIC ISLANDERS

By

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Bachelor of Arts, University of Tennessee, Knoxville, TN 2012

Master's Thesis  
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## Evaluating Morphoscopic Trait Frequencies of Southeast Asians and Pacific Islanders

Chairperson: Randall Skelton, Ph.D.

When assessing ancestry in a forensic context, individuals are generally classified into one of four categories: belonging to European, African, Asian, or Native American ancestry. With only these four assessments, individuals from Southeast Asia and the Pacific Islands are usually phenotypically classified as Asian. While the oceanic regions of Southeast Asia and the Pacific Islands will most likely have trait frequencies similar to those of mainland Asia because of their shared ancestral lineages, there is still a great deal of variability in this region that could cause these trait frequencies to differ. To address this variability, sixteen morphoscopic traits were recorded using the program Osteoware (2011). Skeletal specimens include (n=135) from the Smithsonian National Museum of Natural History and (n=30) from the University of Pennsylvania Museum of Archaeology and Anthropology, for a total of (n=165). Populations collected include individuals from Island Southeast Asia, Melanesia, and Polynesia. These were compared closely with data on 7 morphoscopic traits collected for mainland Asians (n=74), as well as for 5 morphoscopic traits of larger groups found throughout the world: American Indian, African American, European American, and Eskimo groups.

The results indicated that the trait distributions of the Pacific were not similar to any of the other larger groups of the world for all five traits examined. Further, it was found that 7 out of 9 traits were significantly different in their frequencies between mainland Asians and groups of the Pacific. A clinal pattern of trait expression was noted across the geography on a west-east orientation for 6 traits. In correspondence analyses and cluster analyses, the Southeast Asians, Melanesians, and Polynesians were found to be more similar to each other than to mainland Asia. The Melanesians and the Southeast Asians showed the greatest correlation of morphoscopic trait frequency distribution. Overall, the Pacific group had a higher inclination for larger posterior zygomatic tubercles and a much higher prevalence of a straight zygomaticomaxillary suture than other groups of the world examined. The expression of these traits should be kept in mind when estimating the biological affinity of an individual.

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## CHAPTER I

### INTRODUCTION

Anthropologists strive to know and understand all aspects of our species from the wide-ranging cultures, to innumerable languages, to the expansive spectrum of biological variability. In today's world, forensic anthropologists are tasked with providing insight about an individual from their skeletal remains in hopes of a positive identification. Of the many things that can be learned from skeletal remains, estimating the biological ancestry of an individual can be the most difficult. Adding ancestral background to the biological profile of skeletal remains can aid law enforcement in the identification process of the individual. Using morphological and metric analyses of the skeleton, forensic anthropologists are tasked with associating unknown remains with those of a culturally perceived race that would have been assigned to an individual when they were alive (Sauer, 1992). While many anthropologists reject the idea of biological race, law enforcement still expects an estimation of race as part of the biological profile for identification. Society has a tendency to classify individuals rather than focus on subtle variations which leads to this interpretation of race in the views of law enforcement officials and the general public (Gill, 1998).

Human biological variability is vast and is the product of numerous forces over an expansive amount of time. Human variability changes over the geography of the world, however the majority of variability can be found within groups rather than between groups (Lewontin, 1972; Ossenberg, 1976; Templeton, 1998; Edgar & Hunley, 2009). This variability does not conform to discrete sets called "races" (Livingstone, 1962; Gill, 1998), thus causing difficulties when estimating an individual's biological ancestry and explaining it to the public



(Sauer, 1992; Brace, 1995). During the era of racial classification, typologists even admitted that many times racial lines between groups were arbitrary, that groups were constantly in a state of change, and that “races” were hard to pinpoint (Coon et al., 1950) thus, unknowingly, providing support for the dismissal of biological race.

Clines have been suggested as a better representation of human variability across the globe and are defined as systems where a gene, feature, or trait frequency gradually changes from one geographic area to another (Huxley, 1938, 1955; Brues, 1972; Bellwood, 1979; Brace, 1995; Relethford, 2008). Clinal patterns of variability better illuminate the overall spectrum of human biological variability, often leaving no clear demarcation between groups (Huxley, 1938; Livingstone, 1962; Relethford, 2009), consequently making the estimation of ancestry more difficult and debatable (Lieberman, 2008; Edgar & Hunley, 2009). Livingstone (1962) further explains clines as the result of 1- A recent advance of an advantageous gene, 2- Gene flow between populations which have different equilibrium gene frequencies or 3- A gradual change in the equilibrium significance of the gene along the cline. It has been noted by Dobzhansky (1962) that clines are not always uniform and may be sharper in regions where cultural or natural obstructions for travel or reproduction are in place or more gradual in areas where the exchange of genes is more open.

Many evolutionary forces are acting on the cranial morphology of individuals from around the world. Differential environmental adaptation, natural selection, genetic drift, founder events, geographic isolation, and gene flow all influence the clines and degree of variability that we see today in human biology (Bellwood, 1979; Lahr, 1996). In populations from islands of the Pacific, geographic isolation, genetic drift, and founder’s effect will have a larger effect on the

local population than other evolutionary forces. On the contrary, populations that reside on large, continuous land masses will be more effected by forces like gene flow.

Looking at the larger picture of these clines all over the world, patterns and general clusters can usually be distinguished. Numerous craniometric studies and statistical programs have illustrated this point (Howells, 1973, 1989, 1995; Jantz & Ousley, 2005; Pietrusewsky, 2008a, 2008b; Relethford, 2009) though as explained above, these clusters are not always easily divisible and often show clinal patterns of craniometric variability across the geography. More homogenous populations with little gene flow will generally exhibit a smaller and more distinguishable cluster. More heterogeneous populations will often times overlap clusters with populations that they have had admixture with in the past or present as well as any ancestral populations or geographically adjacent populations. This same concept can also be applied to the distribution of non-metric traits and morphoscopic traits for populations across the geography.

## **Morphoscopic Traits**

Morphological variation and indications of ancestry can be explored by looking closely at morphoscopic traits. Morphoscopic traits, once referred to as macromorphoscopic traits, are quasicontinuous morphological variables that can be seen as soft tissue differences in living individuals (Hefner, 2009; Hefner et al., 2012). Quasi-continuous or threshold dichotomy traits have been described by Grüneberg (1952) as discontinuous phenotypes that do not follow Mendel's laws for simple dominant-recessive inheritance but instead have a complex or polygenic inheritance. Most quasicontinuous traits exhibit variation in expression. The

continuous genetic basis can be envisioned as two overlapping normal distributions where individuals with a genotype above the threshold exhibit a visible phenotype that can be scored as slight, moderate, or pronounced depending on the distance from the threshold and individuals below the threshold fail to display any visible trait expression (Scott & Turner, 1997). The visible phenotype is generally discontinuous but the underlying distribution is continuous, determined by both environmental and genetic factors, thus creating a quasicontinuous distribution (Grüneberg, 1952; Berry & Berry, 1967; Scott & Turner, 1997). Alice Brues (1958) defined traits similar to morphoscopic traits in her “second class of traits” that are described as being seen in both living individuals and their skeleton due to the contour of the bone where it closely follows the surface. The main groups of morphoscopic traits include assessing bone shape, bony feature morphology, suture shape, presence/absence data, and feature prominence/protrusion (Hefner et al., 2012).

Morphoscopic trait expression varies within all major human populations and no trait is found solely in only one human group, contrary to what may be believed (Gill, 1998; Digangi & Hefner, 2012; Hefner et al., 2012). With this in mind, it has been suggested that close consideration be given to frequency distributions of expected traits for major populations (Hefner et al., 2012). Recording the frequencies of morphoscopic traits for human groups is a useful way to display the variability of these traits between groups and avoids strictly adhering to typological lists. For many decades, morphological assessment of ancestry or even racial groups was derived from typological lists of traits that groups supposedly exhibited. As seen in Figure 1, Polynesians are expected to have a medium nasal bone trait expression, a highly variable nasal spine, a dull or absent nasal sill (inferior nasal aperture), a curved or angled zygomaticomaxillary suture, and projecting malars, to name a few. While some Polynesian individuals may possess

many of the traits from typological lists, some Polynesian individuals will share almost none of the traits from the lists, thus making these typological lists dangerous when attempting to estimate an individual's ancestral background.

Distributions of trait frequencies have been created and explored for forensic and physical anthropological contexts for non-metric frequency occurrence (Rhine, 1990; Lahr, 1996; Hanihara & Ishida, 2001a,b,c,d,e) and morphoscopic trait occurrence (Hefner 2009). Frequency distributions of morphoscopic traits created by Hefner (2009) show that a relationship does exist between populations and expressions of these traits. However, the distributions also show that inter- and intra-group variation is much higher than one would expect from solely looking at a trait list. From this information, I am interested in the immense variability found within groups that are considered as one major ancestral population and the associated implications of this grouping.

**Table 1: Typological trait lists including Polynesians taken from Gill (1998)**

<b>CRANIOFACIAL TRAIT VARIATIONS COMMON TO EACH GEOGRAPHIC RACE</b>					
<i>Characteristics</i>	<i>East Asian</i>	<i>American Indian</i>	<i>White</i>	<i>Polynesian</i>	<i>Black</i>
Cranial form	broad	medium-broad	medium	highly variable	long
Sagittal outline	high, globular	medium-low sloping frontal	high, rounded	medium	highly variable post-bregmatic depression
Cranial sutures	complex	complex	simple	complex	simple
Nose form	medium	medium	narrow	medium	broad
Nasal bone size	small	medium/large	large	medium	medium/small
Nasal bridge form	flat	medium/tented	high/step-like	medium	low/quonset hut
Nasal profile	concave	concavo-convex	straight	concave/concavo-convex	straight/concave
Interorbital projection	very low	low	high, prominent	low	low
Nasal spine	medium	medium, tilted	prominent, straight	highly variable	reduced
Nasal sill	medium	medium	sharp	dull/absent	dull/absent
Incisor form	shovelled	shovelled	blade	blade/shovelled	blade
Facial prognathism	moderate	moderate	reduced	moderate	extreme
Alveolar prognathism	moderate	moderate	reduced	moderate	extreme
Malar form	projecting	projecting	reduced	projecting	reduced
Zygomaticomaxillary suture	angled	angled	curved	curved/angled	curved/angled
Palatal form	parabolic/elliptic	elliptic/parabolic	parabolic	parabolic	hyperbolic/parabolic
Palatine suture	straight/jagged	straight	jagged	highly variable	arched/jagged
Orbital form	round	rhomboid	rhomboid	rhomboid	round
Mastoid form	wide	wide	narrow, pointed	wide	oblique, posterior tubercle
Mandible	robust	robust	medium cupped below incisors	robust, rocker form	gracile oblique gonial angle
Chin projection	moderate	moderate	prominent	moderate	reduced
Chin form	median	median	bilateral	median	median

## Divisions of the Pacific

The first used divisions of the major areas of the Pacific came about from Dumont D'Urville in the 1820s who separated the area into three regions: Micronesia, Melanesia, and Polynesia (Figure 2). These divisions were not founded on any deep concerns of human biology (Houghton, 1996). Other divisions based on archaeological habitation dates have been introduced such as that proposed by Robert Green and the concept of Near and Remote Oceania (Kirch, 2010). Near Oceania is comprised of the island of Papua New Guinea and goes as far east as the Solomon Island chain, having much greater antiquity in human occupation. Remote

Oceania contains islands of much younger human occupation and is located to the north, east, and south of this region. It is marked by much larger stretches of ocean where land is no closer than 350 kilometers to another island (Houghton, 1996). In this research, the variability of the Pacific will be explored by examining different groupings to see which groupings show more homogeneity for better assessments in forensic contexts.

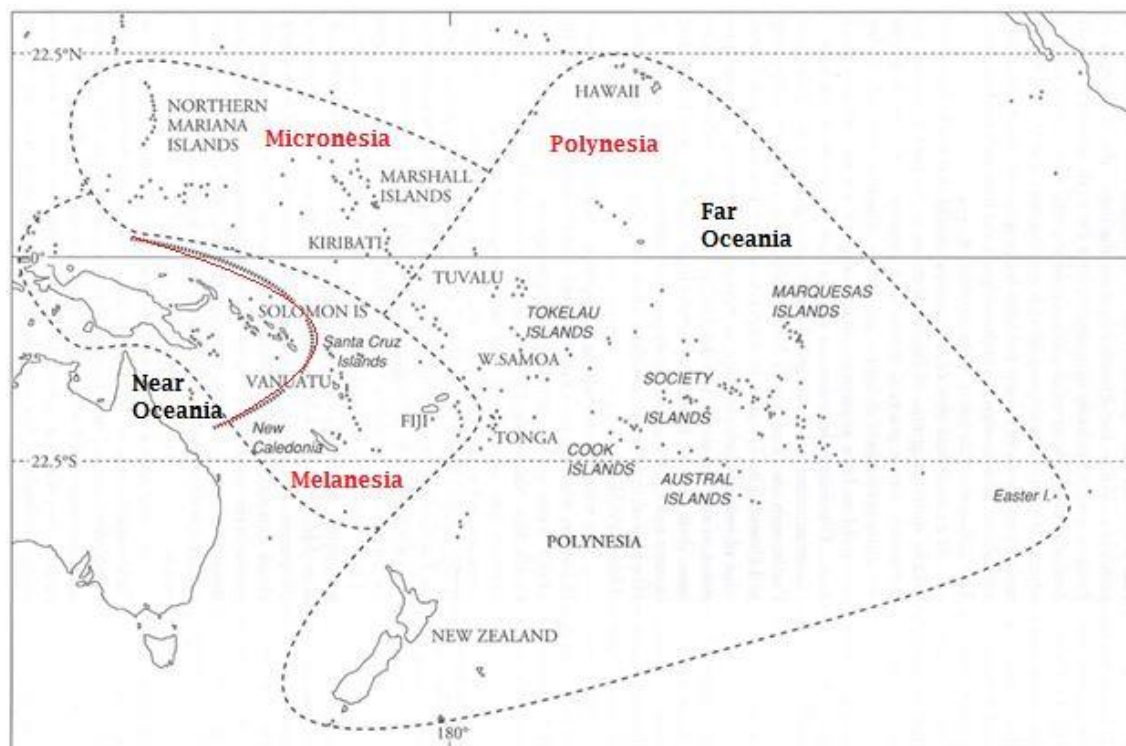
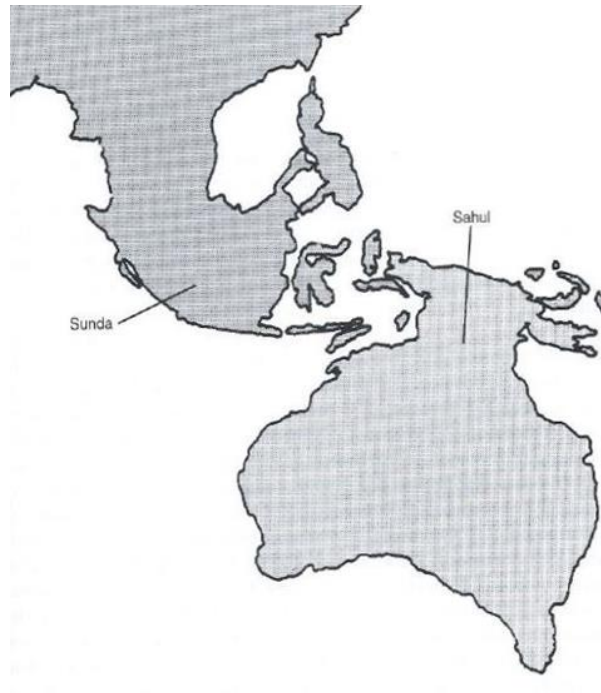


Figure 1: Division of Micronesia, Melanesia, and Polynesia and Near and Remote Oceania; Taken from Houghton (1996).

## Peopling of the Pacific

It is believed that Pleistocene hunter-gatherers crossed from Sundaland, modern day Indonesia and Southeast Asia, to the Sahul landmass, which comprises the areas of Australia, New Zealand, Tasmania, and Papua New Guinea, as seen in Figure 3 (Bellwood, 1987; Lahr, 1996; Bellwood, 1997; Deka et al., 2001; Glover & Bellwood, 2004). The Sunda and Sahul

landmasses were exposed due to low sea levels during glacial periods (Bellwood 2013). A common hypothesis among researchers follows that late Pleistocene Sundaland may have been the geographic central location from which all Pacific Basin and Rim populations may have radiated (Hanihara, 1993).



**Figure 2: Sunda landmass (mainland and island Southeast Asia, extending along the eastern Asian coast to Japan) and the Sahul landmass (Australia, New Guinea, and Tasmania) exposed at low sea-levels during periods of last glacial maxima. Taken from Lahr (1996).**

While parts of our understanding concerning Polynesian expansion remain unsure, what is known is this expansion seems to have occurred relatively rapidly when compared to other major human migrations, especially given the harsh oceanic terrain and the great distances that would have had to have been crossed. The main disagreement lies in the homeland of the migratory groups that eventually inhabited Polynesia and the amount of admixture that occurred along the way. Bellwood (1997) has proposed the “Out of Taiwan” model that describes a large-

scale migration around 6,000 years ago from southern China migrating east to Taiwan. He argues that these explorers were cereal crop cultivators who had domesticated animals and that approximately 4500 years ago one of these branches crossed the Luzon Strait into the Philippine Islands. With their selective advantage due to farming capabilities, they moved rapidly into regions of Island Southeast Asia, replacing the hunter-gatherers that inhabited the area. They then reached Island Melanesia and then continued on to uninhabited islands of Oceania quite rapidly with little admixture along the way (Gibbons, 2001; Atholl & O'Connor, 2008). Linguistic evidence for origins of the Malayo-Polynesian languages points to a proto-Austronesian language that is spoken in Taiwan and provides support for Bellwood's theory (Gibbons, 2001).

The 'Express Train to Polynesia' model proposed by Diamond (1988), based on archaeological and linguistic data, suggests that the islands were colonized by Neolithic voyagers from the South Asia and the island Southeast Asia region during a rapid eastward population migration around 4,000-6,000 years (Redd et al., 1995; Deka et al., 2001). This model holds that this rapid migration largely bypassed the indigenous Melanesians as they spread to the Pacific (Gibbons, 2001). Associated with this rapid migration was the spread of the Austronesian languages and the Lapita culture (Deka et al., 2001). In more recent years, this model has been further explored and built upon to include ideas of 'Express Train from Taiwan to Polynesia' that describes farmers from Taiwan and their culture replacing hunter-gatherers of Indonesia (Diamond & Bellwood, 2003; Oppenheimer, 2004). Bellwood and Dizon (2008) explained that while it was "express", it still required 3,000 years from the time of settlement in Taiwan before explorers reached areas of New Zealand. It was also later clarified that the Lapita culture that



moved through Melanesia and western Polynesia is the main “express” dispersal episode that occurred (Bellwood & Dizon, 2008).

An alternative theory holds that Polynesian ancestors came from the original inhabitants of mainland and island Southeast Asia at an earlier time, around 5,000 BC, not from the farmers from Taiwan who supposedly replaced the hunter-gatherers of Southeast Asia (Terrell, 1986; Oppenheimer, 2004). This model is sometimes termed the ‘slow boat’ theory and maintains that these Southeast Asian migrants moved slowly through Melanesia which allowed time for biological admixture and integration of Melanesian and Austronesian cultures between the migrants from Southeast Asia and Melanesia before colonizing the rest of the Pacific (Gibbons, 2001). This ‘slow boat’ idea of a prolonged delay of migration and heavy admixture is in opposition with the ‘Express train to Polynesia’ theory that holds that migration occurred more rapidly with minimal admixture along the way. Both arguments provide different lines of support for their theories and the findings contradict one another at times, resulting in many of these uncertainties between researchers. A review of evidence found for both arguments is discussed below.

### *Archaeological Evidence*

In Southeast Asia, the oldest evidence of humans comes from Laos and dates between 46,000 and 64,000 years ago (Bellwood, 2013). Moving away from the mainland, human evidence was found in both Borneo and the Philippines dating to 45,000 years ago (Glover & Bellwood, 2004; Bellwood, 2013). These sites in mainland and island Southeast Asia overlap with late surviving populations of *Homo erectus* and *Homo floresiensis*. As of today, there has been no evidence found for *H. floresiensis* in Australia (Bellwood, 2013).

In Melanesia, the oldest human settlements found are located on the western edges of the Pacific on the Huon peninsula of Papua New Guinea and date to approximately 40,000 years ago with a general consensus of the first population expansion leading to the colonization of Papua New Guinea and Australia around 40,000 and 50,000 years ago (Irwin, 1992; Houghton, 1996; Deka et al., 2001; Bellwood, 2013). Stone tools have been recovered on the highest areas of coral terraces on this peninsula and are dated to 45-54,000 years ago. A rise in sea levels within the last 16,000 years has likely destroyed a great deal of evidence of early humans in this region. To the east of the Huon peninsula, the island of New Britain produces human settlement dates of 35,000 years ago and a site found on New Ireland dates to 33,000 years ago (Lahr, 1996) while others argue that the Solomon Islands and the Bismarck Archipelago containing these two sites were reached by peoples of eastern New Guinea around 20,000 years ago (Bellwood, 2013).

In Micronesia and western Polynesia, a spread of related cultural complexes can be seen through the Philippines into Indonesia and reaching Guam by 1500 BC and Tonga and Samoa by 900BC (Bellwood, 2013). The first settlers to reach the Mariana Islands came from the Philippines as seen by the parallels in the cultural content of the archaeological evidence. Between 1350 and 900 BC, the Lapita cultural complex left a clear trail of sites in Island Melanesia (excluding New Guinea) and western Polynesia as seen in Figure 4 (Irwin, 1992; Bellwood, 2013). On islands such as Fiji, Vanuatu, New Caledonia, Tonga, and Samoa this cultural complex marked the first documented human settlement (Figure 5). The Lapita complex however has only been found sparsely in New Guinea and only late sites have been found. This supports the notions of Lapita culture favoring coastline areas with coral reefs and lagoons, most of which is lacking in New Guinea (Bellwood, 2013).

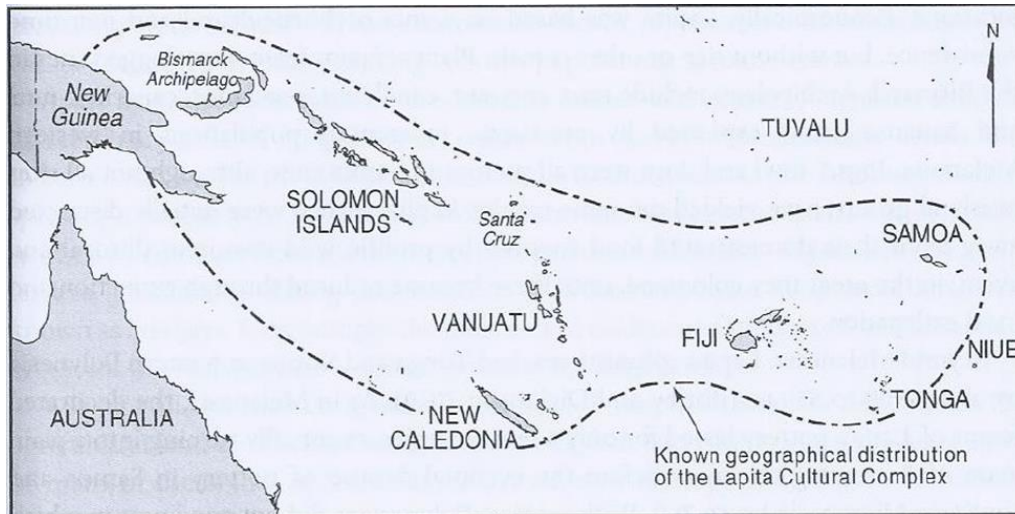


Figure 3: Distribution of Lapita sites in Oceania taken from (Bellwood, 2013)

In east Polynesia, many researchers agree that two distinct phases of colonization took place (Figure 5). It is believed that the first phase occurred between 1025-1120 AD in the Society Islands and the second phase occupied the remaining islands and occurred in one major push between 1190-1290 AD (Wilmshurst et al., 2011; Bellwood, 2013). Easter Island, located on the furthest reaches of Oceania, contains stone statues dating to 1200 AD (Bellwood, 2013). Others have argued for an earlier colonization of some of the islands including assertions that the Marquesas Islands were settled as early as 0 AD and that earlier Lapita sites in eastern Polynesia have just yet to be uncovered (Irwin, 1992). It has also been suggested that while some Polynesian islands were colonized early, such as the Marquesas Islands, others remained uninhabited until human migration spread outwards in first few centuries AD. While there is some disagreement on colonization times, what is generally agreed upon is human settlement in Polynesia occurred in the central and eastern islands after a long migratory break. Samoa was colonized around 800 BC but a nearly 2,000 year pause followed before migration occurred into eastern Polynesia (Wilmshurst et al., 2011). Bellwood (2013) has suggested that this rapid

expansion occurred after a long migratory pause because up until approximately 1000 AD many atolls were under sea level thus making these sea crossings much longer. Also during this expansion occurred what is known as a reverse 'Polynesian Outlier' migration that went east to west that led to the assimilation and replacement of former populations in many cases (Atholl & O'Connor, 2008; Bellwood, 2013).

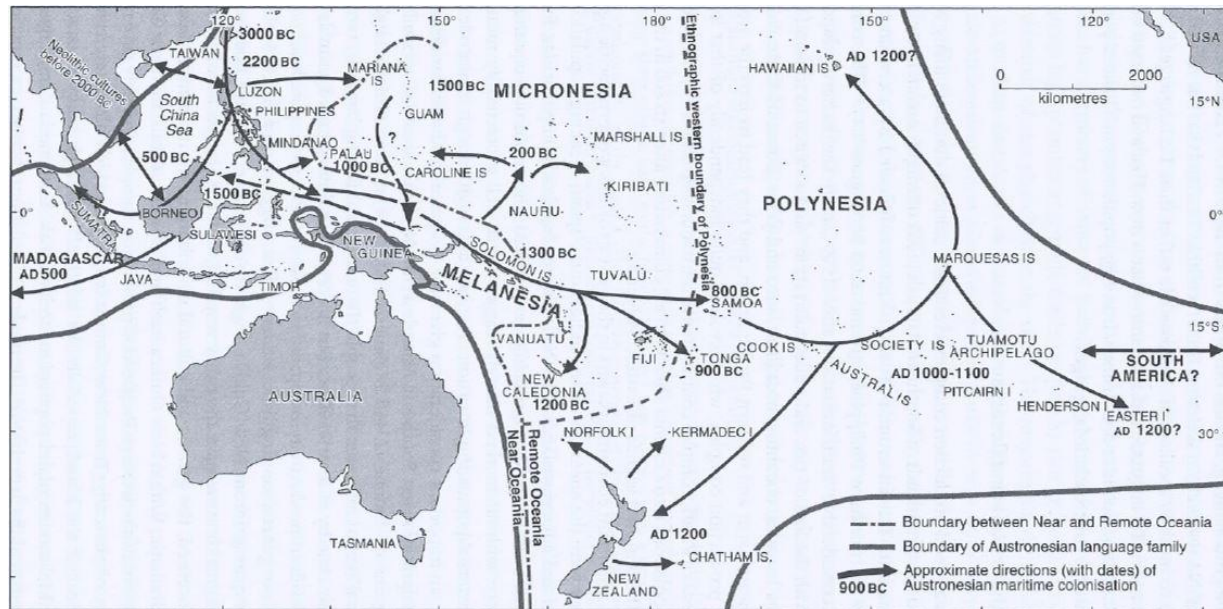


Figure 4: Holocene population movement according to archaeological and comparative linguistic data taken from (Bellwood, 2013)

### *Morphological Evidence*

Lahr (1996) asserts that genetic and morphological analyses separate Australo-Melanesians as a distinct cluster as either the first divergence from an African cluster or an earlier division of a non-African group. Other researchers have observed this noticeable distinction between the Australo-Melanesians and Asian populations. It was also argued by Howells (1989) that the Australo-Melanesian and the Asian populations could not have shared a common origin in the east. In 1992, Pietrusewsky and colleagues supported this theory through craniometric data analysis. Two distinct clusters were noted: one that contained East Asia,

Southeast Asia, Micronesia, and Polynesia and another cluster containing the Aborigines of Australia and Melanesia. The authors expressed the opinion that this separation was of great antiquity. From this, it is suggested that Southeast Asia, not Melanesia, is the ancestral homeland to the founding populations of Micronesia and Polynesia (Pietrusewsky, 1988; Pietrusewsky et al., 1992; Scott & Turner, 1997; Bellwood, 2013). This is also supported with genetic evidence to be discussed below. Additionally, dental morphology points to Southeast Asia as the origin for Polynesians and Micronesians because they all belong to the same dental complex that differs from that of Melanesia (Scott & Turner, 1997).

Further, it was also concluded by Pietrusewsky et al. (1992) that Southeast Asia was a recognizable subgroup of the larger Asian group that is distinct from northern Asia since at least the Neolithic. Pietrusewsky (1997) asserted that craniometric analyses linked Polynesians more closely with island Southeast Asia and only remotely linked them with China and Taiwan. Through other craniofacial measurements of individuals from this area, Hanihara (1993) suggested that the Polynesians possibly share a common gene pool with the Jomon which can possibly be linked back to Southeast Asians, most likely Island Southeast Asians with less admixture with mainland Asian populations.

### *Genetic Evidence*

Genetic analyses have reinforced ideas that Asian populations entered Island Southeast Asia in large groups between 2000-1000 BC (Bellwood, 2013). While Melanesia was already inhabited, admixture increasingly took place between Asian and Melanesian populations toward Papua New Guinea (Hill & Serjeantson, 1989). Polynesia and Micronesia were not inhabited at this time and were thus it is believed that they were mainly colonized by the migrating Asian

populations (Oppenheimer, 2004; Bellwood, 2013) though Oppenheimer (2004) notes that this is not a specific link to Taiwan. Genetically, the peoples of southeastern Indonesia, Vanuatu, New Caledonia Island, and the Solomon Islands are mainly of indigenous Melanesian origin (Bellwood, 2013) which is logical considering the proximity of these islands to Papua New Guinea and Australia. Cox (2013) asserts that multiple lines of genetic evidence show the Polynesian population contains about 80% Asian autosomal ancestry. The opposite is true for western Pacific populations around New Guinea as these groups carry about 20% Asian autosomal ancestry.

In Indonesia, a major shift is seen between Bali and Flores from Asian to Melanesian genotypes. Also, there is a sharp rise in Melanesian ancestry from nearly zero percent in Bali to approximately 50% near Timor (Cox, 2013). Strong support is given for significant population migration from the north and west going into eastern Indonesia dating to 2000 BC using an autosomal molecular clock (Bellwood, 2013). This is in agreement with the archaeological and linguistic evidence of the region. Also within Indonesia, Bellwood (2013) notes that western populations were found to carry mtDNA and NRY haplogroups that were brought by migrants from the Asian mainland while eastern populations carry Asian haplogroups but mainly carry indigenous Melanesian haplogroups, expressing genetic clinality.

A Polynesian motif has been documented that is found within 75-90% of Polynesians and 25-50% of Micronesians. This motif is characterized as a branch of the Asian B mtDNA haplogroup that contains three specific mutations at three nucleotides. This Polynesian motif is also found in substantial frequencies of island Melanesians and lowland New Guineans but is not found in Taiwanese or most of mainland Southeast Asia for that matter. However, this motif is found just east of Southeast Asia near island Southeast Asia. The distribution of this motif

suggests Wallacea, the area between Sundaland and Near Oceania in present day island Southeast Asia, is the likely source of this genotype in lowland Oceania (Oppenheimer, 2004). In agreement, Redd et al. (1995) and Bellwood (2013) suggest that Indonesia, a part of Wallacea, may be the source of this genotype, attributing its high frequency to a product of founder's effect. Aside from this mutation, Hill and Serjeantson (1989) assert that the Polynesians share very little genetic ancestry with Melanesia but rather have strong ancestral ties to Southeast Asia.

Oppenheimer (2004) also provides evidence for a Wallacea origin of Polynesia through paternal links. The dominant Y haplotype of Polynesia is haplogroup 10 that is defined by an RPS4Y marker. It belongs to approximately 50-80% of Polynesians but is absent in Taiwan and the Philippines. After an early introduction to Asia and Australia during the Late Pleistocene, the root ancestral form of this haplogroup has only been found in India, Borneo, and Wallacea. In Wallacea, a new Oceanic mutation was acquired, M38, and is the only haplogroup 10 type found in the rest of the Pacific. Oppenheimer (2004) suggests that this haplotype ultimately came from Asia and mutated in Wallacea and spread to Polynesia from this region.

Concerning the opinion of Taiwanese origins, Oppenheimer (2004) states that a combination of genetic studies reveals dissimilarity between Polynesia and Taiwan at multiple loci including in their type, specificity, and proportion. He goes on to assert that there are insufficient genetic connections to support even a small spread from Taiwan. Hill and Serjeantson (1989) are also in concordance with Oppenheimer concluding that no specific links between Polynesians and Chinese were found but instead, several connections between the Pacific and Southeast Asia were noted.

## **Modern Day Variability in Southeast Asia and the Pacific**

When assessing ancestry in a forensic context today, individuals are generally classified into one of four categories: belonging to European ancestry, African ancestry, Asian ancestry, or Native American ancestry, though recent research for Hispanic individuals is on the rise. Throughout history, these groupings have undergone change, at one time even incorporating 6 major groups: Black (Negroid), White (Caucasoid), East Asian (Mongoloid), Melanesian/Australian (Australoid), American Indian, and Polynesian (Gill, 1998). It is known and has been noted that members of Southeast Asian, Melanesian, Australoid, and Polynesian groups are often not included in many studies due to a lack of data or because many studies are directed toward forensic identification in North America (Gill, 1998) even though knowledge of individuals from these regions are of increasing importance for forensic anthropologists due to the growing number of people who are relocating to the United States from this region (Rhine, 1990). With only 4 main ancestral classifications, individuals from the Southeast Asian and Pacific Island regions have been phenotypically classified in the Asian categorization (Howells, 1989; Pietrusewsky, 2008b, 2010) though as previous analyses have shown there is a range of different and tentative affinities found in Southeast Asia, Melanesia, and Polynesia (Irwin, 1992) that would cause individuals from these regions to have differing frequencies of traits than those of mainland Asia.

### *Morphological Variation*

Inter-regional clinal patterns of variation and overall patterned geographic variation in Southeast Asia have been observed by previous researchers using both craniometric and non-metric data (Hanihara, 1992; Lahr, 1996; Hanihara & Ishida, 2001d,e; Hanihara, 2005;



Pietrusewsky, 2008a). In 2001, Hanihara and Ishida examined major human populations and their frequency distributions of discrete cranial traits over a number of publications. In their research they observed that the Polynesians, along with other outlying groups of the region, fell outside the range of the East Asian grouping. It was noted that the distinctiveness of a peripheral group like the Polynesians may indicate discontinuities in local morphology (Hanihara & Ishida, 2001c). In further studies, they also observed patterns of interregional clinality and intraregional discontinuity, asserting that genetic drift could have been the cause for this (Hanihara & Ishida, 2001d).

Studies of this region using craniometric data have shown a separation between Southeast Asia and North/East Asia (Pietrusewsky et al., 1992; Pietrusewsky, 2010), while also noting a close connection between Island Southeast Asia and mainland Southeast Asia (Pietrusewsky, 2008a,b). Other researchers have noted this geographical separation through morphological variants of teeth (Scott & Turner, 1997). Turner (1987,1990) brought attention to a specific dental complex termed sundadonty that is exhibited in individuals of Southeast Asia, Polynesia, Micronesia, and southern China while a second and different complex, sindodonty, appeared in individuals of northern China, Japan, Mongolia, and Korea. Some Melanesians and New Guineans are excluded from either dental complex though they do show more dental similarities to sundadonty than to sindodonty (Scott & Turner, 1997).

Overall size has always been a noted characteristic of populations from Far Oceania. Individuals from this region fall within the largest and most muscular people found around the world (Houghton, 1996). Shapiro (1933) recorded cranial indices of living individuals from Pacific groups. It was noted that as you move east across the geography, the cranial size increases. Two populations of Papua New Guinea, the Loyalty Islands, Solomon Islands, and

Java reported a cranial index of around 73, while the Society Islands and Hawaii reported cranial indices of 85. Populations found centrally located between these two regions like Fiji, Samoa, and Tonga all report indices of 81, intermediately ranked between the two far reaching localities. As seen in Figure 6, this shows clinality of increased cranial size from east to west across the Pacific. This increase in cranial size and musculature has been suggested as being the result of selective pressures of the oceanic environment. Houghton (1996) noted that phenotypic plasticity would be able to cope to an extent with this changing environment but over time, genetic selection would occur and provide a higher chance of survival. It was further suggested that being able to maintain more heat, larger-bodied and more muscular individuals were better suited to the wet-cold oceanic conditions while traversing areas of the Pacific.

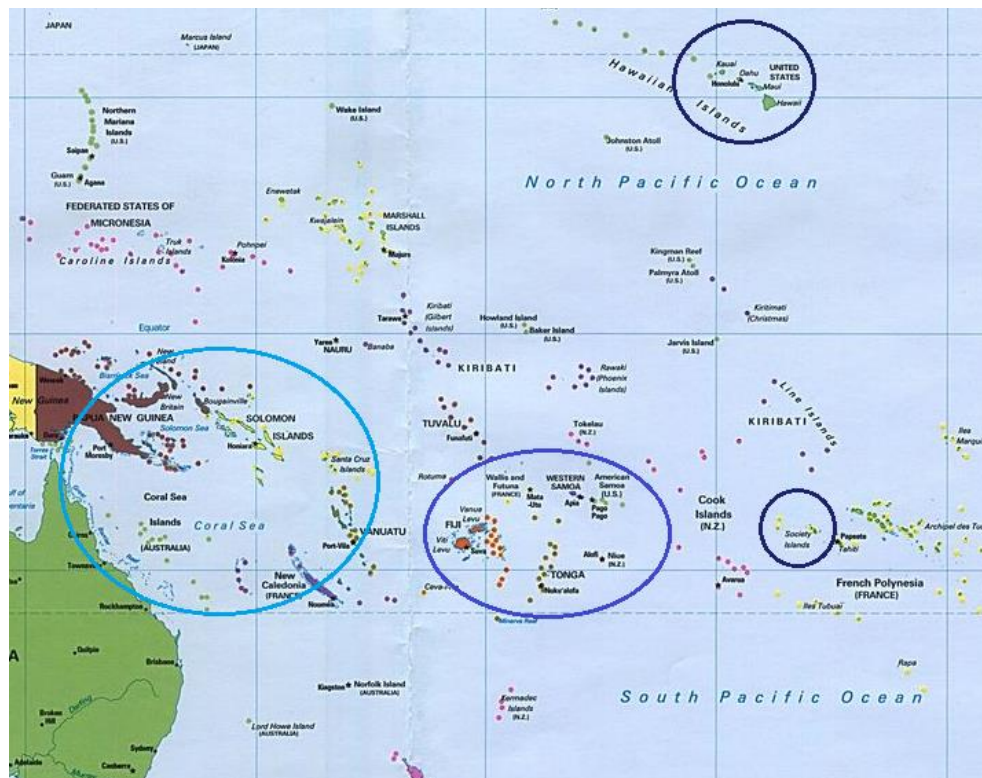


Figure 5: Map showing clinal clusters of increased cranial indices

## *Genetic Variation*

Aside from morphological variability, genetic clines have been observed in the populations of the Pacific Islands. Redd and colleagues (1995) examine a 9 base pair deletion that has been used as a genetic marker in peoples of East Asia origin to trace descent, as mentioned earlier. It is often found in Asian, Polynesian, and Native American individuals (Lahr, 1996; Gibbons, 2001). A geographic cline of the deletion frequency was observed across populations of the Pacific Islands. From Indonesia to Papua New Guinea to Samoa, they noted a clinal increase of this deletion across the geography and found a decrease in the diversity of the control region sequence which is consistent with founder events. They suggest that this final mutation probably occurred in Indonesia and spread eastward.

Looking more closely at the populations, it has been noted that Melanesia comprises individuals of varying affinities such as Polynesians, Indonesians, Negritos, and Australians. As Lahr (1996) points out, elements like the Polynesians and the Indonesians within Melanesia are a result of recent admixture. The amount of Polynesian admixture in areas of Melanesia varies from island to island. This is shown with the 9 base pair deletion distribution mentioned above. This deletion is not commonly found among Melanesian groups but is common among Asian groups, pointing to Polynesian ancestral ties to Southeast Asia instead of Melanesia. This deletion is completely absent in the highlands of New Guinea but is present in low frequencies in coastal New Guinea populations (Lahr, 1996) suggesting admixture of coastal Melanesian groups and Polynesian groups.

## Hypotheses

Differential adaption to local environments, geographic separation and isolation, genetic drift, differential ancestral makeup, founder's effect, and differing models of gene flow all contribute in numerous ways to the human biological variability seen in Oceania. Genetic variability, dental morphological variants, craniometric distinctions, and differing frequencies of non-metric traits in this region provide evidence that a substantial amount of variability would be added to the larger Asian grouping when Southeast Asian and Pacific Island groups are included. This also suggests it may be possible to differentiate between morphoscopic trait frequencies of populations of the oceanic region and those of mainland Asia.

Multiple lines of evidence show that Polynesians are more similar to Southeast Asians than to Melanesians probably due to their founding population originating from Southeast Asia. However, Polynesia is geographically isolated and has less exposure to other groups for gene flow to take place and for admixture to occur, thus making them more distinct from their Southeast Asian ancestors. I would expect the Polynesian group to display a distribution of trait expression different from the distribution of Southeast Asia because of this but I also would expect the Polynesian group to display a distribution more similar to the Southeast Asian distribution than to the mainland Asian distribution.

I expect that the trait distribution for the Melanesian group could manifest in two manners. The first would be an intermediate distribution of trait expression between the Southeast Asians and the Polynesians due to admixture with Southeast Asian groups and intermediate geographical location. This would more closely follow the 'slow boat' model. The second would be that the Melanesians may display a very different distribution of trait

expression from the Southeast Asians and the Polynesians due to different ancestral founding populations during the first Pleistocene migrations and also because the Melanesians experienced little admixture with the Polynesians. This expression more closely follows the ‘Express train to Polynesia’ model. In this model, it would be likely that the Southeast Asians and the Polynesians would be more similar in trait distribution while the Melanesian group would be the least similar.

Because of its close geographic proximity and consistent gene flow, the Island Southeast Asian population should theoretically be more similar to mainland Asia while, if going by the ‘slow boat’ model, Polynesians should be the least similar to mainland Asian groups due to longer ancestral separation and extensive admixture with Melanesians. If going by the ‘Express train to Polynesia’ model, the Polynesians should theoretically be more similar to Southeast Asians and less similar to the Melanesians due to little admixture with Melanesian groups during initial migration from Southeast Asia. From the evidence in support of the ‘Express train to Polynesia’ model, I propose four hypotheses.

Hypothesis 1: Many of the morphoscopic trait frequencies for Southeast Asians and Pacific Islanders will vary significantly from documented mainland Asian trait frequencies.

Hypothesis 2: The morphoscopic trait frequencies of mainland Asian, Island Southeast Asian, and Polynesian individuals will exhibit a clinal pattern from west to east geographically.

Hypothesis 3: Morphoscopic trait frequencies of Melanesians will show the greatest dissimilarity from the frequency distributions of mainland Asia, Island Southeast Asia, and Polynesia.

Hypothesis 4: The morphoscopic trait frequencies of Melanesians will be more similar to the Southeast Asians than to the Polynesians or mainland Asians.

## CHAPTER II

### MATERIALS & METHODS

Table 2: Samples collected for groups of the Pacific

<b>PACIFIC SAMPLES COLLECTED</b>		
	# of Individuals	Collection
<b>Island Southeast Asia</b>		
Borneo	3	Penn Museum
Indonesia	40	Penn Museum; Smithsonian
Malaysia	5	Penn Museum
Philippines	35	Penn Museum; Smithsonian
Sri Lanka	1	Penn Museum
Sumatra	10	Smithsonian
<b>TOTAL</b>	<b>94</b>	
<b>Melanesia</b>		
Fiji	13	Smithsonian
Papua New Guinea	40	Smithsonian
Solomon Islands	6	Smithsonian
Vanuatu	1	Smithsonian
<b>TOTAL</b>	<b>60</b>	
<b>Polynesia</b>		
Easter Island	3	Smithsonian
Samoa	1	Smithsonian
Tahiti	7	Penn Museum; Smithsonian
<b>TOTAL</b>	<b>11</b>	
<b>TOTAL INDIVIDUALS</b>	<b>165</b>	

Table 3: Frequency data set for larger groups of the world used for comparison with the Pacific groups (Taken from Hefner 2009)

<b>FREQUENCY DATA COMPARISON SAMPLE</b>		
TAKEN FROM HEFNER (2009)		
	# of Individuals	Collection
<b>African</b>		
Native African	32	Smithsonian
American Blacks	188	Terry Collection;
TOTAL	220	Bass Collection
<b>American-Indian</b>		
		Smithsonian
Arikara	42	Smithsonian
Hawikuh	40	Smithsonian
Doyon Eskimo	39	Smithsonian
Pastolik Eskimo	12	Smithsonian
Pueblo Bonito	7	Smithsonian
Santa Barbara	57	Smithsonian
Almeda	26	Smithsonian
Perico Island	17	Smithsonian
Canaveral	19	Smithsonian
St. Lawrence Eskimo	9	Smithsonian
TOTAL	268	
<b>Asian</b>		
China	59	Smithsonian
Japan	15	Smithsonian
TOTAL	74	
<b>European</b>		
American Whites	170	Terry Collection
Native Europeans	15	Smithsonian
TOTAL	185	

Table 4: Larger groups of the world data set used for comparison with the Pacific groups provided by Dr. Joe Hefner

<b>LARGER GROUPS OF THE WORLD COMPARISON</b>		
	# of Individuals	Collection
African American	61	Terry Collection
American Indian	43	Smithsonian
Asian	48	Smithsonian
Eskimo	21	Smithsonian
European American	50	Terry Collection
TOTAL	223	



Table 5: Asian data set used for comparison with the Pacific groups provided by Dr. Joe Hefner

COMPARISON ASIAN SAMPLE		
	# of Individuals	Collection
China	59	Smithsonian
Japan	15	Smithsonian
TOTAL	74	

### *Sample*

Morphoscopic traits were scored for 30 individuals from the University of Pennsylvania Museum of Archaeology and Anthropology's physical anthropology skeletal collection and 135 individuals from the Smithsonian National Museum of Natural History for a total of (n=165). The Island Southeast Asian population sample consists of 94 individuals from the Philippine Islands, Indonesia, Malaysia, Borneo, Sumatra, and Sri Lanka. The Melanesian population sample consists of 60 individuals from Fiji, Papua New Guinea, Solomon Islands, and Vanuatu. The Polynesian sample consists of 11 individuals from Easter Island, Samoa and Tahiti (French Polynesia). For purposes of this research, what will be referred to as the Pacific Island population contains the Polynesian and Melanesian populations (n=71) unless stated otherwise.

Cranial morphoscopic data were collected using the Macromorphoscopy module of the program Osteoware (2011) which provides the user with a particular set of assessments in order to help standardize the measurements. Osteoware (2011) allows for the recording of 16 morphoscopic traits and additional comments about the specimen. All present and observable traits were recorded for each of the crania. Any obstructions, excessive wearing, broken, or missing regions of the skull where traits were to be recorded were left blank and noted as unobservable. The traits are as follows: anterior nasal spine (ANS), inferior nasal aperture (INA), interorbital breadth (IOB), malar tubercle (MT), nasal aperture shape (NAS), nasal

aperture width (NAW), nasal bone contour (NBC), nasal bone shape (NBS) nasal overgrowth (NO), nasofrontal suture (NFS), orbit shape (OS), post-bregmatic depression (PBD), posterior zygomatic tubercle (PZT), supranasal suture (SNS), zygomaticomaxillary suture course (ZSC), and transverse palatine suture (TPS). A full description, illustration, and photo of each trait are listed below.

### Trait Descriptions

The following trait descriptions and illustrations are taken from the Macromorphoscopies chapter of the Osteoware manual written by Hefner (2011). All photographs were taken by the author.

The Anterior Nasal Spine (ANS) is scored as a 1, 2, or 3.

1= Slight; minimal to no projection of the anterior nasal spine beyond the inferior nasal aperture.

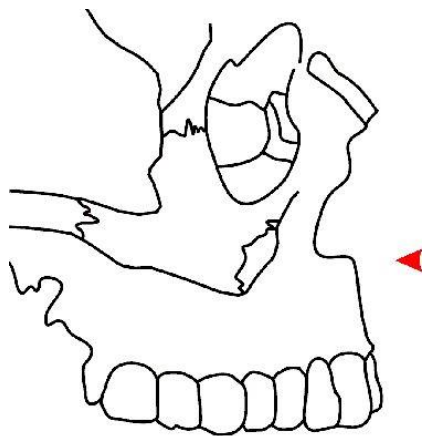


Figure 6a: ANS (1) Illustration (Osteoware, 2011)



Figure 6b: ANS (1)

2= Intermediate; a moderate projection of the anterior nasal spine beyond the inferior nasal aperture

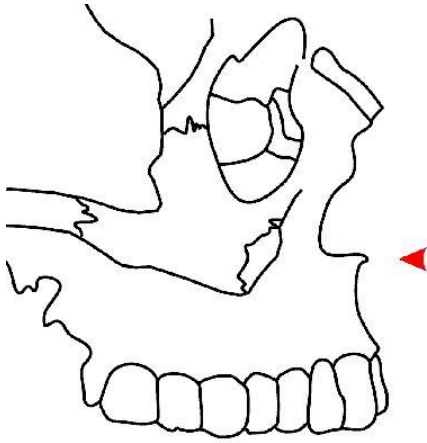


Figure 7a: ANS (2) Illustration (Osteoware, 2011)



Figure 7b: ANS (2)

3=Marked; a pronounced projection of the anterior nasal spine beyond the inferior nasal aperture

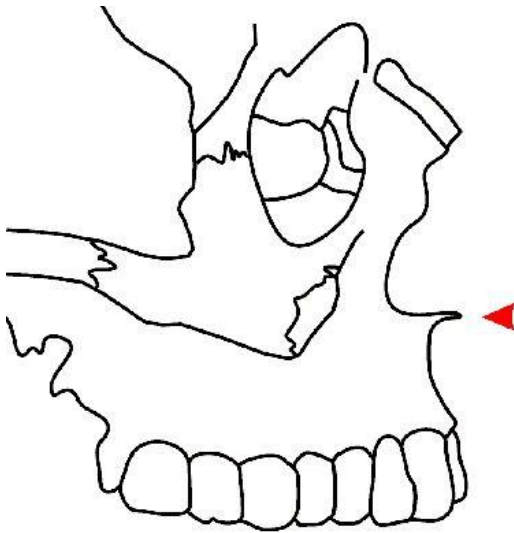


Figure 8a: ANS (3) Illustration (Osteoware, 2011)



Figure 8b: ANS (3)

The Inferior Nasal Aperture (INA) is scored as 1, 2, 3, 4, or 5.

1=An inferior sloping of the nasal floor which begins within the nasal cavity and terminates on the vertical surface of the maxilla, producing a smooth transition.

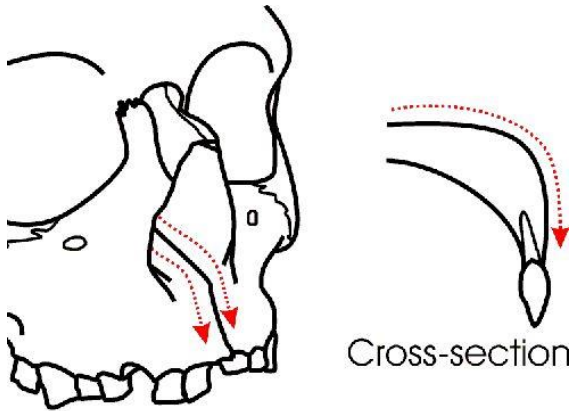


Figure 9a: INA (1) Illustration (Osteoware, 2011)



Figure 9b: INA (1)

2=Sloping of the nasal aperture beginning more anteriorly than in INA 1 and with more angulation at the exit of the nasal opening.

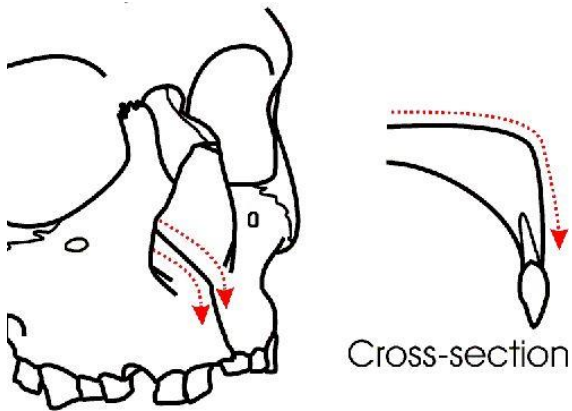


Figure 10a: INA (2) Illustration (Osteoware, 2011)



Figure 10b: INA (2)

3=The transition from nasal floor to the vertical maxilla is not sloping, nor is there an intervening projection, or sill.

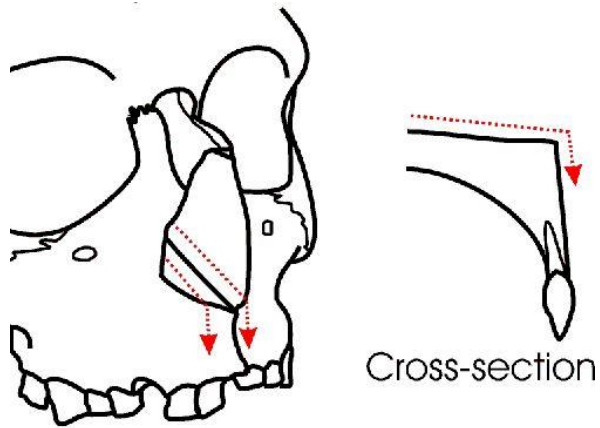


Figure 11a: INA (3) Illustration (Osteoware, 2011)



Figure 11b: INA (3)

4= Any superior incline of the anterior nasal floor, creating a weak (but present) vertical ridge of bone that traverses the inferior nasal border (partial nasal sill)

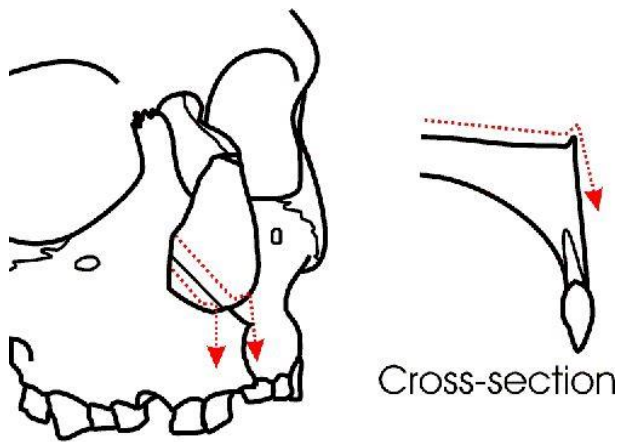


Figure 12a: INA (4) Illustration (Osteoware, 2011)



Figure 12b: INA (4)



5= A pronounced ridge (nasal sill) obstructing the nasal floor-to-maxilla transition.

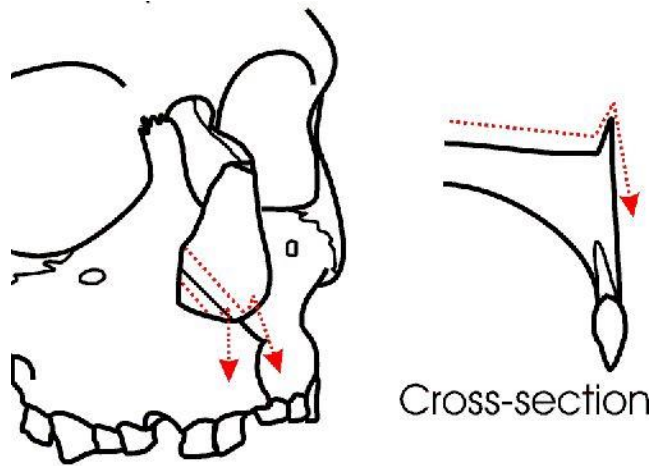


Figure 13a: INA (5) Illustration (Osteoware, 2011)



Figure 13b: INA (5)

The Interorbital Breadth (IOB) is scored 1, 2, or 3.

1=A narrow IOB relative to the facial skeleton.

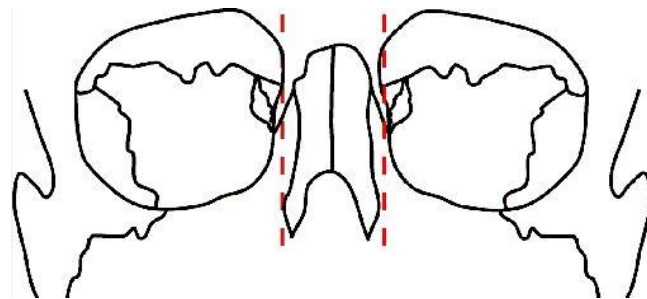


Figure 14a: IOB (1) Illustration (Osteoware, 2011)

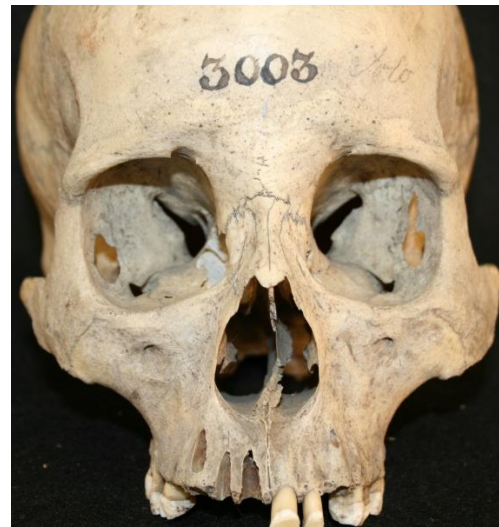


Figure 14b: IOB (1)

2=A medium IOB relative to the facial skeleton.

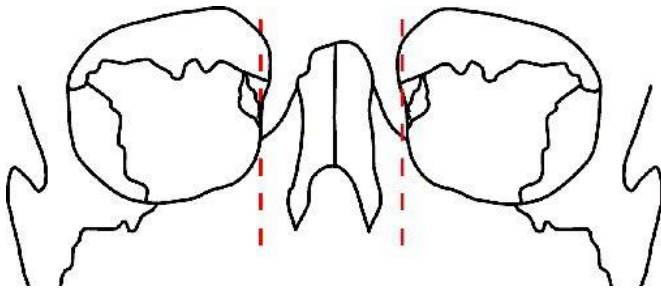


Figure 15a: IOB (2) Illustration (Osteoware, 2011)

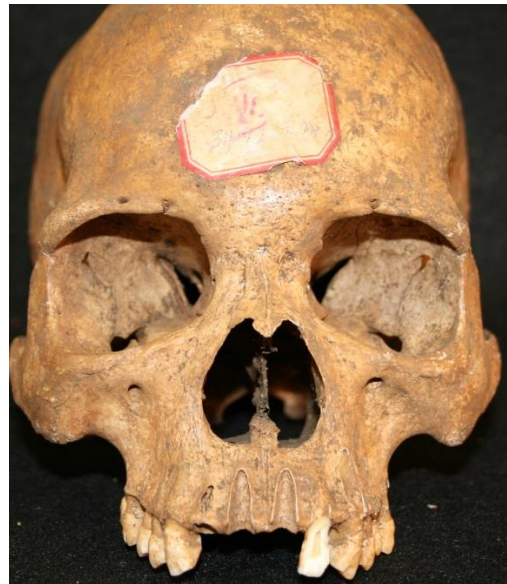


Figure 15b: IOB (2)

3=A broad IOB relative to the facial skeleton.

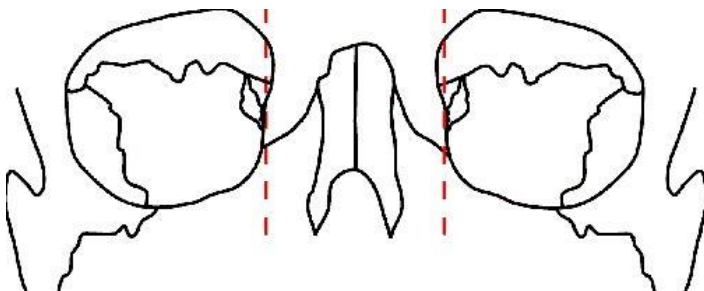


Figure 16a: IOB (3) Illustration (Osteoware, 2011)



Figure 16b: IOB (3)

The Malar Tubercle (MT) is a protruding tubercle located on the inferior margin of the maxilla and zygomatic bone in the region of the zygomaticomaxillary suture. This can be scored by placing a transparent ruler from the intersection of the zygomaticomaxillary suture and the inferior margin of the malar to the deepest point on the curvature of the maxilla. An assessment is then made on the extent of the protrusion beyond the ruler's edge. In instances where the suture is directly on the tubercle, the ruler is placed from the deepest curvature of the maxilla to the deepest anterior curvature on the zygomatic. The malar tubercle may be placed on the maxilla, zygomatic, or along the Zygomaticomaxillary suture. Observations should not be made on the tubercles on the lateral zygomatic arch.

0=No projection of the bone.

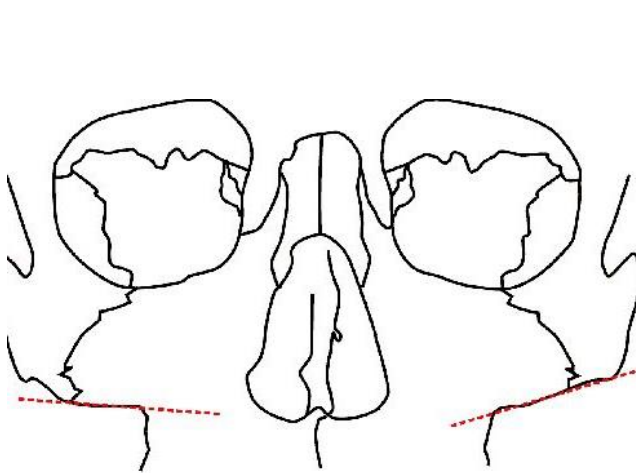


Figure 17a: MT (0) Illustration (Osteoware, 2011)



Figure 17b: MT (0)



1=A trace tubercle below the ruler's edge (about 2 mm or less)

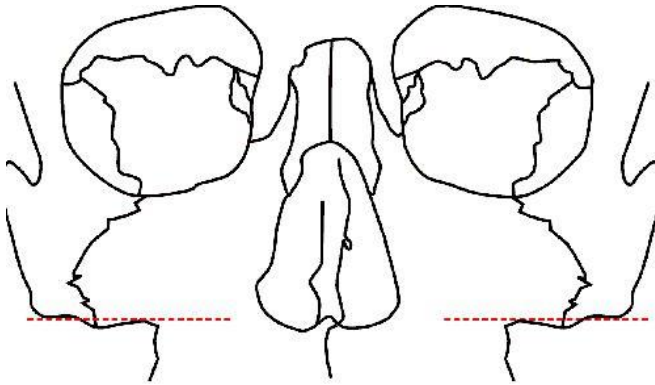


Figure 18a: MT (1) Illustration (Osteoware, 2011)



Figure 18b: MT (1)

2=A medium protrusion below the ruler's edge (roughly 2 to 4 mm)

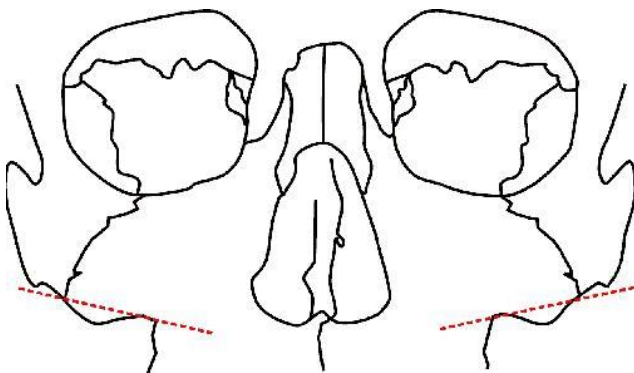


Figure 19a: MT (2) Illustration (Osteoware, 2011)



Figure 19b: MT (2)

3=A pronounced tubercle below the ruler's edge (roughly 4mm or more)

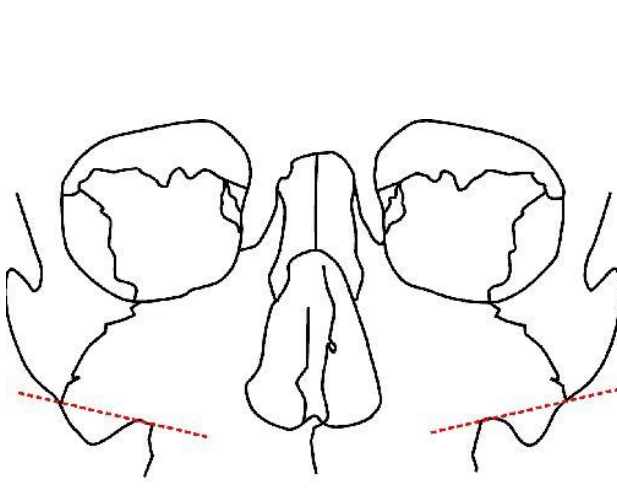


Figure 20a: MT (3) Illustration (Osteoware, 2011)



Figure 20b: MT (3)

The Nasal Aperture Shape (NAS) is scored as a 1, 2, or 3. It is assessed by observing both of the lateral contours of the nasal aperture and, directly related, the position of greatest lateral projection of the margin.

1=Teardrop; lateral projection intermediate to 2 and 3.

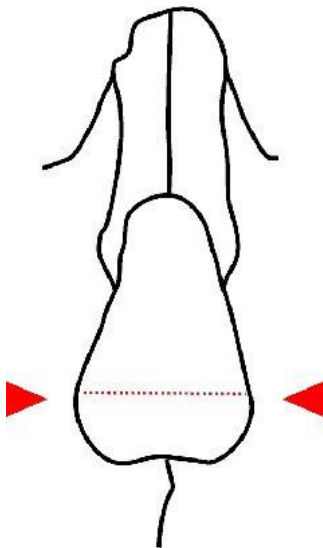


Figure 21a: NAS (1) Illustration (Osteoware, 2011)



Figure 21b: NAS (1)

2= Bell shape; greatest lateral projection at the inferior margin

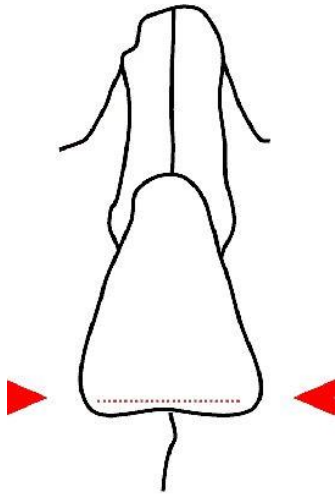


Figure 22a: NAS (2) Illustration (Osteoware, 2011)



Figure 22b: NAS (2)

3=Bowed; greatest lateral projection at midline.

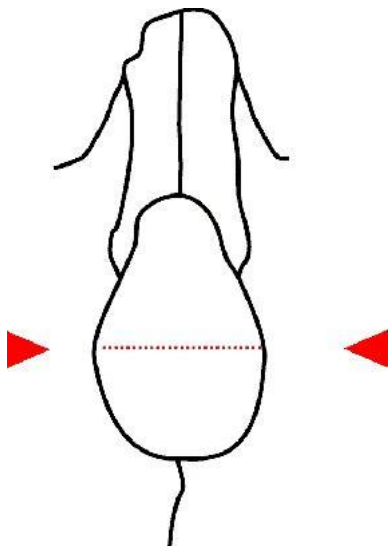


Figure 23a: NAS (3) Illustration (Osteoware, 2011)



Figure 23b: NAS (3)

The Nasal Aperture Width (NAW) is assessed relative to the facial skeleton.

1=Narrow

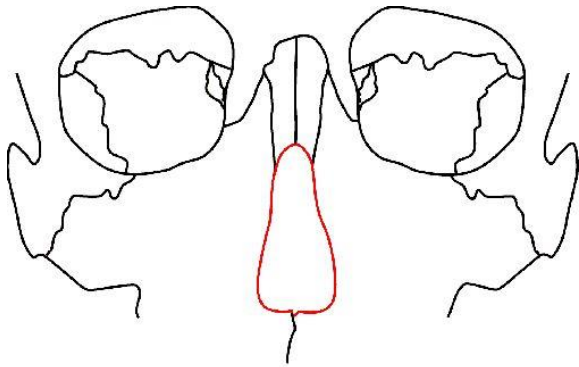


Figure 24a: NAW (1) Illustration (Osteoware, 2011)



Figure 24b: NAW (1)

2=Medium

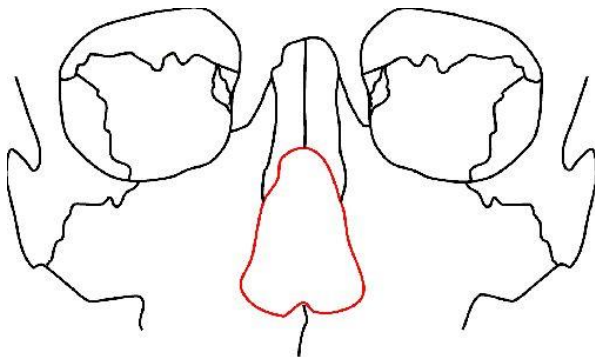


Figure 25a: NAW (2) Illustration (Osteoware, 2011)



Figure 25b: NAW (2)



3=Wide

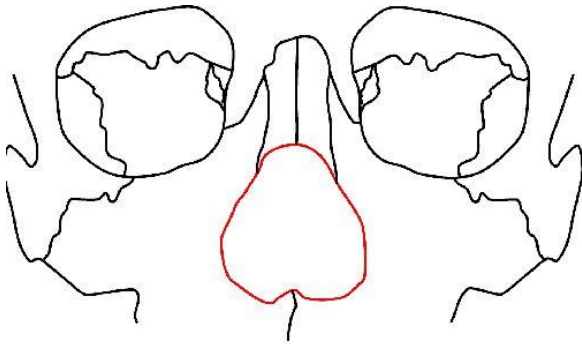


Figure 26a: NAW (3) Illustration (Osteoware, 2011)



Figure 26b: NAW (3)

The Nasal Bone Contour (NBC) is defined as the contour the nasal bones and the frontal process of the maxilla approximately 1 cm below nasion. Visual interpretation of the nasal contour is not the most effective manner of analysis because of high inter- and intra-observer error. Using a contour gauge permits more reliable and consistent assessment of nasal contour.

0=Low and rounded nasal bone contour

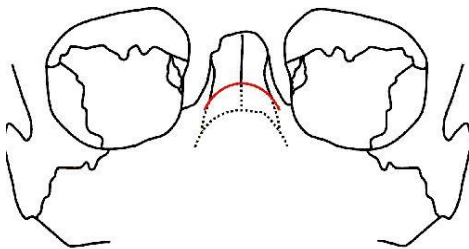


Figure 27a: NBC (0) Illustration (Osteoware, 2011)



Figure 27b: NBC(0)



Figure 27c: NBC (0)

1=An oval contour, with elongated, high, and rounded lateral walls

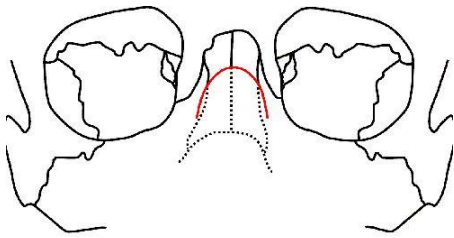


Figure 28a: NBC (1) Illustration (Osteoware, 2011)

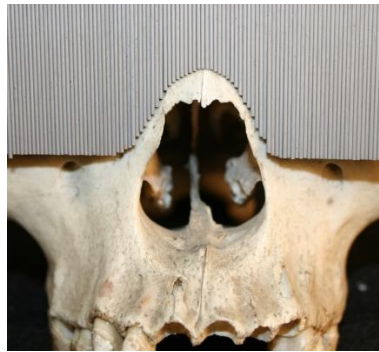


Figure 28b: NBC (1)

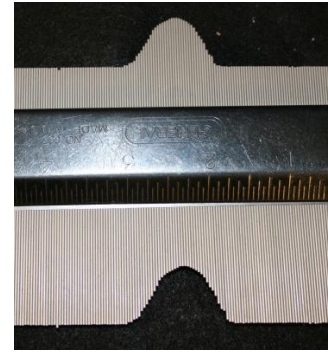


Figure 28c: NBC (1)

2=Steep lateral walls and a broad (roughly 7 mm or more), flat superior surface “plateau”

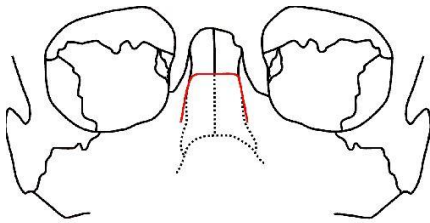


Figure 29a: NBC (2) Illustration (Osteoware, 2011)



Figure 29b: NBC (2)



Figure 29c: NBC (2)

3=Steep-sided lateral walls and a narrow superior surface “plateau”

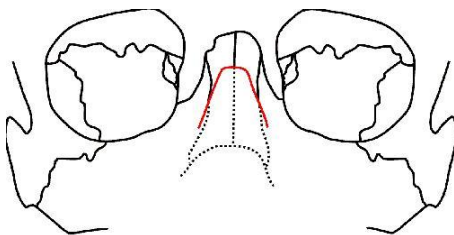


Figure 30a: NBC (3) Illustration (Osteoware, 2011)



Figure 30b: NBC (3)

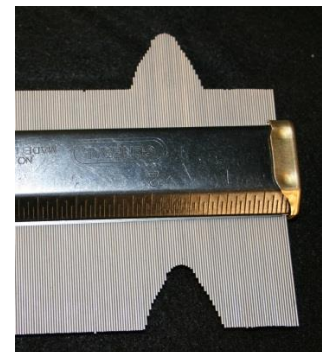


Figure 30c: NBC (3)

4=Triangular cross section, lacking a superior surface “plateau”

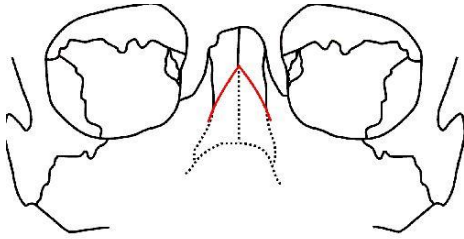


Figure 31a: NBC (4) Illustration (Osteoware, 2011)



Figure 31b: NBC (4)



Figure 31c: NBC (4)

The Nasal Bone Shape (NBS) is a determination is made regarding 1-the position of the nasal pinch if there is any and 2-the amount of lateral bulging. The observer should not consider the frontonasal suture, nasal suture, or the symmetry of the nasal bones. Rather, an assessment is made of the lateral contours of the nasal bones.

1=Nasal bones with no nasal pinch

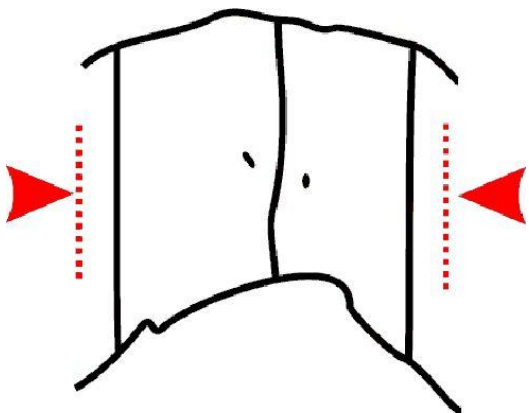


Figure 32a: NBS (1) Illustration (Osteoware, 2011)



Figure 32b: NBS (1)



2=Nasal bones with a superior pinch and minimal lateral bulging

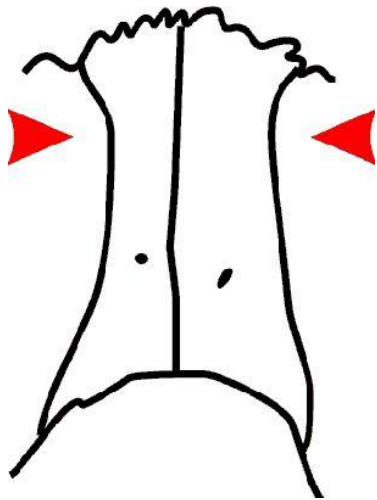


Figure 33a: NBS (2) Illustration (Osteoware, 2011)



Figure 33b: NBS (2)

3=Nasal bones with a superior pinch and pronounced lateral bulging of the inferior region. To differentiate between a score of 2 or 3, the amount of lateral bulging in the inferior region should be observed.

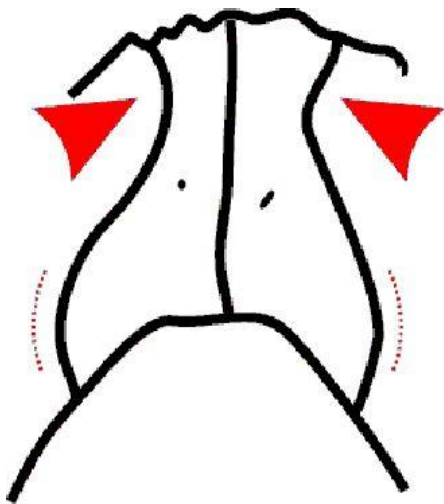


Figure 34a: NBS (3) Illustration (Osteoware, 2011)



Figure 34b: NBS (3)



4=Triangular-shaped nasal bones

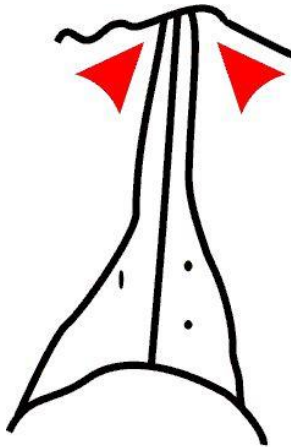


Figure 35a: NBS (4) Illustration (Osteoware, 2011)

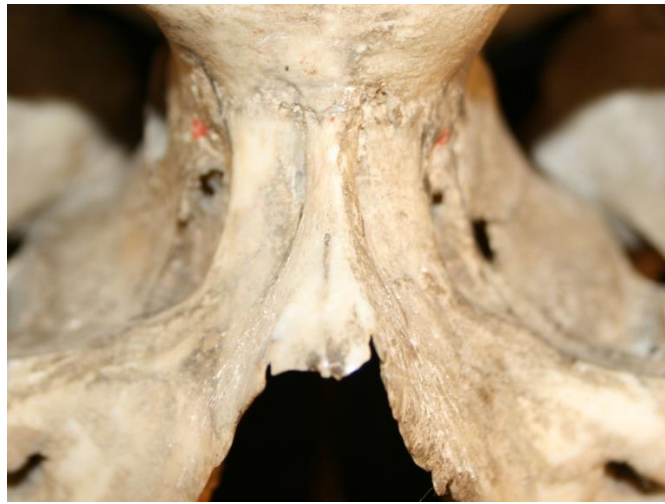


Figure 35b: NBS (4)

The Nasofrontal Suture (NFS) is the suture separating the nasal bones from the frontal bone. The shape of this suture is assessed. The symmetry of the nasal bones should be ignored. In the case of extreme pinching of the superior border as in NBS (4), observation should be left blank.

1=Round and lacking angles

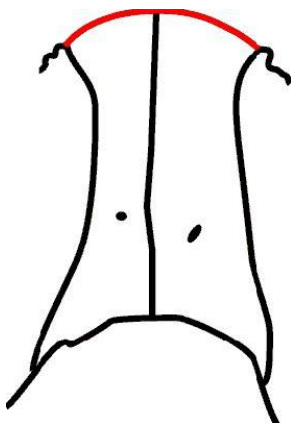


Figure 36a: NFS (1) Illustration (Osteoware, 2011)



Figure 36b: NFS (1)

2=Square; approximate right angles at *nasale superious*

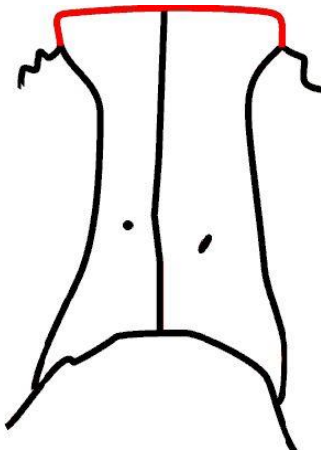


Figure 37a: NFS (2) Illustration (Osteoware, 2011)



Figure 37b: NFS (2)

3=Triangular

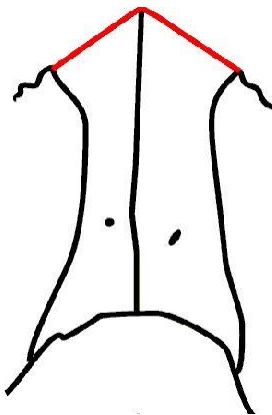


Figure 38a: NFS (3) Illustration (Osteoware, 2011)



Figure 38b: NFS (3)

4=Irregular; lacking any definitive shape

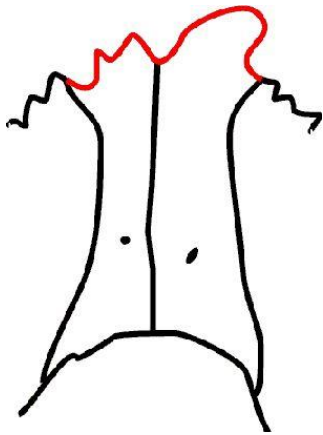


Figure 39a: NFS (4) Illustration (Osteoware, 2011)



Figure 39b: NFS (4)

The Nasal Overgrowth (NO) is an inferior projection of the lateral border of the nasal bones beyond the maxillae at *nasale inferious*. Assessment of nasal overgrowth does not include anterior bulging of the nasal bones.

0=No overgrowth

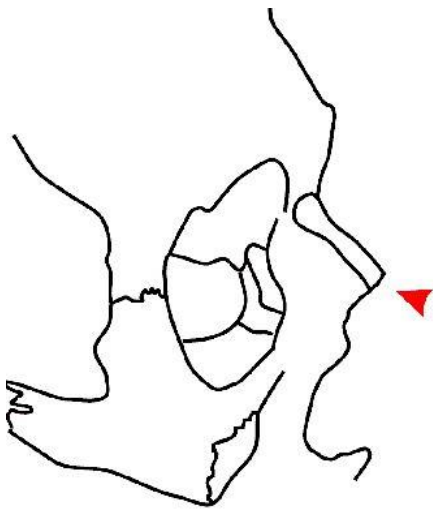


Figure 40a: NO (0) Illustration (Osteoware, 2011)



Figure 40b: NO (0)

1=Any projection of the lateral border of the nasal bones beyond the maxillary border

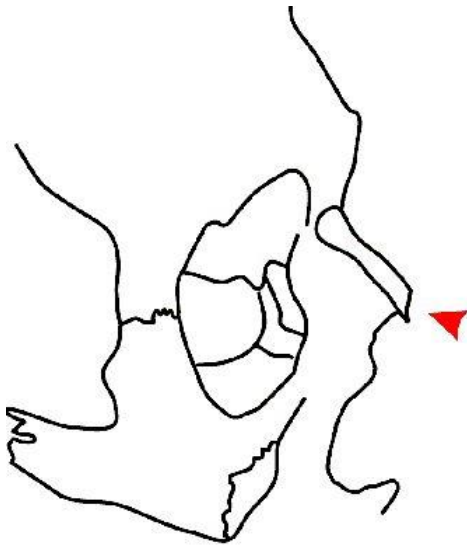


Figure 41a: NO (1) Illustration (Osteoware, 2011)



Figure 41b: NO (1)

The Orbital Shape (OS) assesses the shape orbital margins. The medial border of the orbit is defined by the anterior lacrimal crest and the maxillary process of the frontal bone.

1=Rectangular; orbits with horizontal margins longer than the vertical margins, but otherwise parallel

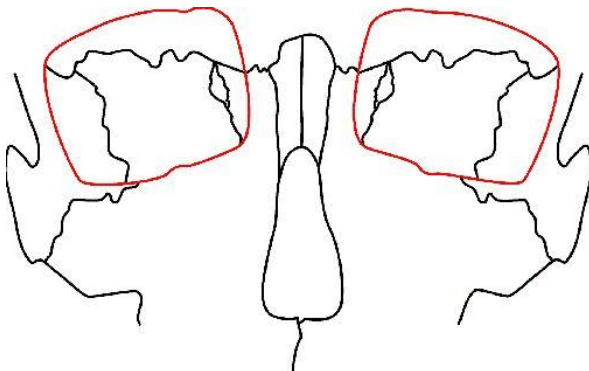


Figure 42a: OS (1) Illustration (Osteoware, 2011)



Figure 42b: OS (1)



2=Circular; orbital margin is approximately equidistant from center on all sides

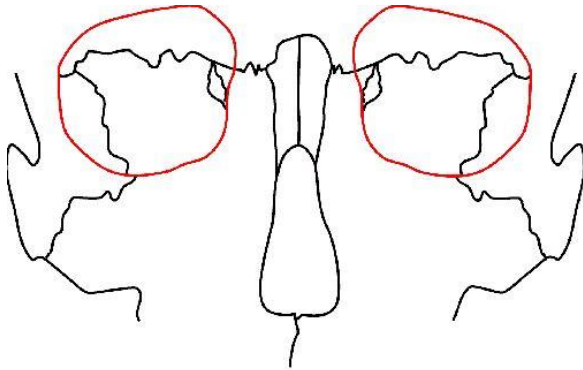


Figure 43a: OS (2) Illustration (Osteoware, 2011)



Figure 43b: OS (2)

3=Rhombic; medial border height is shorter than lateral border height similar to aviator sunglasses

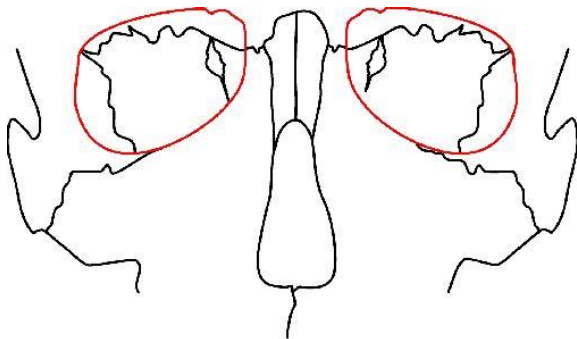


Figure 44a: OS (3) Illustration (Osteoware, 2011)



Figure 44: OS (3)

The Postbregmatic Depression (PBD) is a slight to broad depression along the sagittal suture, posterior to bregma, which is not the result of pathology. It is observed in a lateral profile and scored as present or absent.

0=No depression present

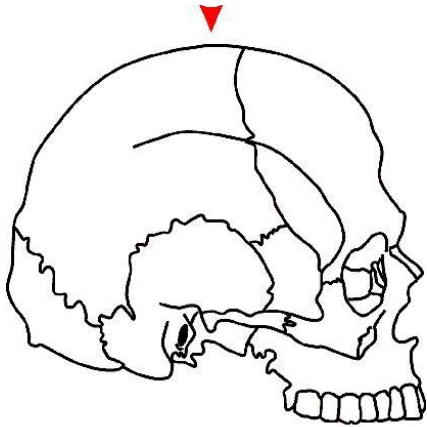


Figure 45a: PBD (0) Illustration (Osteoware, 2011)



Figure 45b: PBD (0)

1=Present; a marked depressed area posterior to bregma along the mid-sagittal plane

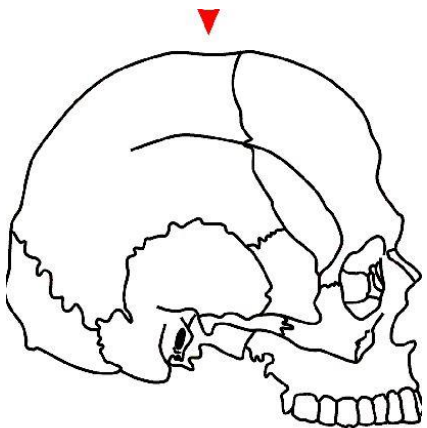


Figure 46a: PBD (1) Illustration (Osteoware, 2011)

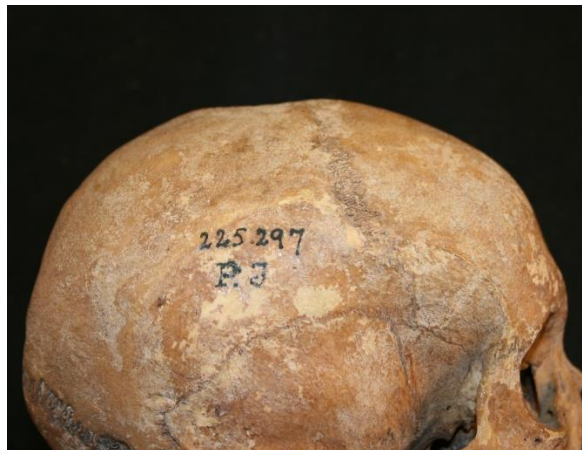


Figure 46b: PBD (1)

The Posterior Zygomatic Tubercle (PZT) is a posterior projection of the zygomatic bone at approximately midorbit as viewed in the lateral plane. A small transparent ruler is placed on the frontal process of the zygomatic from the landmarks frontomolare posterale to jugale. The extent of bony protrusion beyond the ruler's edge is then assessed.

0=No projection of bone

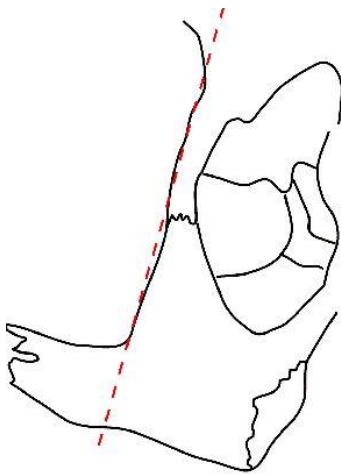


Figure 47a: PZT (0) Illustration (Osteoware, 2011)

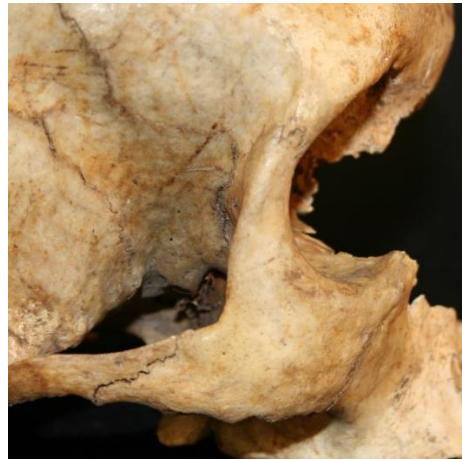


Figure 47b: PZT (0)

1=A weak projection of bone (less than 4 mm)

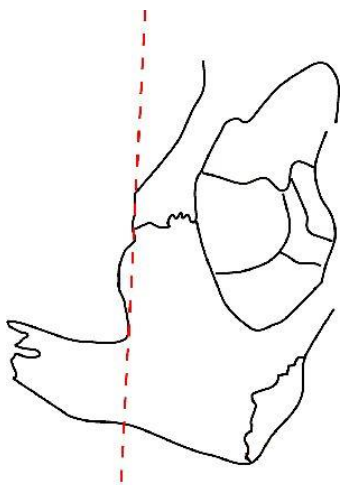


Figure 48a: PZT (1) Illustration (Osteoware, 2011)

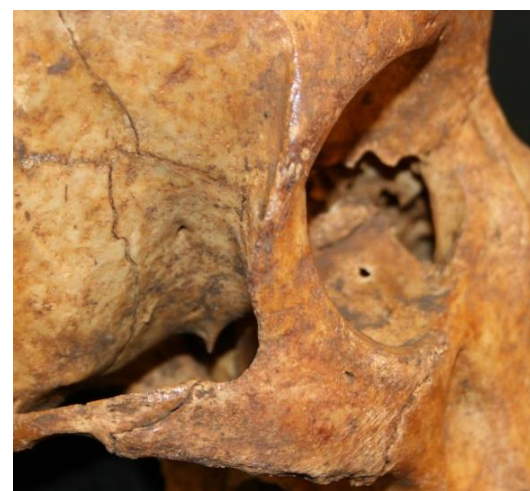


Figure 48b: PZT (1)

2=A moderate projection of bone (approximately 4 to 6 mm)

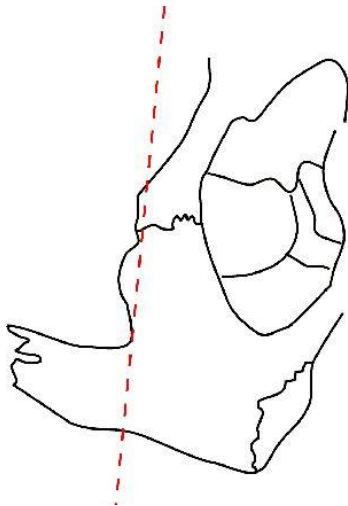


Figure 49a: PZT (2) Illustration (Osteoware, 2011)



Figure 49b: PZT (2)

3=A marked projection of bone (generally > 6mm)

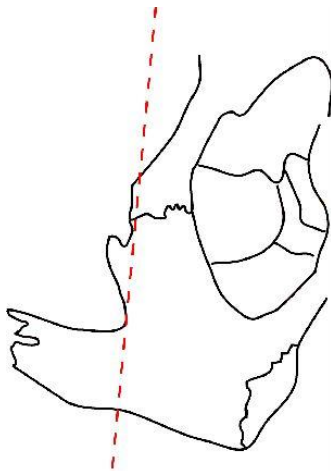


Figure 50a: PZT (3) Illustration (Osteoware, 2011)



Figure 50b: PZT (3)

The Supranasal Suture (SNS) is a secondary complex suture that may persist. It does not represent the nasal portion of a persistent metopic suture, which is generally a single, non-oscillating line but rather is the fusion of the nasal portion of a frontal suture. It appears as a complex of interlocking bony spicules at glabella.



0=Completely obliterated

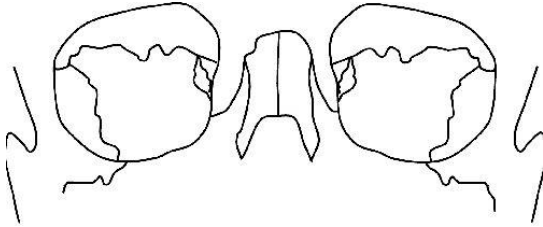


Figure 51a: SNS (0) Illustration (Osteoware, 2011)

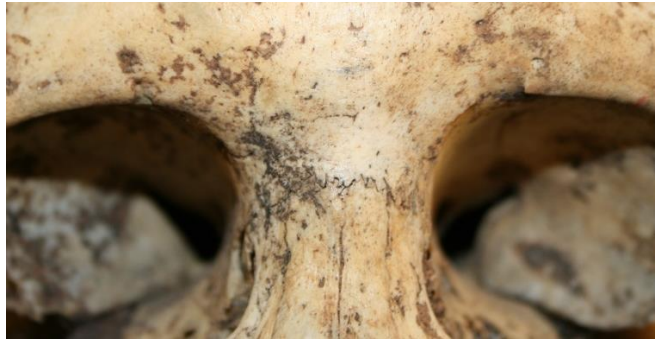


Figure 51b: SNS (0)

1=Open (unfused)

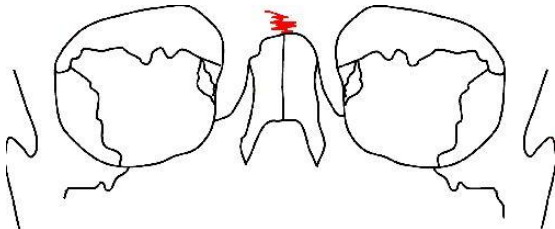


Figure 52a: SNS (1) Illustration (Osteoware, 2011)



Figure 52b: SNS (1)

2=Closed, but visible

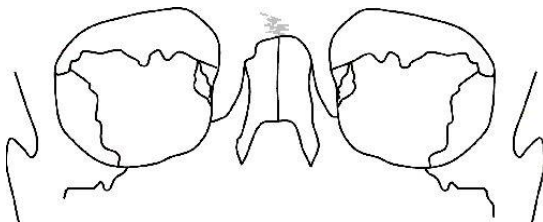


Figure 53a: SNS (2) Illustration (Osteoware, 2011)



Figure 53b: SNS (2)

The Transverse Palatine Suture (TPS) is not scored unilaterally although asymmetrical sutures are not uncommon. The entire suture is observed but the observer should focus on the medial one-half in the region of the palatine suture. When an asymmetrical suture is present, that is the two branches of the suture do not come into contact at the midline, the general theme is recorded. Slight undulations of the suture should not be considered when assessing the trait. If the right and left halves of the suture do not make contact at the midline but the suture is otherwise straight, score the suture as 1.

1=Straight; the suture crosses the palate perpendicular to the median palatine suture with no significant anterior or posterior deviations.

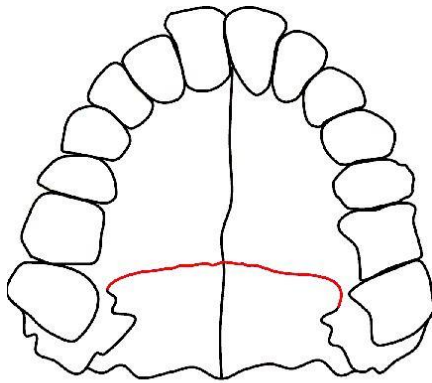


Figure 54a: TPS (1) Illustration (Osteoware, 2011)



Figure 54b: TPS (1)

2=Anterior bulging; the suture crosses the palate perpendicular to the median palatine suture but near this junction is a significant anterior deviation.

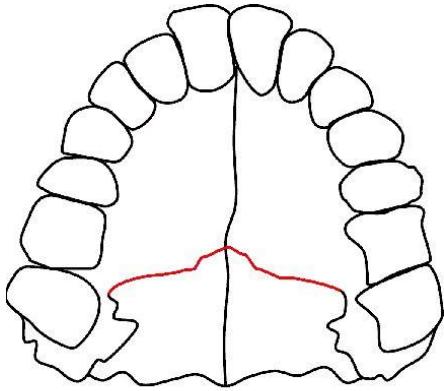


Figure 55a: TPS (2) Illustration (Osteoware, 2011)

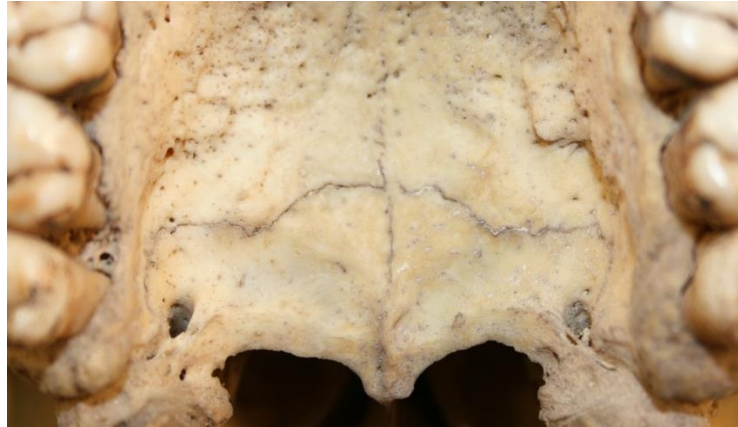


Figure 55b: TPS (2)

3=M-shaped; the suture crosses the palate but deviates anteriorly and posteriorly in the regions of the median palatine suture (similar to an EKG reading)

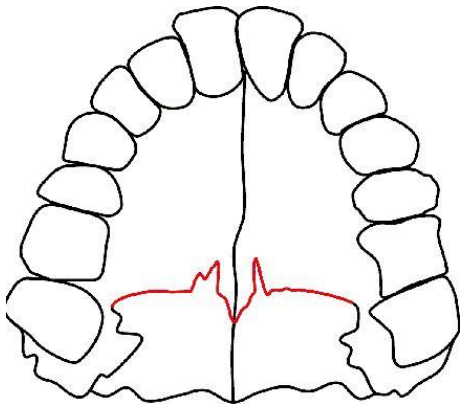


Figure 56a: TPS (3) Illustration (Osteoware, 2011)



Figure 56b: TPS (3)



4=Posterior bulging; the suture crosses the palate perpendicular to the median palatine suture but near this juncture a posterior deviation is present.

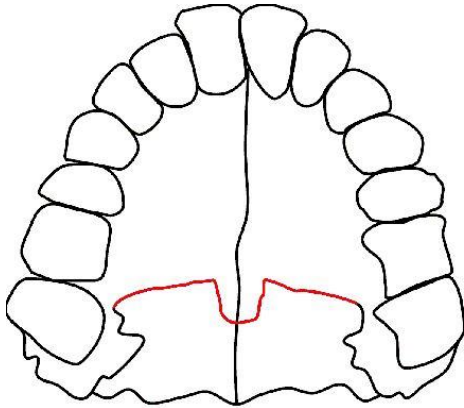


Figure 57a: TPS (4) Illustration (Osteoware, 2011)



Figure 57b: TPS (4)

The Zygomaticomaxillary Suture Course (ZSC) is the suture between the maxilla and the zygomatic. The course of the suture is best observed in the anterior view. The assessment is based primarily on the approximate location of the greatest lateral projection of the suture and also on the number of major angles present.

0=A suture with no angles and greatest lateral projection at the inferior margin of the malar.

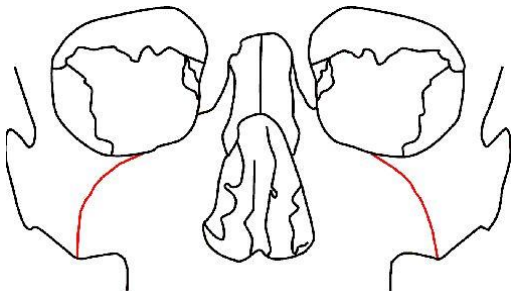


Figure 58a: ZSC (0) Illustration (Osteoware, 2011)



Figure 58b: ZSC (0)

1=A suture with one angle and greatest lateral projection near the midline

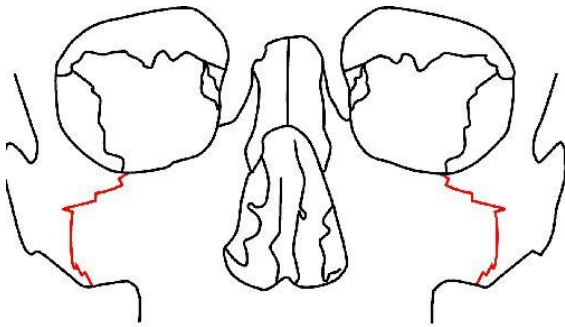


Figure 59a: ZSC (1) Illustration (Osteoware, 2011)



Figure 59b: ZSC (1)

2=A suture with two or more angles (jagged and/or S-shaped appearance) with variable greatest lateral projection

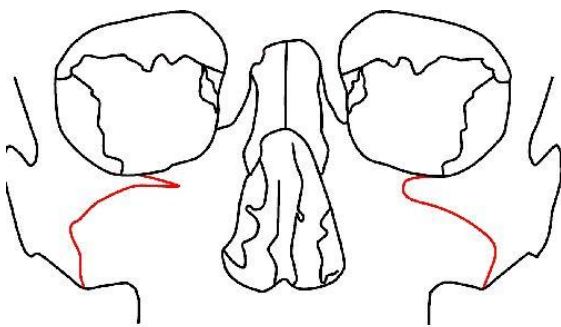


Figure 60a: ZSC (2) Illustration (Osteoware, 2011)



Figure 60b: ZSC(2)

## Frequency Comparison

Examining the frequencies of character states for each trait within a group will illuminate the percentages of each trait expression without making blanket statements concerning the traits found within groups. Typological lists used in the past are examples of these blanket expectations of all individuals within a particular group. Examples include a highly variable sagittal outline and a present postbregmatic depression in individuals of African ancestry (Gill, 1998) while Hefner (2009) found less than half (47.2%) of individuals of African ancestry actually expressed a post-bregmatic depression. In fact, all groups contained individuals who expressed a present post-bregmatic depression, to a lesser extent, but are often cited as exhibiting no depression, often misrepresenting the true variability found within groups.

### *Larger Groups of the World, Southeast Asia, and the Pacific Islands*

To recognize the true variability found within the groups examined, frequencies of the morphoscopic traits were calculated for each group. The trait frequencies of the Southeast Asian and Pacific Islander samples were calculated using SPSS 21.0 (2012). Frequency distribution tables were created for these samples for comparison with the trait frequencies of Asian, European, American Indian, and African samples. This was done to see if these two groups were visually distinguishable in their frequencies from one another and from other major groups of the world. The African, American Indian, European, and Asian sample frequencies used for comparison (Table 3) were collected and published by Hefner (2009) and contain frequencies for 11 of the 16 original traits. Only 10 of the published 11 traits were used for frequency comparison due to changes in the scoring methods in Osteoware from the time of the Hefner

(2009) publication and the time of this study. The traits used include ANS, INA, IOB, MT, NAW, NBC (also labelled NBS (Hefner, 2009)), NO, PBD, SNS, and TPS.

### *Larger Groups of the World and the Pacific*

The Southeast Asian and Pacific Islander samples were combined to form an overall Pacific group (Table 2) and their frequencies calculated using SPSS 21.0. This Pacific group was then compared with the frequencies of Asian, European, American Indian, and African samples (Table 3). This was done to see if the overall Pacific group frequencies were visually distinguishable from the other group frequencies.

## **Significance Tests**

### *Pacific Islanders and Southeast Asia*

Chi-square analyses were performed for the Southeast Asian group and the Pacific Island group (which contains Polynesians and Melanesians) to determine if there was a statistically significant difference between the traits of these regions of the Pacific. Using SPSS 21.0, cross-tabulation tables and chi-square analyses were performed for each of the 9 traits, ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, and ZSC, for the Southeast Asian (n=94) and the Pacific Islander (n=71) samples.

### *Mainland Asia and the Pacific*

Chi-square analyses were performed to determine if there was a statistically significant difference between the traits of the mainland Asians and the groups of the Pacific. Using SPSS 21.0, cross-tabulation tables and chi-square analyses were performed for each trait for an Asian

data sample and the collective Southeast Asian/Pacific Island data (n=165). Data from the Asian sample were graciously provided by Dr. Joe Hefner and is outlined above in Table 5. This sample contains (n=74) total individuals, (n=15) from Japan and (n=59) China. A total of 9 traits were provided: ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, and ZSC.

#### *Mainland Asia, Southeast Asia, Melanesia, and Polynesia*

Chi-square analyses were performed for the mainland Asian, Southeast Asian, Melanesian, and Polynesian groups to determine if there was a statistically significant difference between the groups when they are not grouped together as one 'Pacific' population. Using SPSS 21.0, cross-tabulation tables and chi-square analyses were performed for each of the 9 traits, ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, and ZSC, for the Asian (n=74), Southeast Asian (n=94), Melanesian (n=60), and Polynesian (n=11) samples.

#### *Larger Groups of the World*

Chi-square analyses were performed for the larger groups of the world including the overall Pacific group to determine if there was a statistically significant difference between the larger groups of the world. Using SPSS 21.0, cross-tabulation and chi-square analyses were performed for 5 traits for larger groups of the world (Table 4), American Indians (n=43), Asians (n=48), African Americans (n=61), European Americans (n=50), Eskimos (n=21), and peoples of the Pacific (n=165), to determine if there is a significant difference between these main groups. The Pacific group contains the data collected for Island Southeast Asians, Melanesians, and Polynesians (Table 2). These traits are IOB, NAW, NBC, PZT, and ZSC. Data for these 5 traits



for American Indian, Asian, African American, European American, and Eskimo samples were also graciously provided by Dr. Joe Hefner.

### **Correlation Coefficients**

Pearson's correlation coefficients were calculated to examine the associations between the traits to determine if certain expressions of traits correspond to any expressions of other traits, specifically those of the facial region that are most often associated with differences seen between individuals of varying areas of the world. Conversely, this analysis was also performed to see which expressions of traits, if any, are independent of expressions of other traits. Using the Asian (n=74), Southeast Asian (n=94), and Pacific Islander (n=71) samples, Pearson's correlation coefficients were calculated for 9 traits using SPSS 21.0.

### **Geographic Trait Distribution**

To better illustrate the frequency distributions of the traits across the geography, frequency pie charts were created and overlaid onto a map. This visually displays the variability of the region and makes any clinality of trait expression across the geography more easily recognizable. Using all 16 traits found in Osteoware (2011), frequencies of trait expression using pie charts were determined for Southeast Asians (n=94), Melanesians (n=60), and Polynesians (n=11) using SPSS 21.0. Additionally, pie charts were created for the Japanese (n=15) and Chinese (n=59), provided by Dr. Joe Hefner, for 9 of the 16 traits. These 9 traits are ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, and ZSC.

## **Correspondence Analysis**

Simple correspondence analyses generate independent axes representing patterns of variation and association between states of categorical variables. Similar to principal component axes, these axes summarize patterned information within a matrix of associations between variables. The scores of individuals or mean scores for groups on these axes may be plotted. For correspondence analysis, the measure of association is chi-squared variables whereas for principal components, the measure of association is covariance (Hammer, 2012). While it would have been desirable to have used multiple correspondence analysis in order to consider all the morphological traits simultaneously, software for this type of analysis was not available at the time at the University of Montana. Therefore, simple correspondence analyses were performed for each trait separately.

For analyses of correspondence, groups that fall closely with one another on a plot of the axes have similarities in their patterns of the frequencies of character states for the trait being examined. Conversely, groups that fall far away from one another on a plot of the axes do not have similarities in their frequency patterns for the character states of the trait being examined (Yelland, 2010). Correspondence analysis takes more of a diffusionist approach to viewing group similarity, making it appropriate for analyzing patterns of continuous variation like clines that result to a certain degree from gene flow between groups (Cavalli-Sforza et al., 1993, 1994; Novembre & Stephens, 2008).

### *Larger Groups of the World*

Correspondence analyses were performed for the larger groups of the world and the separated groups of the Pacific to look at the associations between the groups for each trait.

Using PAST 2.17c (Hammer et al., 2001), correspondence analyses were performed for the data containing larger groups of the world (Tables 2 & 4): American Indians (n=43), Asians (n=48), African Americans (n=61), European Americans (n=50), Eskimos (n=21), Southeast Asians (n=94), Melanesians (n=60), and Polynesians (n=11). The 5 traits used were IOB, NAW, NBC, PZT, and ZSC.

#### *Mainland Asia, Southeast Asia, Melanesia, and Polynesia*

Correspondence analyses were performed for the separated groups of the Pacific and mainland Asia to examine associations between these groups for each trait and to see which groups correspond most closely and which do not correspond closely. Using PAST 2.17c, correspondence analyses were performed for the mainland Asian (n=74) sample (Japan and China), Southeast Asia (n=94), Melanesia (n=60), and Polynesia (n=11). This was done for 7 traits: ANS, INA, IOB, NAW, NBC, PZT, and ZSC. NO and PBD were not included in this analysis because their assessment only includes two categories: 0 and 1. Correspondence analysis requires three or more compartments or assessments for a plot to be generated (Hammer et al., 2005).

#### **Hierarchical Cluster Analysis**

Hierarchical cluster analysis can be used to represent similarities between groups. Hierarchical cluster analysis differs from the correspondence analysis approach in that it assumes that at least some of the clustering is due to phylogenetic history (Baum & Smith, 2012). It is generally assumed that shared alleles due to common ancestry or gene flow is the main cause for the similarities seen between groups since the phenotype is at least an indirect expression of the

genotype (Relethford 2012). Therefore, hierarchical cluster analyses can present a view of evolutionary relationships between groups of people. This analysis works by generating a hierarchy of clusters and linking associated populations based on the overall expression of the variables in each group.

Clustering using average linkage takes inter-group distance as an average of all inter-individual distances made up of pairs of individuals, taking one from each group (Landau & Everitt, 2004). In phylogenetics, this is known as UPGMA, or Unweighted Pair-Group Method with Arithmetic Means (Baum & Smith, 2012). The Euclidean distance method of clustering builds the hierarchy by progressively merging clusters from individual elements, showing the geometric distance between groups in the multidimensional space. This method was chosen over other hierarchical clustering methods such as a neighbor joining method because not only are the ancestral linkages being examined with this data but the overall morphological similarities are being examined due to factors like admixture since a varying degree of admixture is generally agreed to have taken place between the groups of the Pacific.

### *Larger Groups of the World*

To examine the overall morphological similarities and dissimilarities of larger groups of the world and groups of the Pacific, a hierarchical cluster analysis was performed. Using SPSS 21.0, a Euclidean distance method dendrogram was created using between-group average linkage clustering for 5 traits for the larger groups of the world: American Indians (n=43), Asians (n=48), African American (n=61), European Americans (n=50), Eskimos (n=21), Southeast Asians (n=94), Melanesians (n=60), and Polynesians (n=11). The traits included in this analysis were IOB, NAW, NBC, PZT, and ZSC.

*Mainland Asia, Southeast Asia, Melanesia, and Polynesia*

To examine the overall morphological similarities of the groups of the Pacific and mainland Asia, a hierarchical cluster analysis was performed. Using SPSS 21.0, a Euclidean distance method dendrogram was created using between-group average linkage clustering for 9 traits for the mainland Asian sample (n=74) (Japan and China), Southeast Asia (n=94), Melanesia (n=60), and Polynesia (n=11). The traits included in this analysis are ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, and ZSC.

## CHAPTER III

### RESULTS

#### Frequency Comparison

##### *Larger groups of the World, Southeast Asia, and the Pacific Islands*

The following are morphoscopic trait frequency tables for African, American Indian, European, and Asian individuals (provided by Hefner, 2009) and Southeast Asian and Pacific Islander individuals. These tables display frequencies for 10 traits: ANS, INA, IOB, MT, NAW, NBC, NO, PBD, SNS, and TPS.

Table 6: ANS Frequencies for Major Populations with SE Asia and Pacific Islands

<b>ANS</b>	<b><u>African</u></b> n=218	<b><u>Am-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=79	<b><u>Pac Islander</u></b> n=57
<b>1</b>	69.7%	67.9%	36.3%	80.0%	60.8%	63.8%
<b>2</b>	20.2%	21.4%	26.0%	13.3%	26.6%	34.5%
<b>3</b>	10.1%	10.7%	37.7%	6.7%	12.7%	1.7%

Table 7: INA Frequencies for Major Populations with SE Asia and Pacific Islands

<b>INA</b>	<b><u>African</u></b> n=218	<b><u>Am-Indian</u></b> n=283	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=90	<b><u>Pac Islander</u></b> n=63
<b>1</b>	29.4%	3.8%	0.7%	12.0%	6.7%	28.1%
<b>2</b>	28.9%	24.0%	3.4%	17.3%	35.6%	51.6%
<b>3</b>	21.6%	56.9%	24.0%	64.0%	47.8%	20.3%
<b>4</b>	13.3%	14.9%	41.1%	4.0%	6.7%	0.0%
<b>5</b>	6.9%	0.4%	30.8%	2.7%	3.3%	0.0%

Table 8: IOB Frequencies for Major Populations with SE Asia and Pacific Islands

<b>IOB</b>	<b><u>African</u></b> n=218	<b><u>Am-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=91	<b><u>Pac Islander</u></b> n=61
1	9.6%	59.2%	30.8%	41.3%	17.6%	21.0%
2	34.4%	36.6%	63.0%	62.0%	63.7%	61.3%
3	56.0%	4.2%	6.2%	6.7%	18.7%	17.7%

Table 9: MT Frequencies for Major Populations with SE Asia and Pacific Islands

<b>MT</b>	<b><u>African</u></b> n=218	<b><u>Am-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=90	<b><u>Pac Islander</u></b> n=68
0	50.5%	40.8%	51.4%	42.7%	4.4%	16.2%
1	27.5%	37.4%	32.2%	33.3%	48.9%	54.4%
2	14.7%	15.3%	12.3%	13.3%	38.9%	27.9%
3	7.3%	6.5%	4.1%	10.7%	7.8%	1.5%

Table 10: NAW Frequencies for Major Populations with SE Asia and Pacific Islands

<b>NAW</b>	<b><u>African</u></b> n=218	<b><u>Am-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=90	<b><u>Pac Islander</u></b> n=62
1	3.7%	8.4%	54.1%	2.7%	7.8%	14.5%
2	40.8%	77.9%	32.9%	86.7%	65.6%	61.3%
3	55.5%	13.7%	13.1%	10.7%	26.7%	24.2%

Table 11: NBC Frequencies for Major Populations with SE Asia and Pacific Islands

<b>NBC</b>	<b><u>African</u></b> n=218	<b><u>Am-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=83	<b><u>Pac Islander</u></b> n=54
0	52.3%	11.5%	7.5%	25.3%	12.0%	11.1%
1	22.9%	25.6%	15.8%	22.7%	74.7%	77.8%
2	10.1%	24.8%	18.5%	38.7%	1.2%	1.9%
3	10.6%	34.4%	25.3%	12.0%	7.2%	9.3%
4	4.1%	3.8%	32.9%	1.3%	4.8%	0.0%

Table 12: NO Frequencies for Major Populations with SE Asia and Pacific Islands

<b>NO</b>	<b><u>African</u></b> n=207	<b><u>Am-Indian</u></b> n=220	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=68	<b><u>Pac Islander</u></b> n=46
<b>0</b>	68.1%	44.1%	52.7%	68.0%	76.5%	80.4%
<b>1</b>	31.9%	55.9%	49.2%	32.0%	23.5%	19.6%

Table 13: PBD Frequencies for Major Populations with SE Asia and Pacific Islands

<b>PBD</b>	<b><u>African</u></b> n=218	<b><u>Am-Indian</u></b> n=253	<b><u>European</u></b> n=184	<b><u>Asian</u></b> n=72	<b><u>SE Asian</u></b> n=94	<b><u>Pac Islander</u></b> n=70
<b>0</b>	52.8%	92.9%	82.9%	90.3%	79.8%	90.1%
<b>1</b>	47.2%	7.1%	17.1%	9.7%	20.2%	9.9%

Table 14: SNS Frequencies for Major Populations with SE Asia and Pacific Islands

<b>SNS</b>	<b><u>African</u></b> n=215	<b><u>Am-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=91	<b><u>Pac Islander</u></b> n=68
<b>0</b>	42.8%	34.3%	39.0%	12.0%	47.3%	46.4%
<b>1</b>	31.2%	31.3%	39.0%	30.7%	3.3%	7.2%
<b>2</b>	26.0%	34.4%	22.0%	57.3%	49.5%	46.4%

Table 15: TPS Frequencies for Major Populations with SE Asia and Pacific Islands

<b>TPS</b>	<b><u>African</u></b> n=180	<b><u>Am-Indian</u></b> n=260	<b><u>European</u></b> n=145	<b><u>Asian</u></b> n=75	<b><u>SE Asian</u></b> n=85	<b><u>Pac Islander</u></b> n=53
<b>0</b>	18.3%	63.5%	29.0%	45.3%	28.2%	18.5%
<b>1</b>	47.2%	27.7%	27.6%	33.3%	44.7%	38.9%
<b>2</b>	25.0%	5.4%	33.8%	14.7%	20.0%	27.8%
<b>3</b>	9.4%	3.5%	9.7%	6.7%	7.1%	14.8%

### *Larger Groups of the World and the Pacific*

The following are morphoscopic trait frequency tables for African, American Indian, European, and Asian individuals (provided by Hefner, 2009) and the overall Pacific (Southeast Asia, Melanesia, and Polynesia combined). These tables display frequencies for 10 traits: ANS, INA, IOB, MT, NAW, NBC, NO, PBD, SNS, and TPS.



Table 16: ANS Frequencies for Major Populations with Pacific

<b>ANS</b>	<b><u>African</u></b> n=218	<b><u>Amer-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=136
<b>1</b>	69.7%	67.9%	36.3%	80.0%	61.8%
<b>2</b>	20.2%	21.4%	26.0%	13.3%	30.1%
<b>3</b>	10.1%	10.7%	37.7%	6.7%	8.1%

Table 17: INA Frequencies for Major Populations with Pacific

<b>INA</b>	<b><u>African</u></b> n=218	<b><u>Amer-Indian</u></b> n=283	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=153
<b>1</b>	29.4%	3.8%	0.7%	12.0%	15.7%
<b>2</b>	28.9%	24.0%	3.4%	17.3%	42.5%
<b>3</b>	21.6%	56.9%	24.0%	64.0%	35.9%
<b>4</b>	13.3%	14.9%	41.1%	4.0%	3.9%
<b>5</b>	6.9%	0.4%	30.8%	2.7%	2.0%

Table 18: IOB Frequencies for Major Populations with Pacific

<b>IOB</b>	<b><u>African</u></b> n=218	<b><u>Amer-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=152
<b>1</b>	9.6%	59.2%	30.8%	41.3%	19.1%
<b>2</b>	34.4%	36.6%	63.0%	62.0%	62.5%
<b>3</b>	56.0%	4.2%	6.2%	6.7%	18.4%

Table 19: MT Frequencies for Major Populations with Pacific

<b>MT</b>	<b><u>African</u></b> n=218	<b><u>Amer-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=158
<b>0</b>	50.5%	40.8%	51.4%	42.7%	9.6%
<b>1</b>	27.5%	37.4%	32.2%	33.3%	51.6%
<b>2</b>	14.7%	15.3%	12.3%	13.3%	33.8%
<b>3</b>	7.3%	6.5%	4.1%	10.7%	5.1%

Table 20: NAW Frequencies for Major Populations with Pacific

<b>NAW</b>	<b><u>African</u></b> n=218	<b><u>Amer-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=152
<b>1</b>	3.7%	8.4%	54.1%	2.7%	10.5%
<b>2</b>	40.8%	77.9%	32.9%	86.7%	63.8%
<b>3</b>	55.5%	13.7%	13.1%	10.7%	25.7%

Table 21: NBC Frequencies for Major Populations with Pacific

<b>NBC</b>	<b><u>African</u></b> n=218	<b><u>Amer-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=137
<b>0</b>	52.3%	11.5%	7.5%	25.3%	11.7%
<b>1</b>	22.9%	25.6%	15.8%	22.7%	75.9%
<b>2</b>	10.1%	24.8%	18.5%	38.7%	1.5%
<b>3</b>	10.6%	34.4%	25.3%	12.0%	8.0%
<b>4</b>	4.1%	3.8%	32.9%	1.3%	2.9%

Table 22: NO Frequencies for Major Populations with Pacific

<b>NO</b>	<b><u>African</u></b> n=207	<b><u>Amer-Indian</u></b> n=220	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=114
<b>0</b>	68.1%	44.1%	52.7%	68.0%	78.1%
<b>1</b>	31.9%	55.9%	49.2%	32.0%	21.9%

Table 23: PBD Frequencies for Major Populations with Pacific

<b>PBD</b>	<b><u>African</u></b> n=218	<b><u>Amer-Indian</u></b> n=253	<b><u>European</u></b> n=184	<b><u>Asian</u></b> n=72	<b><u>Pacific</u></b> n=164
<b>0</b>	52.8%	92.9%	82.9%	90.3%	84.1%
<b>1</b>	47.2%	7.1%	17.1%	9.7%	15.9%

Table 24: SNS Frequencies for Major Populations with Pacific

<b>SNS</b>	<b><u>African</u></b> n=215	<b><u>Amer-Indian</u></b> n=262	<b><u>European</u></b> n=146	<b><u>Asian</u></b> n=75	<b><u>Pacific</u></b> n=159
<b>0</b>	42.8%	34.3%	39.0%	12.0%	46.5%
<b>1</b>	31.2%	31.3%	39.0%	30.7%	5.0%
<b>2</b>	26.0%	34.4%	22.0%	57.3%	48.4%

Table 25: TPS Frequencies for Major Populations with Pacific

<b>TPS</b>	<b><u>African</u></b> <b>n=180</b>	<b><u>Amer-Indian</u></b> <b>n=260</b>	<b><u>European</u></b> <b>n=145</b>	<b><u>Asian</u></b> <b>n=75</b>	<b><u>Pacific</u></b> <b>n=138</b>
<b>1</b>	18.3%	63.5%	29.0%	45.3%	24.5%
<b>2</b>	47.2%	27.7%	27.6%	33.3%	42.4%
<b>3</b>	25.0%	5.4%	33.8%	14.7%	23.0%
<b>4</b>	9.4%	3.5%	9.7%	6.7%	10.1%

## Significance Tests

### *Pacific Islanders and Southeast Asia*

Table 26: Chi-square probabilities for Pacific Islanders and Southeast Asians

<b>Chi-Square Results for Pacific Islanders &amp; Southeast Asians</b>	
	p-value
ANS	0.058
INA	<b>0.000*</b>
IOB	0.848
NAW	0.412
NBC	0.570
NO	0.616
PBD	0.077
PZT	<b>0.003</b>
ZSC	<b>0.011</b>

The following results were taken from the cross tabulation tables and chi-square probabilities of 9 morphoscopic traits (ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, ZSC) using SPSS 21.0 for the Pacific Islanders (Melanesia & Polynesia) and Southeast Asia. Highlighted probabilities indicate significance at the 0.05 level or above, bolded probabilities indicate significance at the 0.01 level or above, and probabilities with an asterisk indicate probabilities at the 0.001 level or above. The INA ( $p < 0.000$ ) showed significant interregional

differences at the 0.001 level of significance. The PZT ( $p<0.003$ ) showed significant interregional differences at the 0.01 level of significance. The ZSC ( $p<0.011$ ) showed significant interregional differences at the 0.05 level of significance. The ANS ( $p<0.058$ ), IOB ( $p<0.848$ ), NAW ( $p<0.412$ ), NBC ( $p<0.570$ ), NO ( $p<0.616$ ), PBD ( $p<0.077$ ) did not exhibit significant interregional differences.

### *Mainland Asia and the Pacific*

**Table 27: Chi-square probabilities of Mainland Asia and the Pacific**

<b>Chi-Square Results for Mainland Asia &amp; the Pacific</b>	
	p-value
ANS	<b>0.006</b>
INA	<b>0.001*</b>
IOB	<b>0.000*</b>
NAW	<b>0.000*</b>
NBC	<b>0.000*</b>
NO	0.390
PBD	0.379
PZT	0.027
ZSC	<b>0.000*</b>

The following results were taken from the cross tabulation tables and chi-square probabilities of 9 morphoscopic traits (ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, ZSC) using SPSS 21.0 for Mainland Asian (Japan & China) and the Pacific (Island Southeast Asia, Melanesia, & Polynesia). The INA ( $p<0.001$ ), IOB ( $p<0.000$ ), NAW ( $p<0.000$ ), NBC ( $p<0.000$ ), and ZSC ( $p<0.000$ ) all showed significant interregional differences at the 0.001 level of significance. The ANS ( $p<0.006$ ) showed significant interregional differences at the 0.01 level of significance. The PZT ( $p<0.027$ ) showed significant interregional differences at the 0.05

level of significance. The NO ( $p < 0.390$ ) and PBD ( $p < 0.379$ ) did not exhibit significant interregional differences.

*Mainland Asia, Southeast Asia, Melanesia, and Polynesia*

**Table 28: Chi-square probabilities of Mainland Asia, Southeast Asia, Melanesia, and Polynesia**

<b>Chi-Square Results for Mainland Asia, Southeast Asia Melanesia &amp; Polynesia</b>	
	p-value
ANS	<b>0.010</b>
INA	<b>0.000*</b>
IOB	<b>0.003</b>
NAW	<b>0.003</b>
NBC	<b>0.000*</b>
NO	0.542
PBD	0.246
PZT	<b>0.003</b>
ZSC	<b>0.000*</b>

The following were taken from the cross tabulation tables and chi-square probabilities of 9 morphoscopic traits (ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, ZSC) using SPSS 21.0 for Mainland Asians, Island Southeast Asians, Melanesians, and Polynesians. The INA ( $p < 0.000$ ), NBC ( $p < 0.000$ ), and ZSC ( $p < 0.000$ ) showed significant interregional differences at the 0.001 level of significance. The ANS ( $p < 0.010$ ), IOB ( $p < 0.003$ ), NAW ( $p < 0.003$ ), and PZT ( $p < 0.003$ ) showed significant interregional differences at the 0.01 level of significance. The NO ( $p < 0.542$ ) and PBD ( $p < 0.246$ ) did not exhibit significant interregional differences.

### *Larger Groups of the World*

**Table 29: Chi-square probabilities of larger groups of the World**

<b>Chi-Square Results for Larger Groups of the World</b>	
	p-value
IOB	<b>0.000*</b>
NAW	<b>0.000*</b>
NBC	<b>0.000*</b>
PZT	<b>0.000*</b>
ZSC	<b>0.000*</b>

The following were taken from the cross tabulation tables and chi-square probabilities of 5 morphoscopic traits (IOB, NAW, NBC, PZT, ZSC) using SPSS 21.0 for American Indians, Asians, African Americans, European Americans, Eskimos, Melanesians, Polynesians, and Southeast Asians. The IOB ( $p < 0.000$ ), NAW ( $p < 0.000$ ), NBC ( $p < 0.000$ ), PZT ( $p < 0.000$ ), and ZSC ( $p < 0.000$ ) all showed significant interregional differences at the 0.001 level of significance.

### **Correlation Coefficient**

The table displayed is the Pearson's correlation coefficient table for 9 traits using mainland Asian, Southeast Asian, Melanesian, and Polynesian data. Bolded correlations are significant at the 0.05 level and correlations that are bolded and have an asterisk are significant at the 0.01 level. This analysis found that 4 trait correlations were significant at the 0.05 level and 6 trait correlations were significant at the 0.01 level. The INA and ANS, INA and PBD, INA and ZSC, and ZSC and IOB were all significantly correlated at the 0.05 level. This analysis also showed that the NBC and ANS, NBC and INA, IOB and NAW, IOB and NBC, NBC and NO, and the ZSC and PZT were all significantly correlated at the 0.01 level. All remaining trait correlations were not found to be significant.

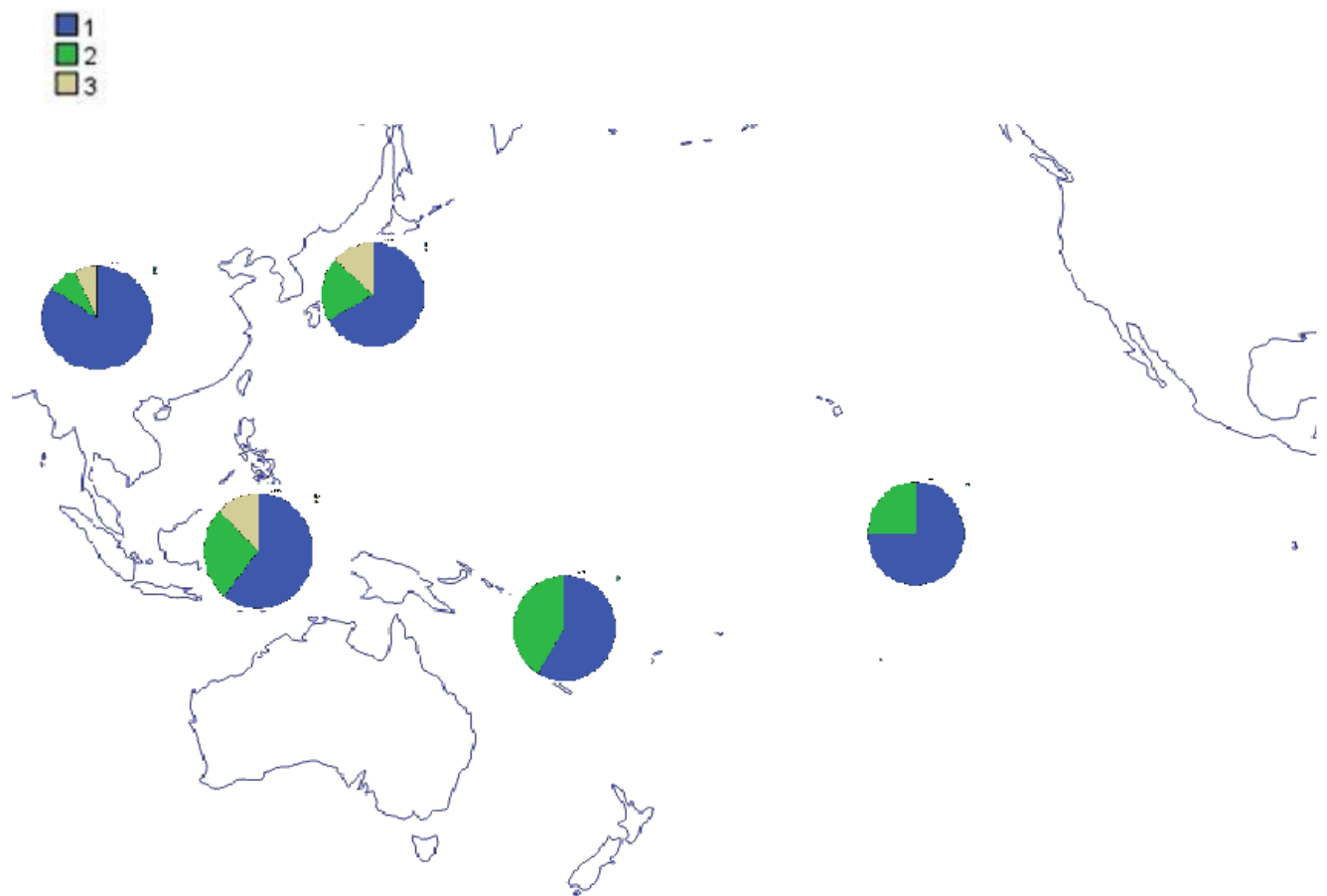
Table 30: Correlation coefficient table for 9 traits: Correlation is significant at the 0.05 level where bolded and at the 0.01 level where \*.

	ANS	INA	IOB	NAW	NBC	NO	PBD	PZT	ZSC
ANS	-								
INA	<b>0.160</b>	-							
IOB	0.052	-0.004	-						
NAW	-0.095	0.027	<b>0.233*</b>	-					
NBC	<b>0.207*</b>	<b>0.189*</b>	<b>-0.212*</b>	-0.125	-				
NO	0.095	-0.033	-0.028	0.083	<b>0.194*</b>	-			
PBD	0.018	<b>0.137</b>	-0.026	-0.033	0.042	0.059	-		
PZT	0.092	0.109	0.028	-0.041	0.051	-0.009	0.029	-	
ZSC	-0.040	<b>0.162</b>	<b>-0.148</b>	-0.038	0.093	-0.043	-0.067	<b>0.276*</b>	-

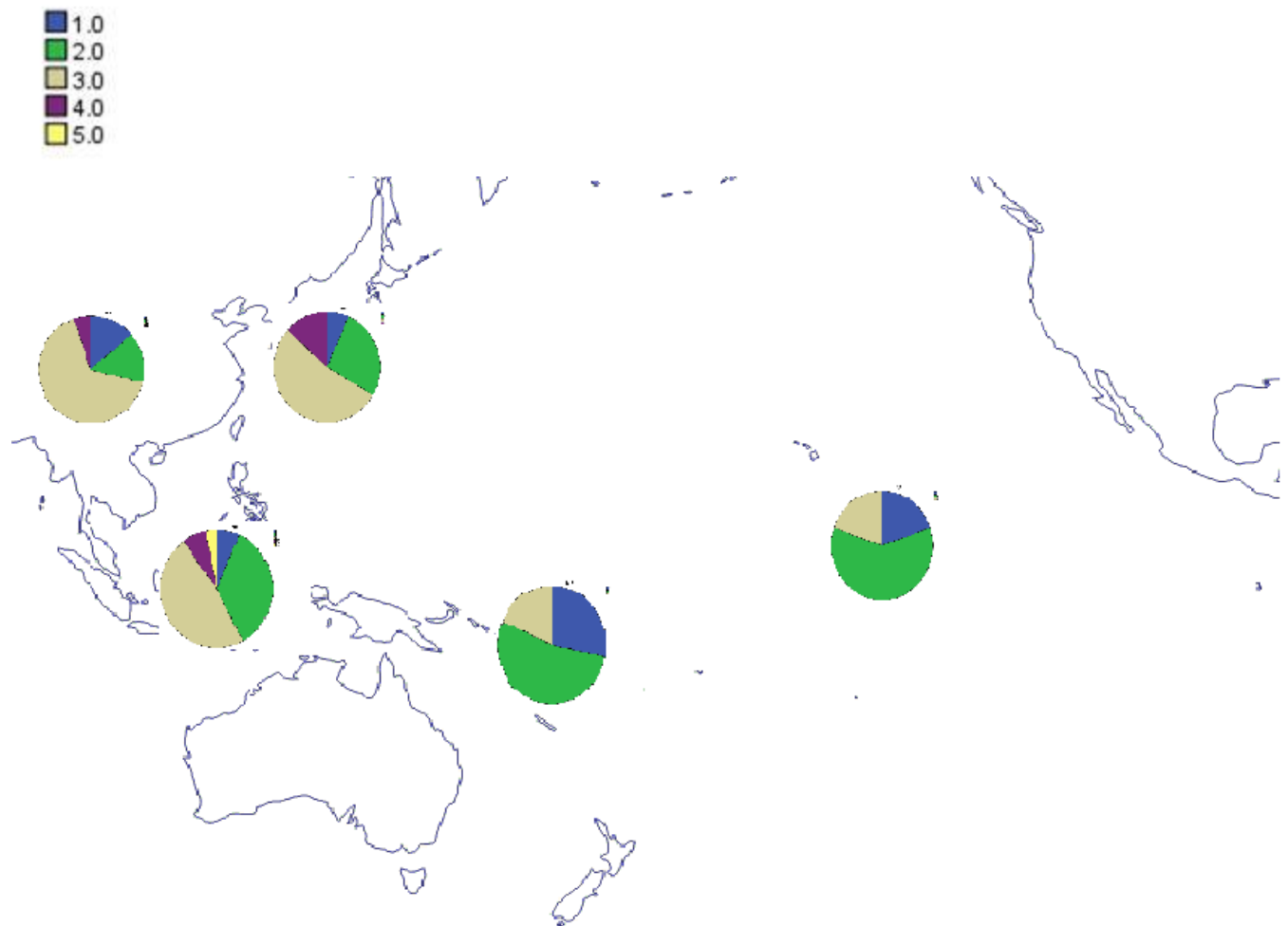
## Geographic Distribution

The graphics represent the geographic frequency distribution for Chinese, Japanese, Southeast Asians, Melanesians, and Polynesians for the anterior nasal spine, inferior nasal aperture, interorbital breadth, nasal aperture width, nasal bone contour, nasal overgrowth, postbregmatic depression, posterior zygomatic tubercle, and zygomaticomaxillary suture course.

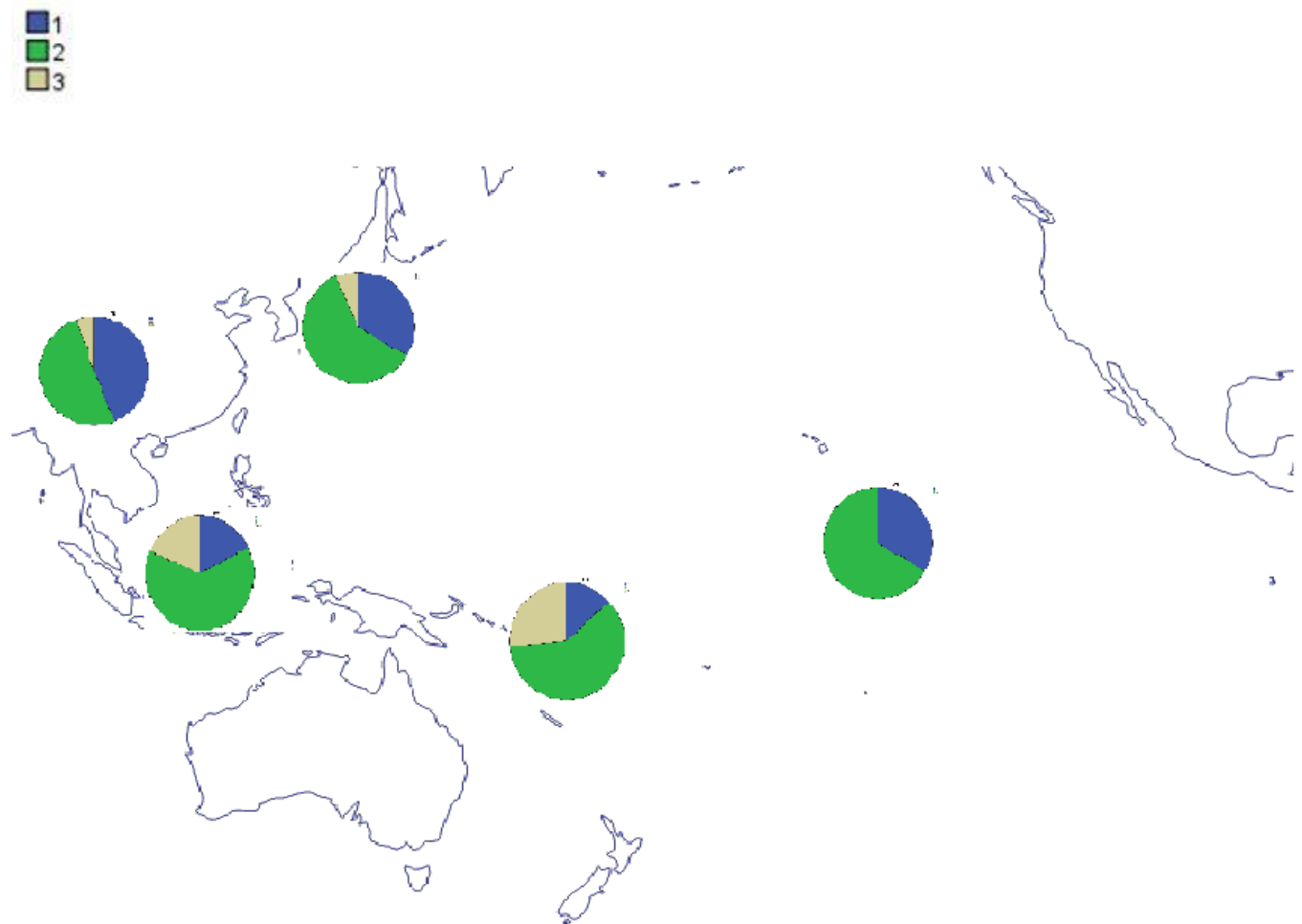




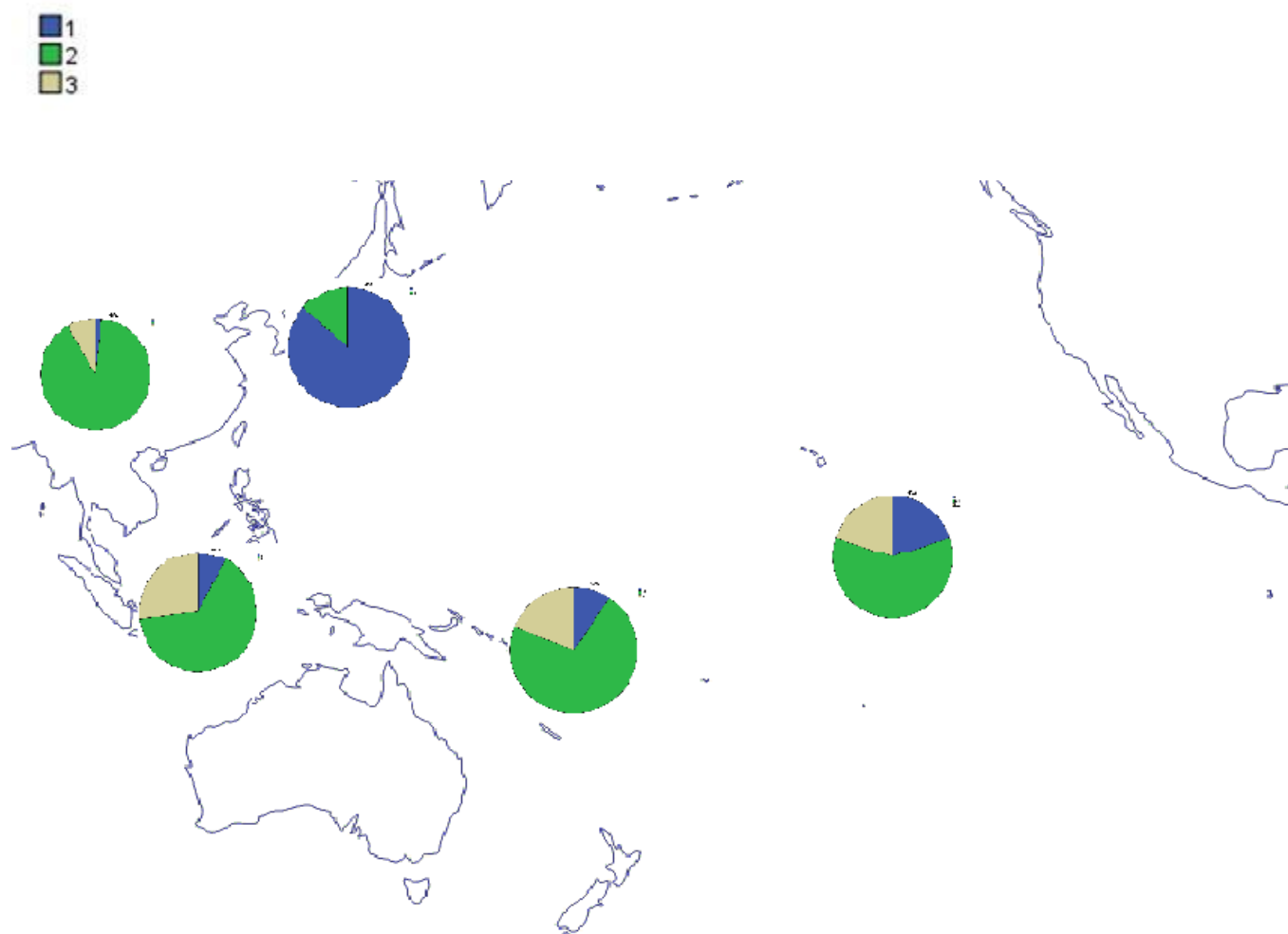
**Figure 61: Anterior nasal spine (ANS) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;**  
**1= slight nasal spine, 2=intermediate nasal spine, 3=marked nasal spine**



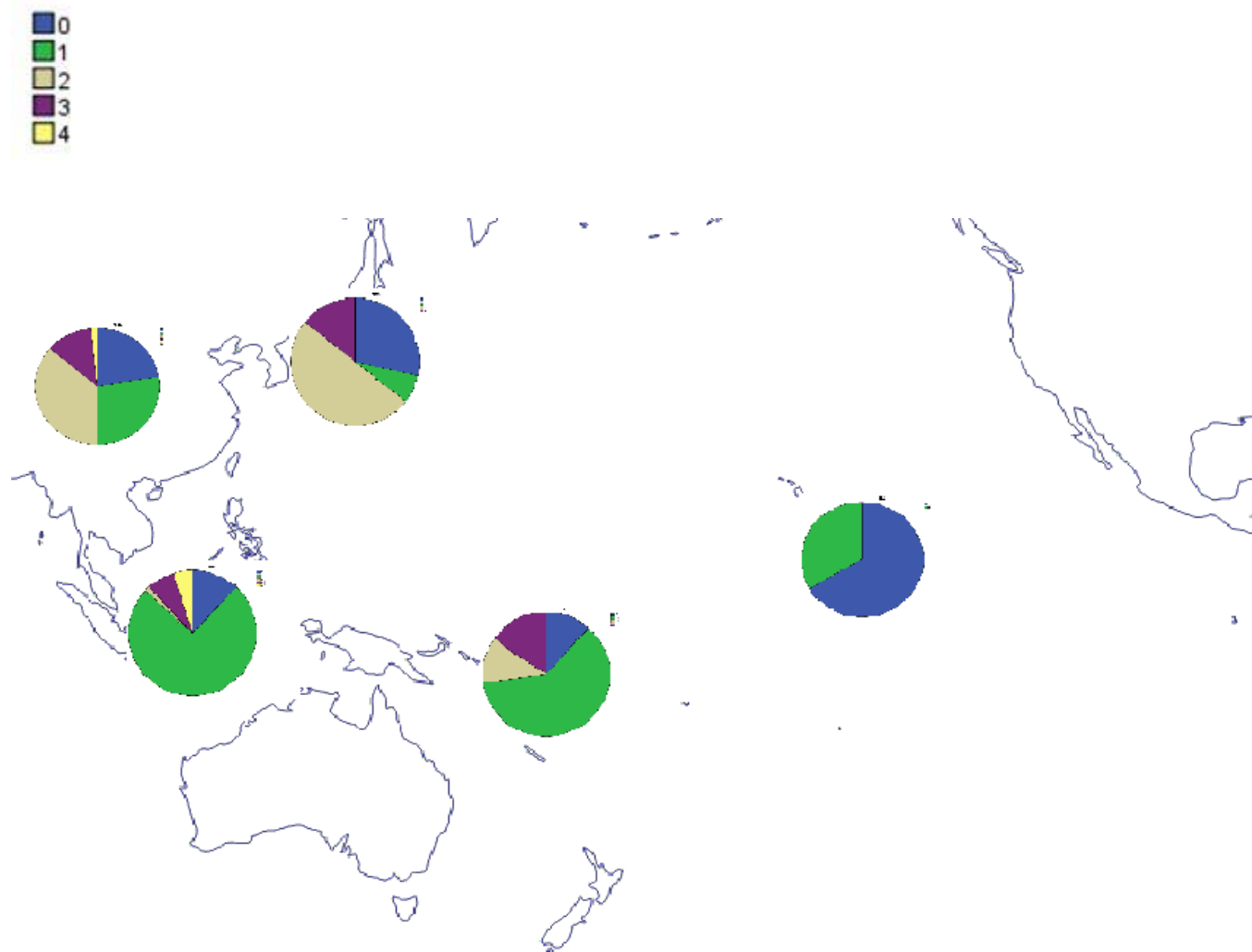
**Figure 62: Inferior nasal aperture (INA) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;**  
**1= heavy sloping, 2= slight sloping, 3= no sloping and no ridge of bone, 4= slight ridge of bone, 5= large ridge of bone**



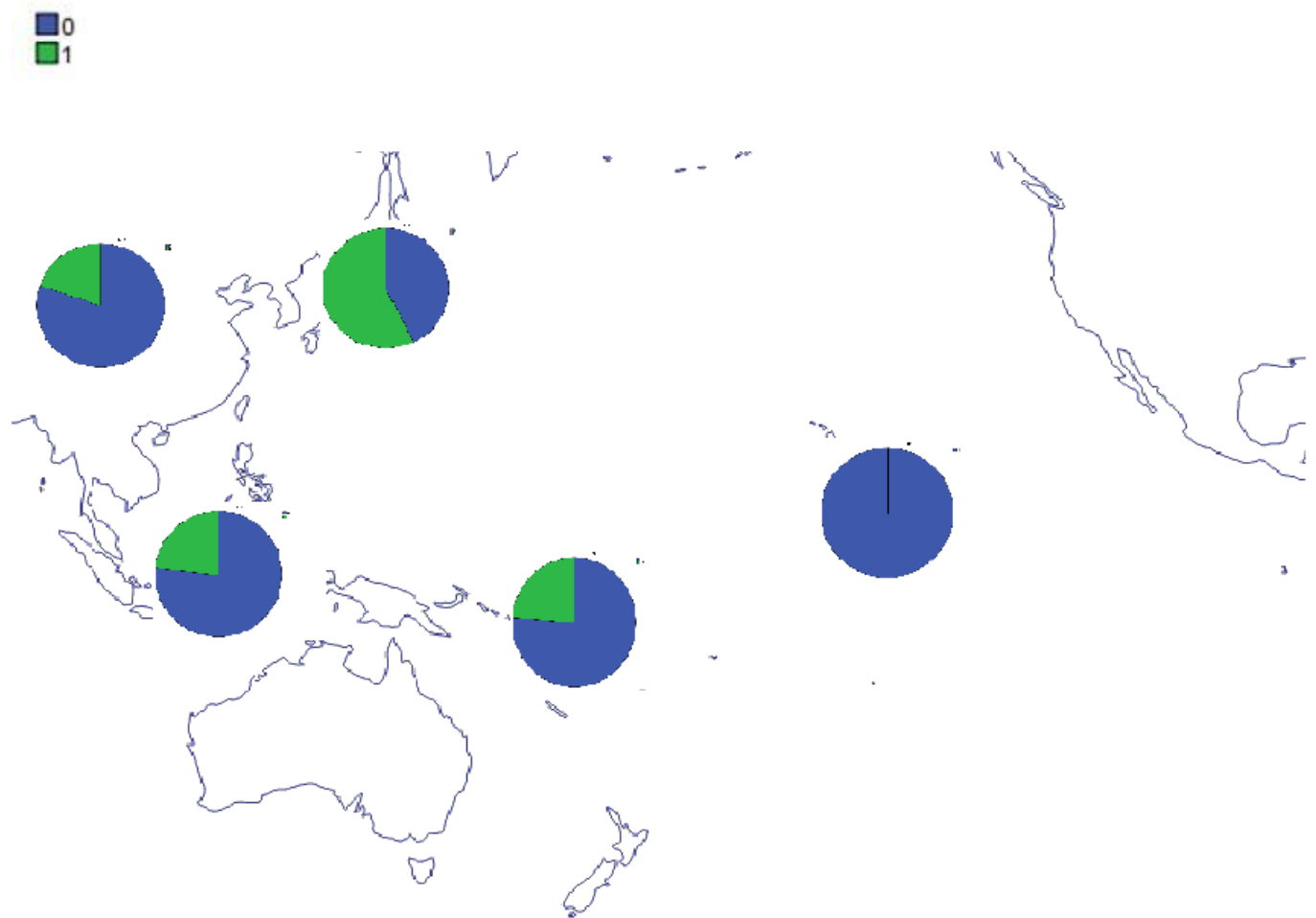
**Figure 63: Interorbital breadth (IOB) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;  
1= narrow, 2= intermediate, 3= broad**



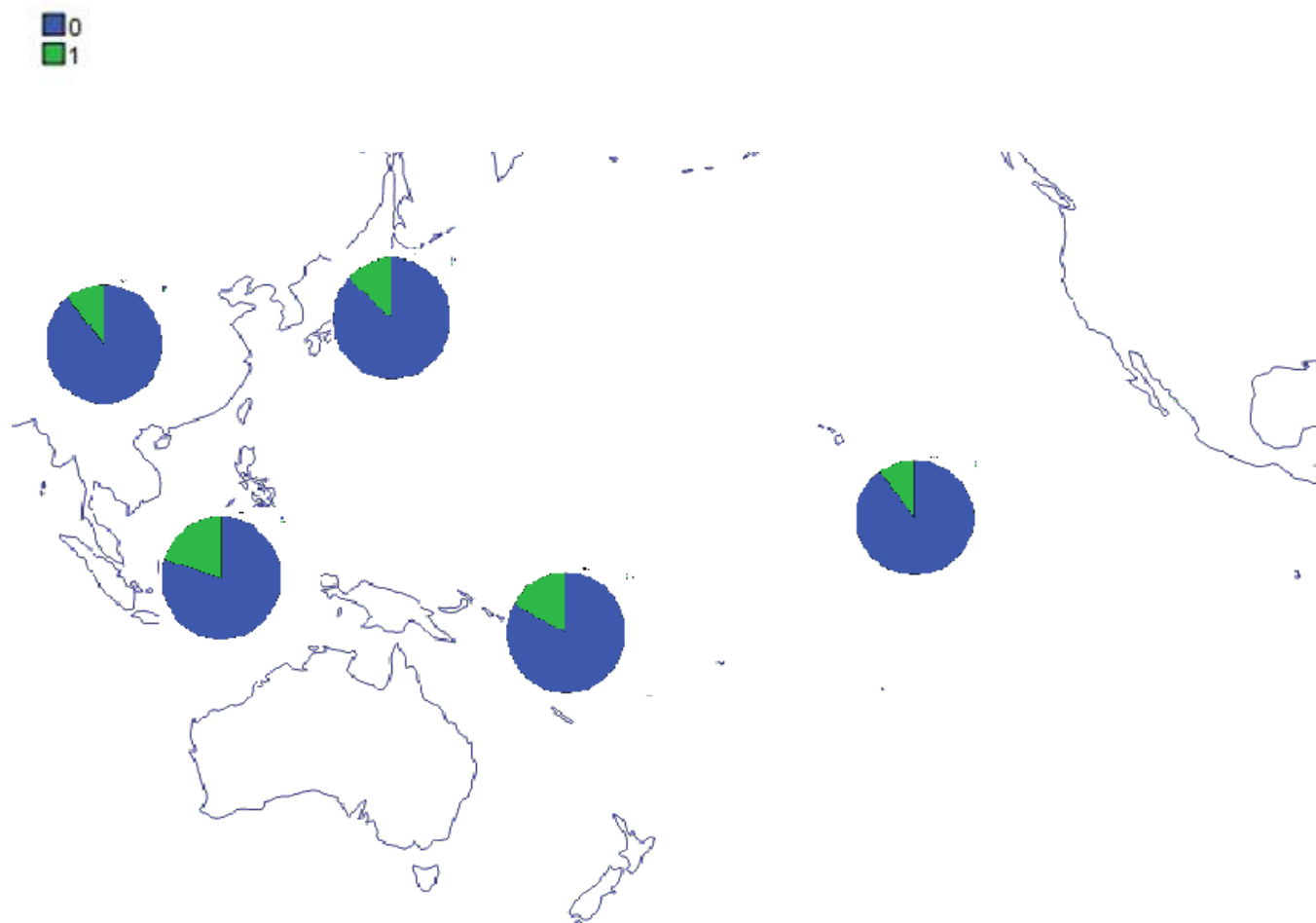
**Figure 64: Nasal aperture width (NAW) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;  
1= narrow, 2= intermediate, 3= wide**



**Figure 65: Nasal bone contour (NBC) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;**  
 1= low and rounded, 2= high and rounded, 3= steep lateral walls with broad plateau, 4= steep lateral walls with narrow plateau, 5= triangular

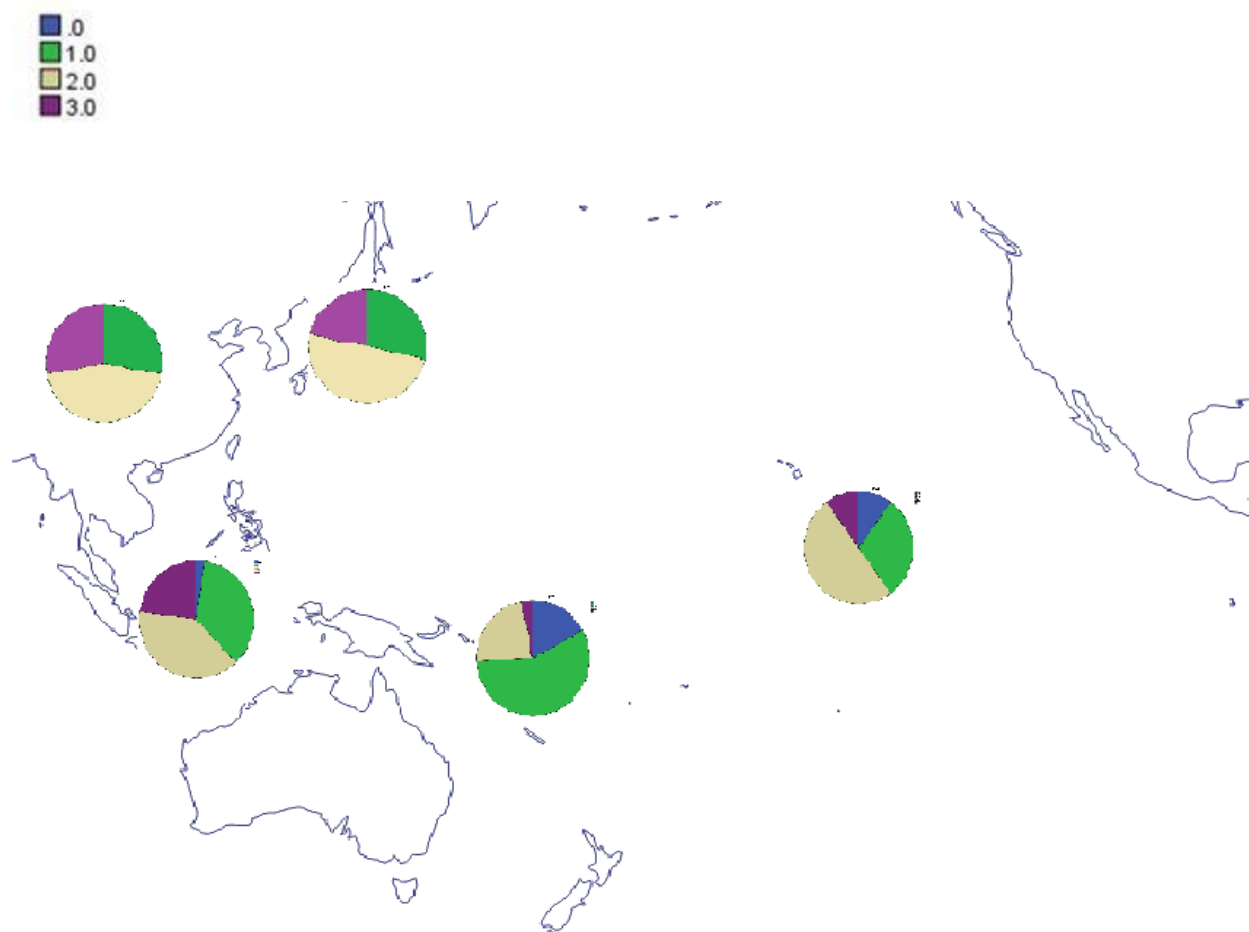


**Figure 66: Nasal overgrowth (NO) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;  
0= overgrowth absent, 1= overgrowth present**

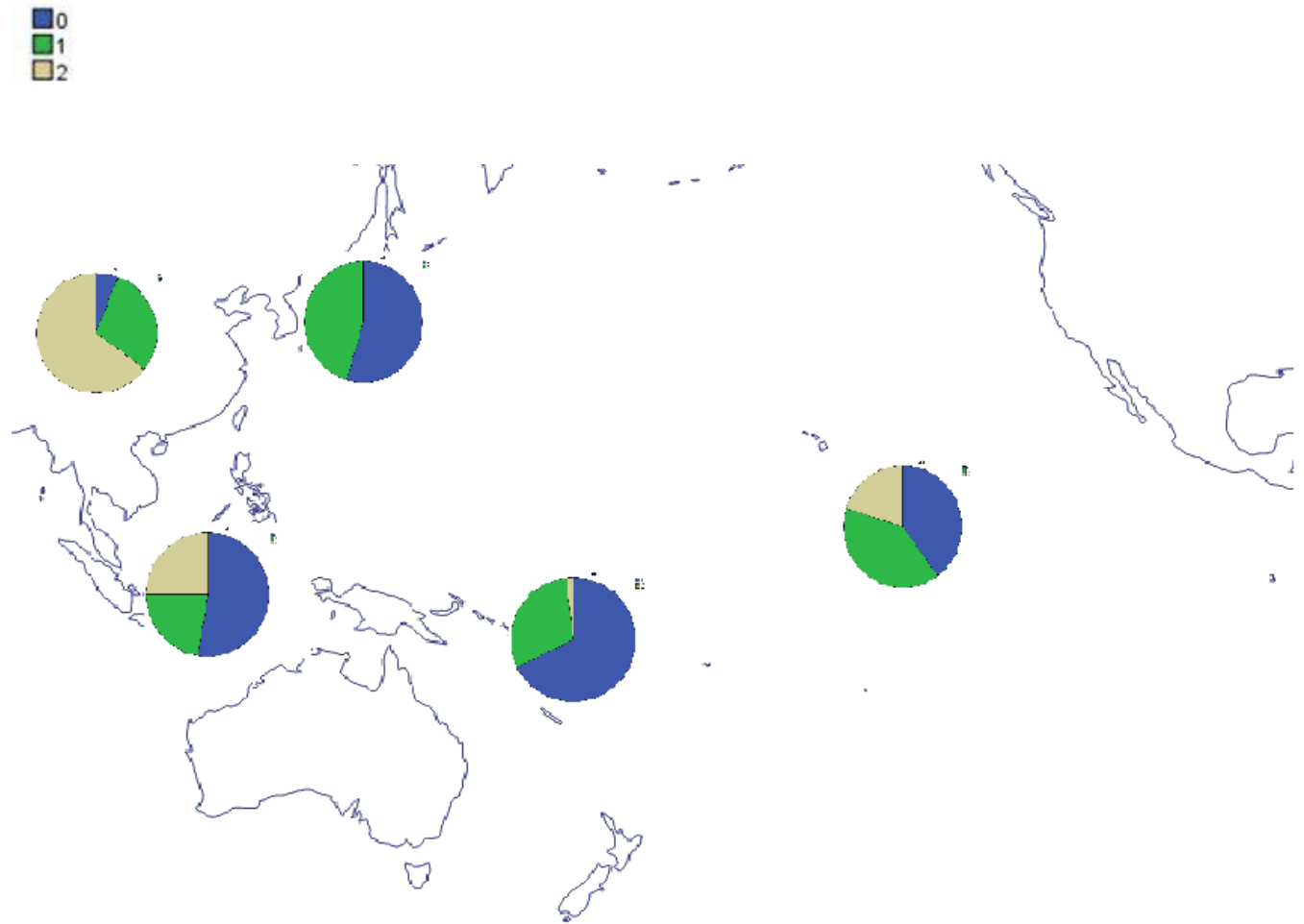


**Figure 67: Postbregmatic depression (PBD) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;  
0= depression absent, 1= depression present**



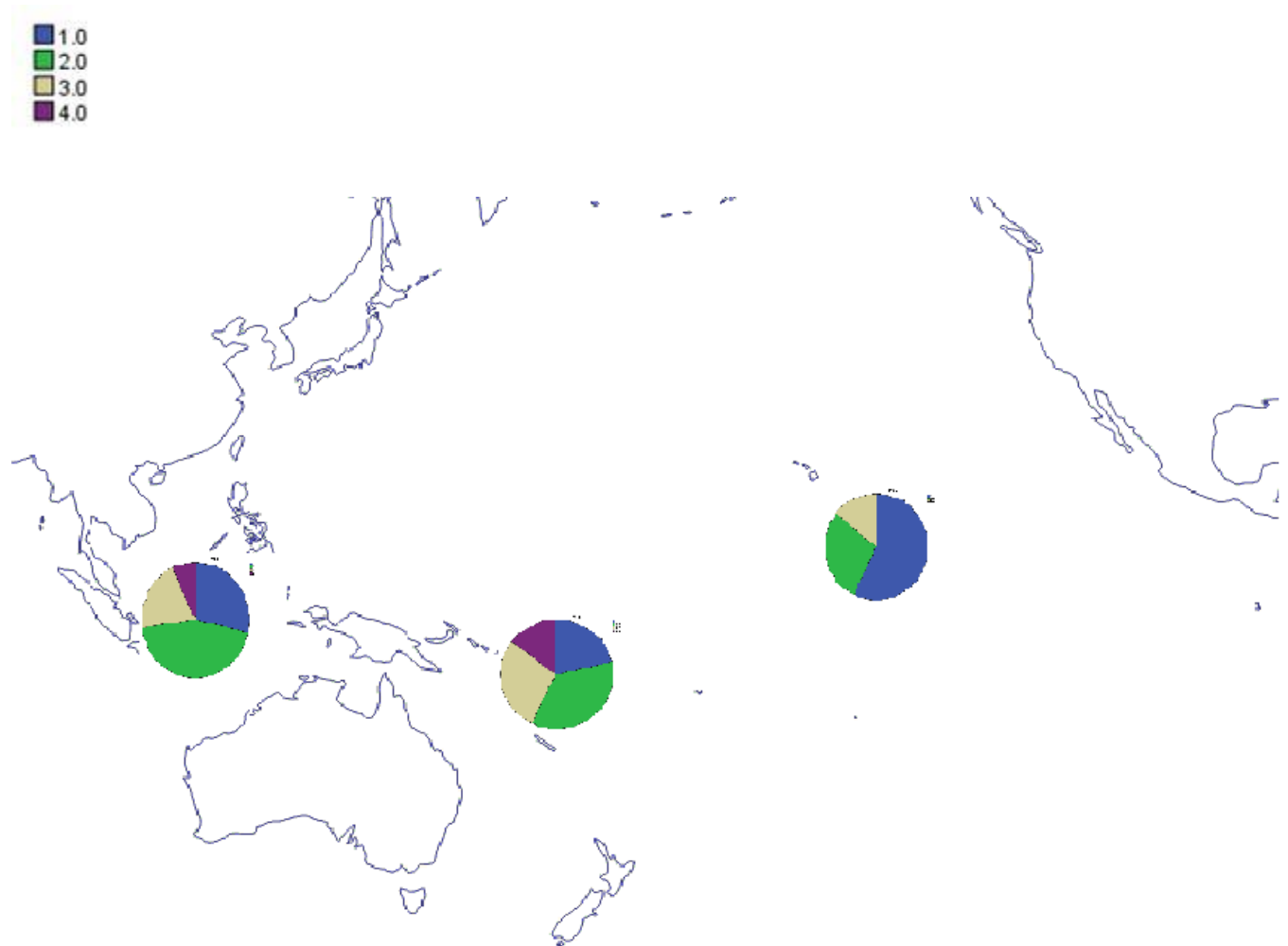


**Figure 68: Posterior zygomatic tubercle (PZT) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia;**  
**0= no projection, 1= weak projection, 2= moderate projection, 3= marked projection**

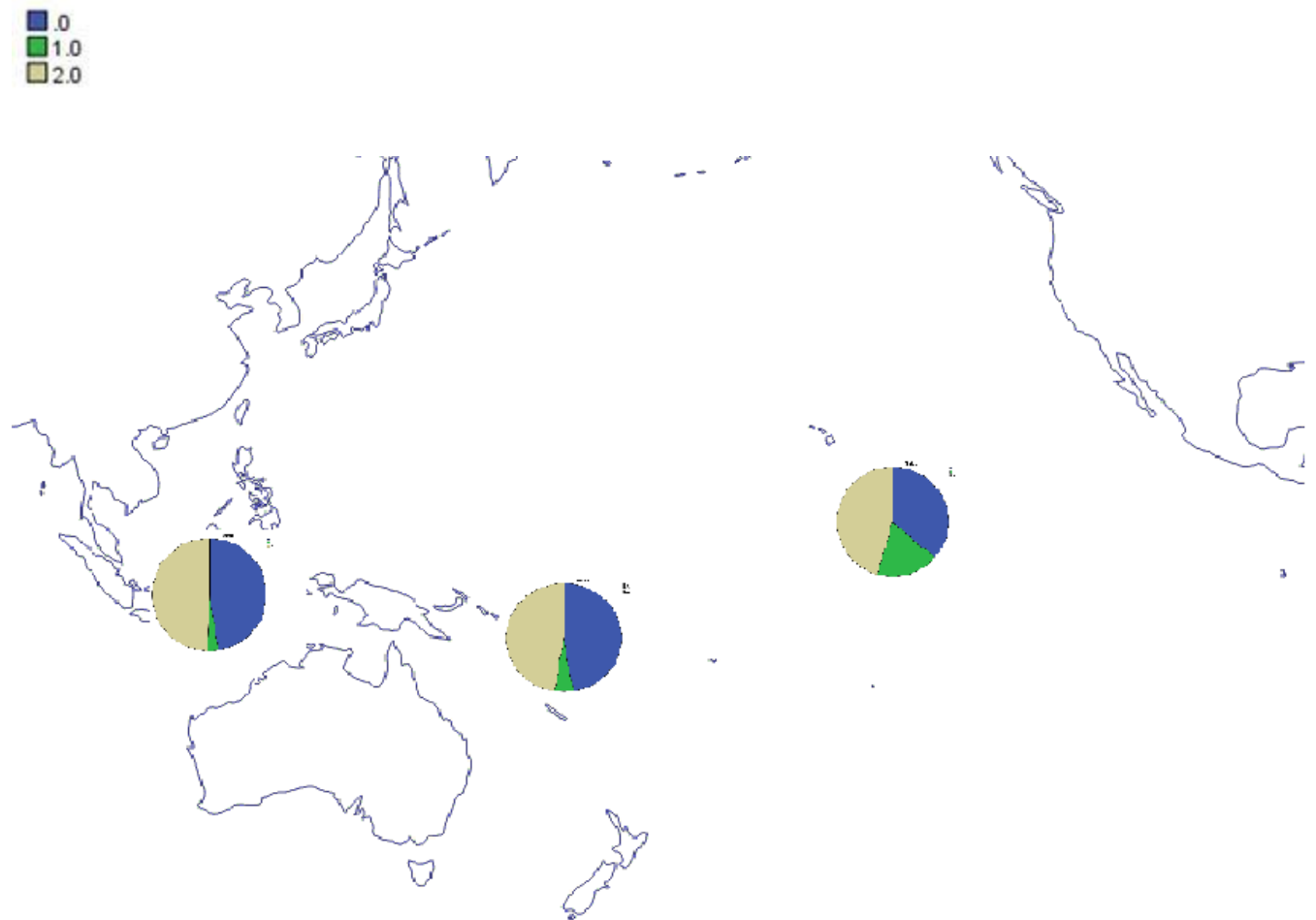


**Figure 69: Zygomaticomaxillary suture course (ZSC) geographic distribution for China, Japan, Southeast Asia, Melanesia, and Polynesia; 0= straight, 1= midline projection, 2= jagged, S-shaped**

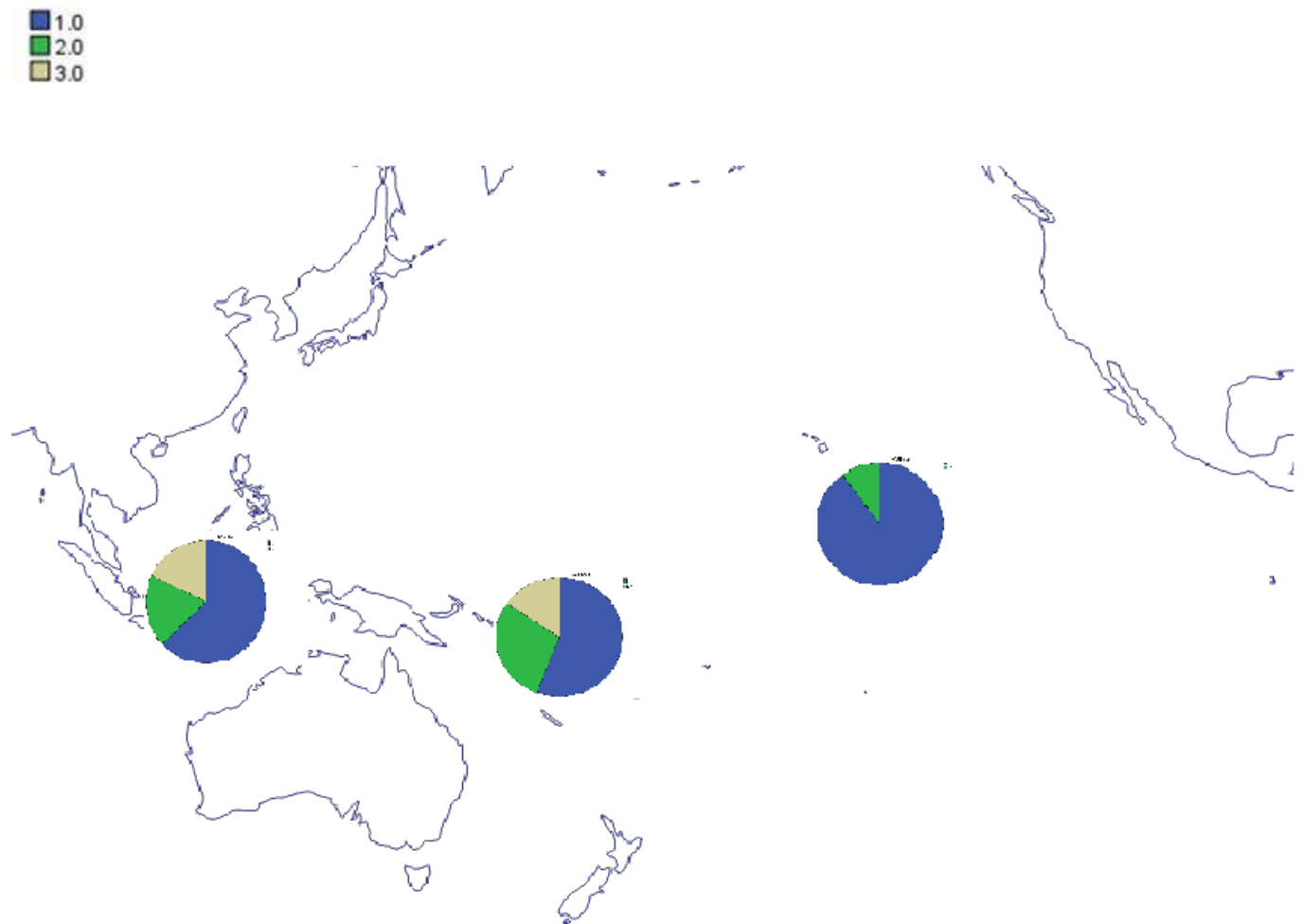
The following graphics represent the geographic frequency distribution for Southeast Asians, Melanesians, and Polynesians for the transverse palatine suture, supranasal suture, nasal aperture shape, nasal bone shape, malar tubercle, orbit shape, and nasofrontal suture.



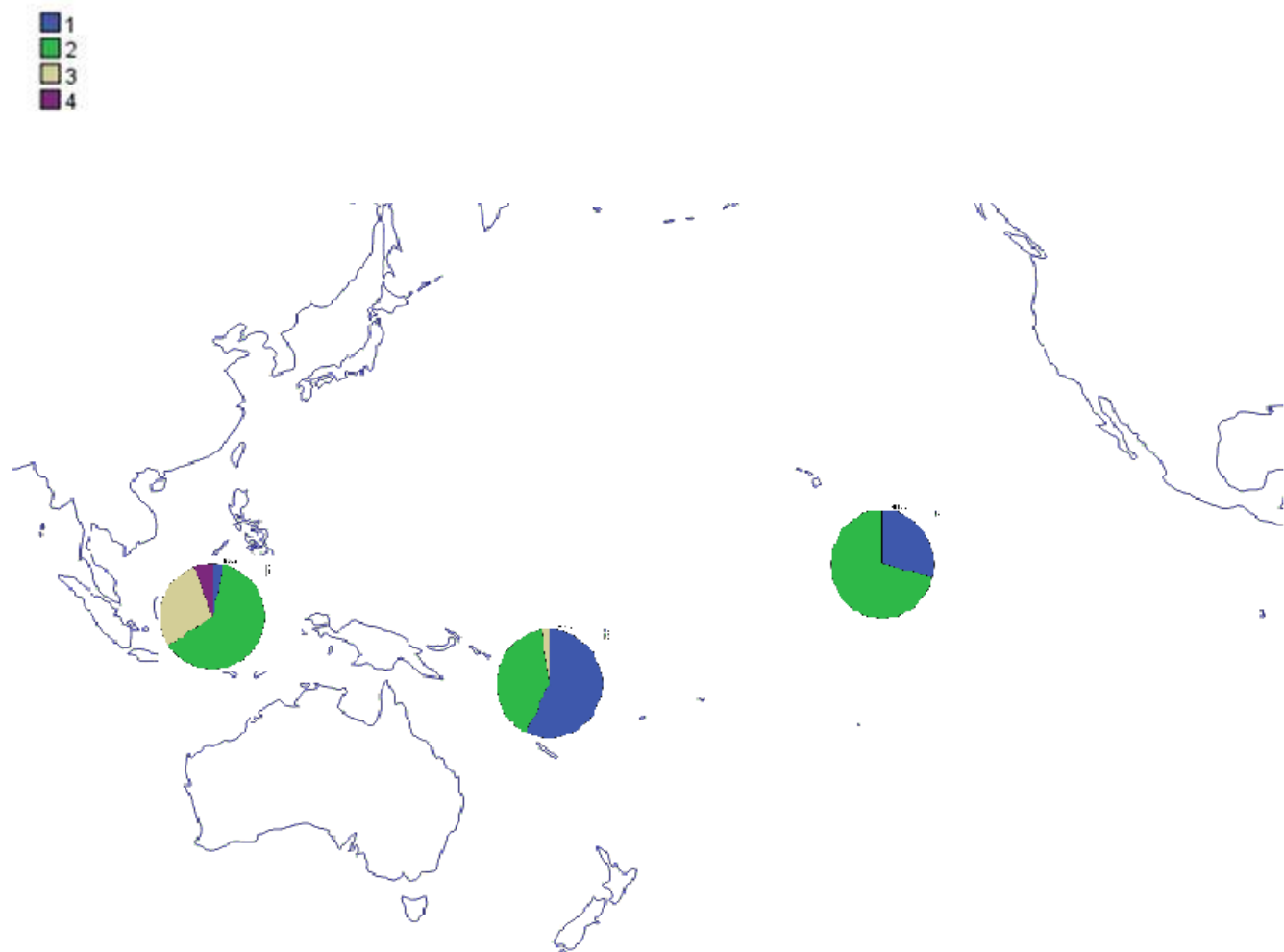
**Figure 70: Transverse palatine suture (TPS) geographic distribution for Southeast Asia, Melanesia, and Polynesia;**  
1= straight, 2= anterior bulging, 3= M-shaped, 4= posterior bulging



**Figure 71: Supranasal suture (SNS) geographic distribution for Southeast Asia, Melanesia, and Polynesia;**  
**0= completely obliterated, 1= open and unfused, 2= closed but visible**

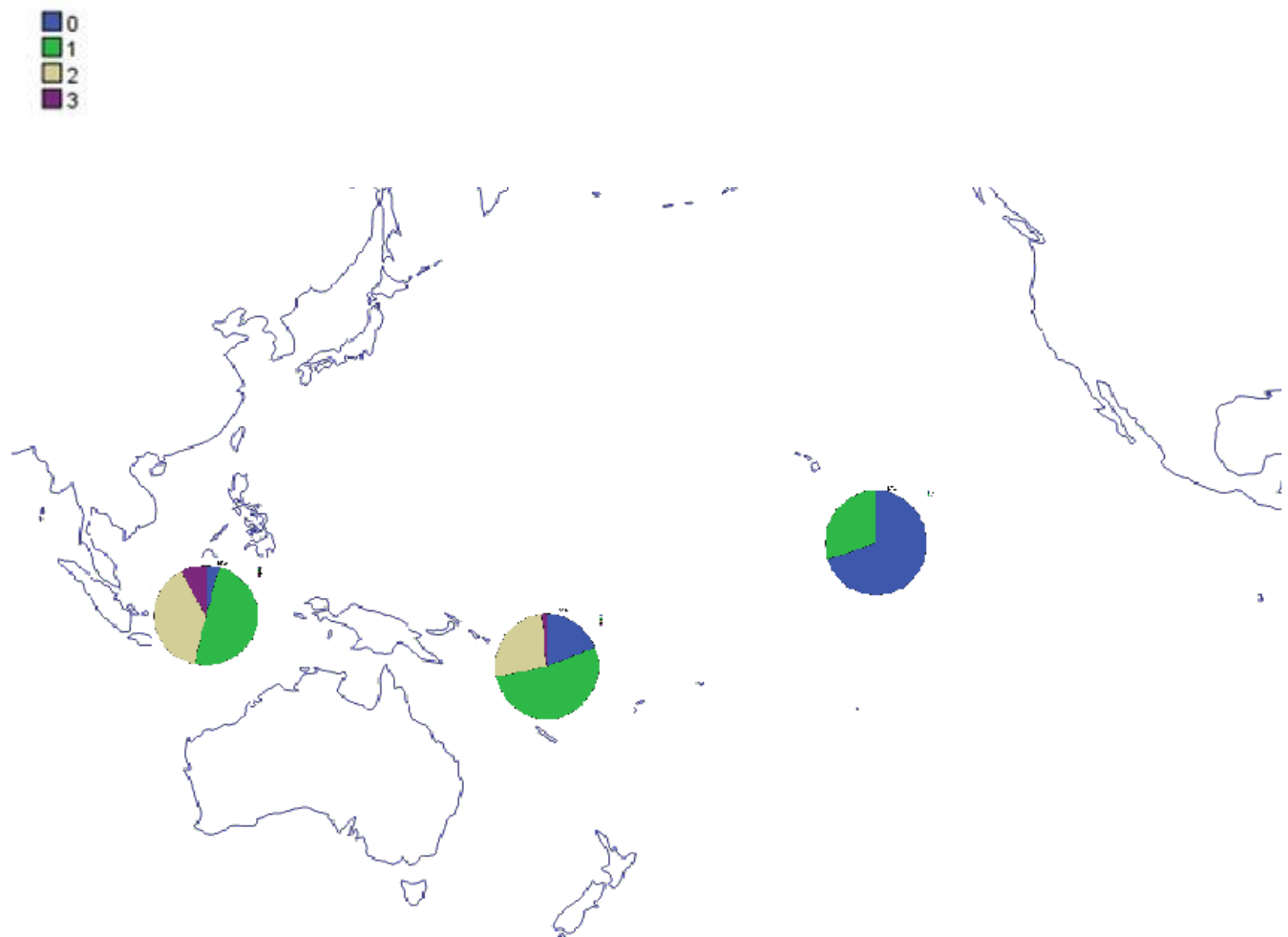


**Figure 72: Nasal aperture shape (NAS) geographic distribution for Southeast Asia, Melanesia, and Polynesia;  
1= teardrop-shaped, 2= bell-shaped, 3= bowed**



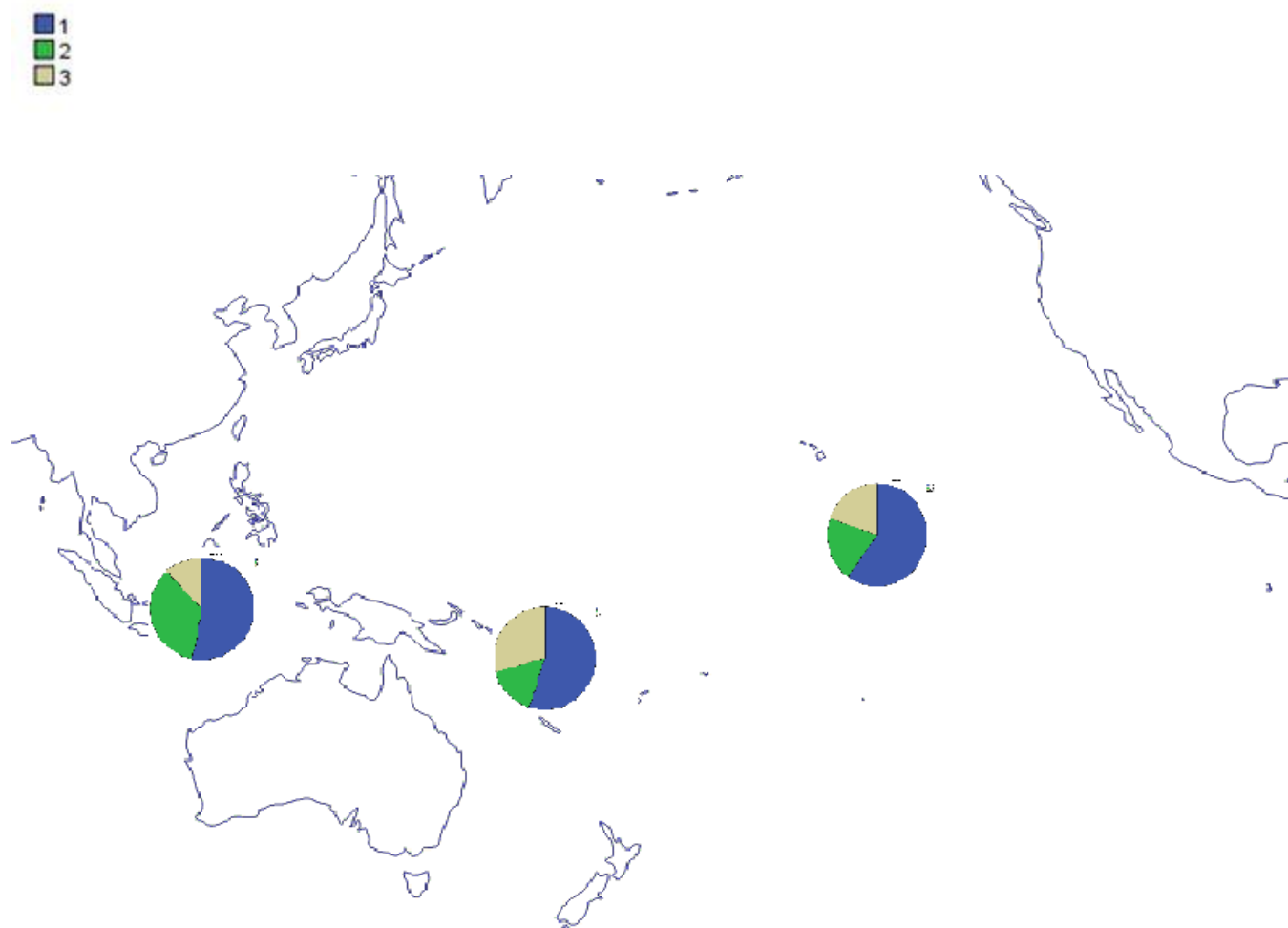
**Figure 73: Nasal bone shape (NBS) geographic distribution for Southeast Asia, Melanesia, and Polynesia;**

**1= no pinching, 2= superior pinching and minimal lateral bulging, 3= superior pinching and significant lateral bulging, 4= extreme pinching/triangular**

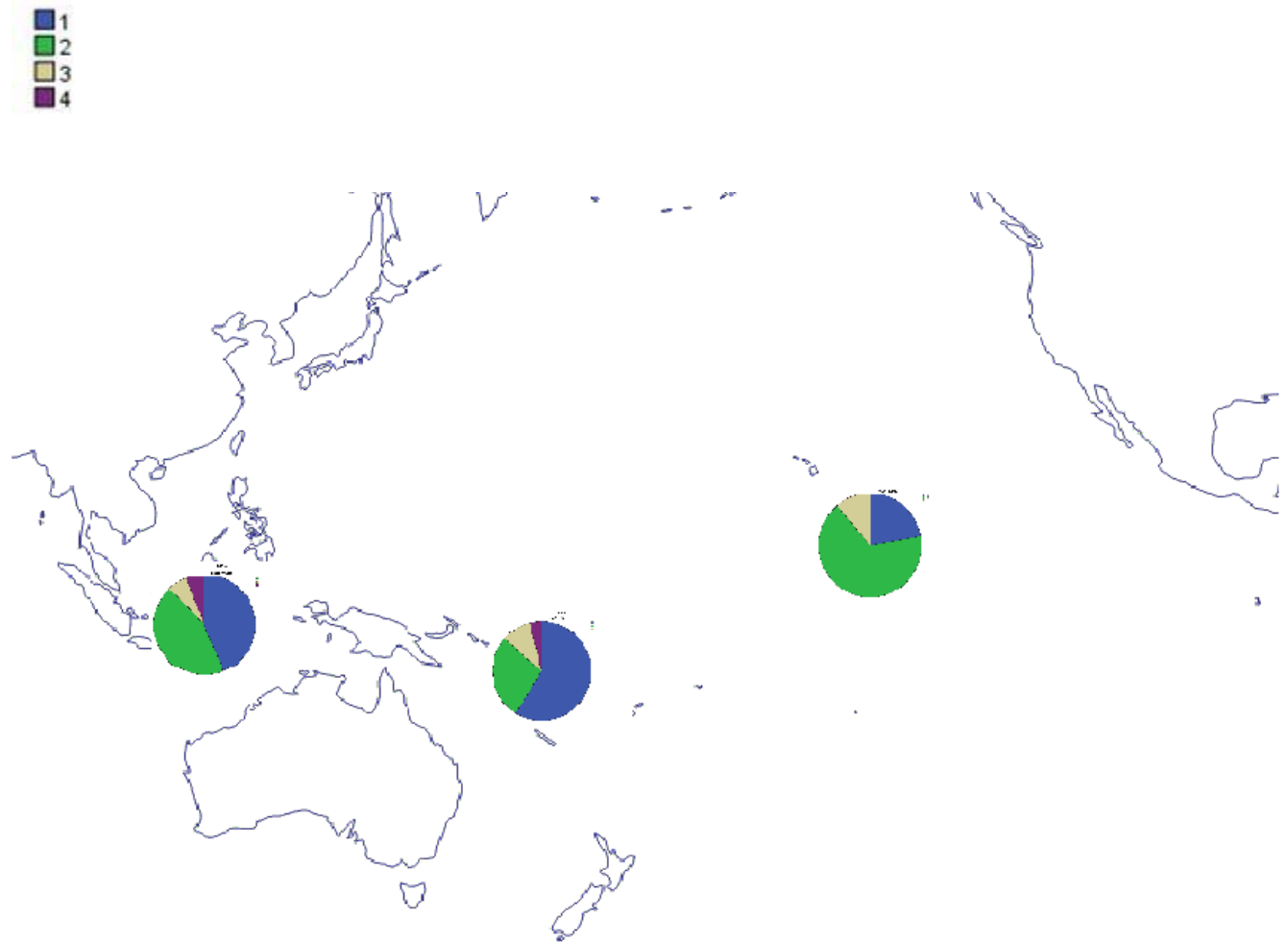


**Figure 74: Malar tubercle (MT) geographic distribution for Southeast Asia, Melanesia, and Polynesia;**  
**1= no tubercle, 2= a trace tubercle, 3= moderate projection, 4= pronounced projection**





**Figure 75: Orbital shape (OS) geographic distribution for Southeast Asia, Melanesia, and Polynesia;**  
**1= rectangular, 2= circular, 3= rhombic**



**Figure 76: Nasofrontal suture (NFS) geographic distribution for Southeast Asia, Melanesia, and Polynesia;  
1= round, 2= square, 3= triangular, 4= irregular**

## Correspondence Analysis Using Single Traits

### *Larger Groups of the World*

The following are the plots of group means on the first two axes from the correspondence analysis for the IOB, NAW, NBC, PZT, and ZSC of American Indians, European Americans, African Americans, Eskimos, Asians, Southeast Asians, Melanesians, and Polynesians. The plot from the interorbital breadth is displayed here. Axis 1 presents a continuum from African Americans to Eskimos with the other groups intermediate. Axis 2 presents a continuum from Polynesians to African Americans with other groups intermediate.

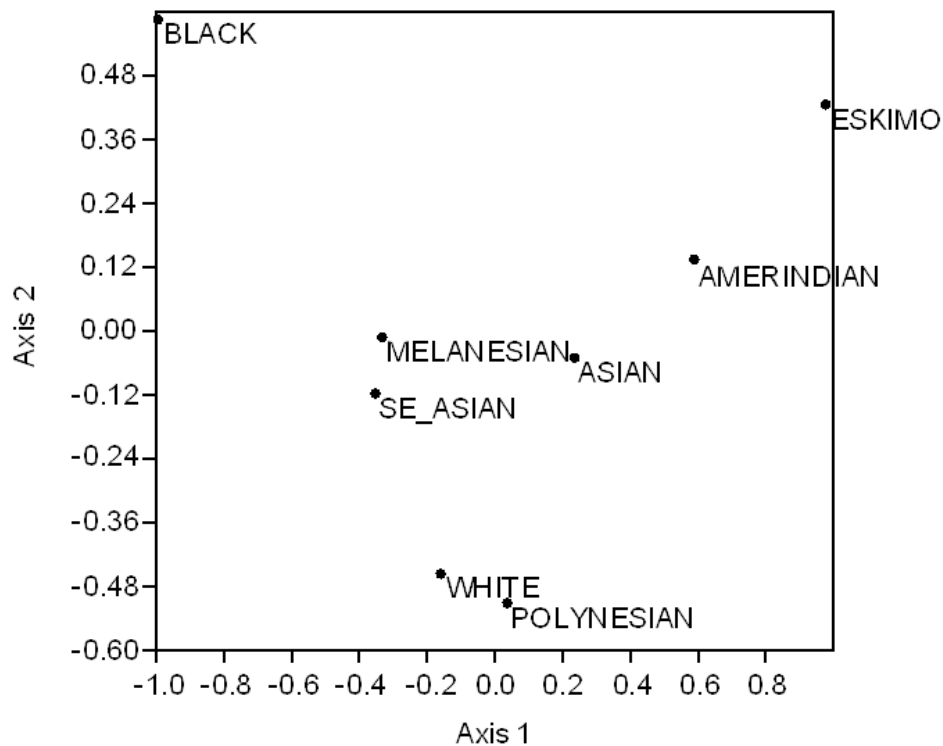


Figure 77: Correspondence analysis of the IOB for larger groups of the world and the Pacific

The plot from the nasal aperture width is displayed here. Axis 1 presents a distribution from European Americans to a cluster of all other groups. Axis 2 presents a continuum from African Americans to Eskimos with the other groups intermediate.

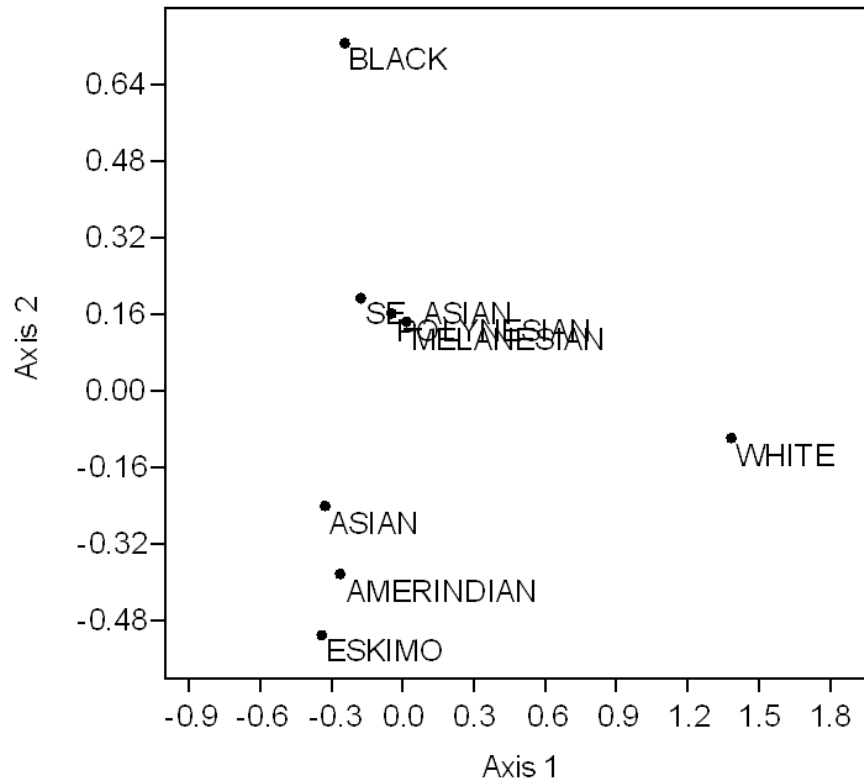


Figure 78: Correspondence analysis of the NAW for larger groups of the world and the Pacific

The plot from the nasal bone contour is displayed here. Axis 1 presents a continuum from European Americans to Polynesians with the other groups intermediate. Axis 2 presents a

continuum from Eskimos and European Americans to African Americans with other groups intermediate.

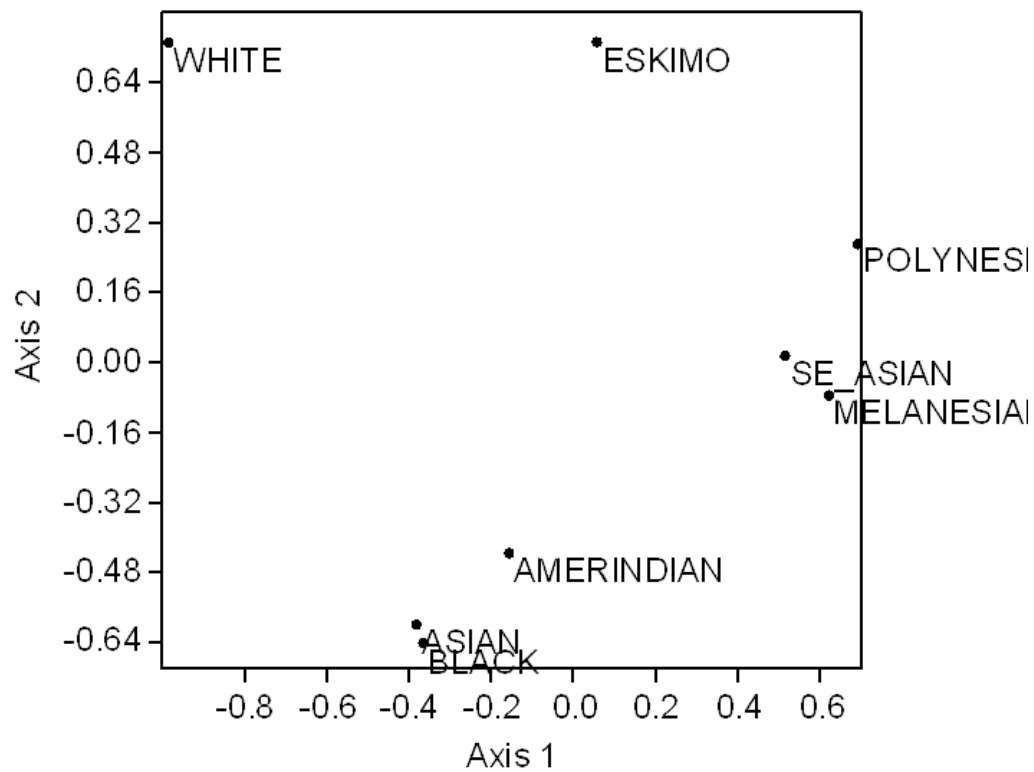


Figure 79: Correspondence analysis of the NBC for larger groups of the world and the Pacific

The plot from the posterior zygomatic tubercle is displayed here. Axis 1 presents a continuum from Southeast Asians to American Indians with the other groups intermediate. Axis 2 presents a continuum from Polynesians to Southeast Asians with other groups intermediate.

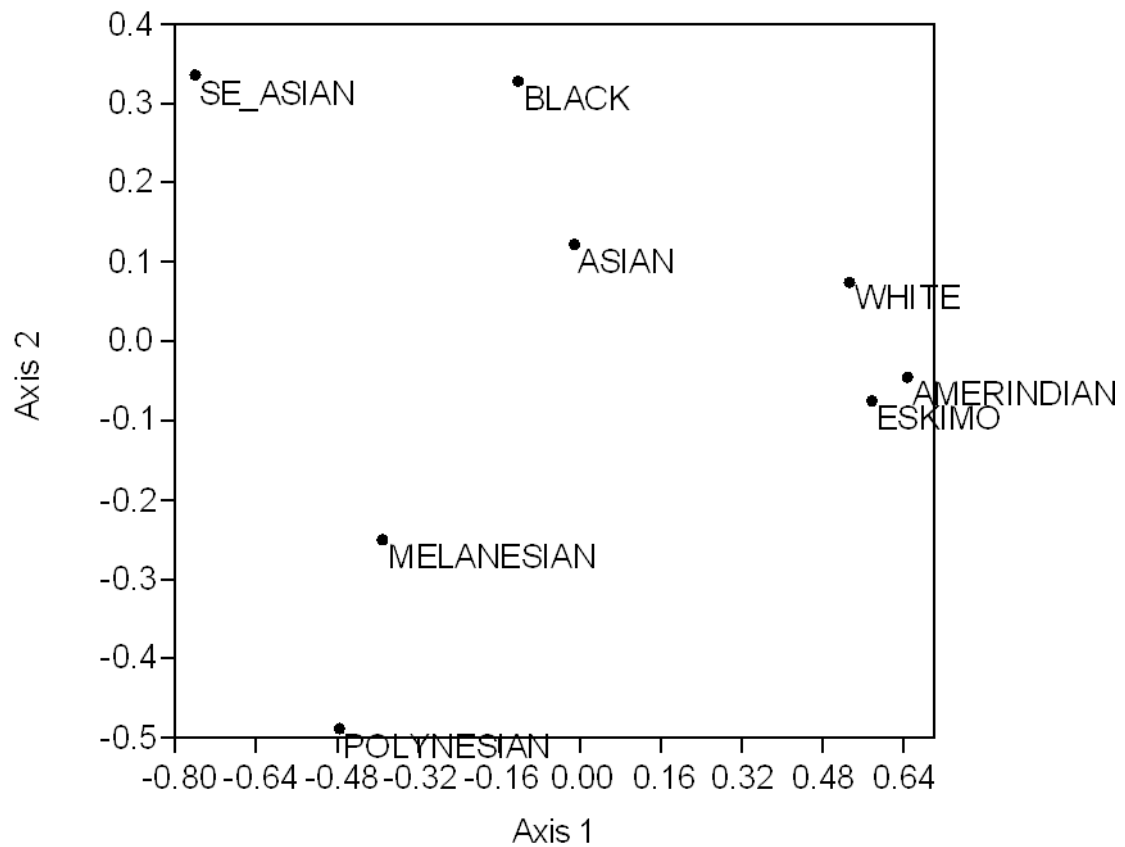


Figure 80: Correspondence analysis of the PZT for larger groups of the world and the Pacific

The plot from the zygomaticomaxillary suture course is displayed here. Axis 1 presents a continuum from Melanesians to a cluster of European Americans, Eskimos, and American

Indians with the other groups intermediate. Axis 2 presents a continuum from European Americans to American Indians with other groups intermediate.

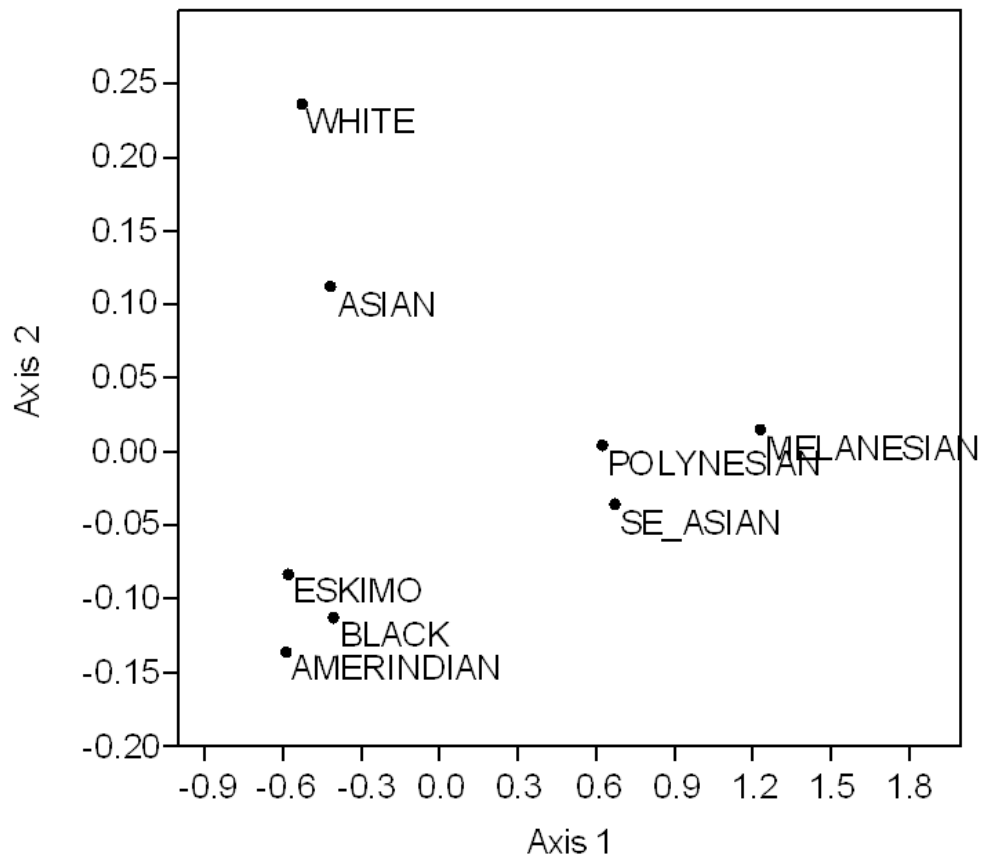


Figure 81: Correspondence analysis of the ZSC for larger groups of the world and the Pacific

*Mainland Asia, Southeast Asia, Melanesia, and Polynesia*

The following are the plots of group means on the first two axes from the correspondence analysis for the ANS, INA, IOB, NAW, NBC, PZT, and ZSC of the mainland Asians, Southeast Asians, Melanesians, and Polynesians. The plot from the anterior nasal spine is displayed here. Axis 1 presents a continuum from Asians to Melanesians with the Southeast Asians very close to the Asians and the Polynesians intermediate. Axis 2 presents a continuum from Polynesians to Southeast Asians with the Asians very close to the Polynesians and the Melanesians intermediate.

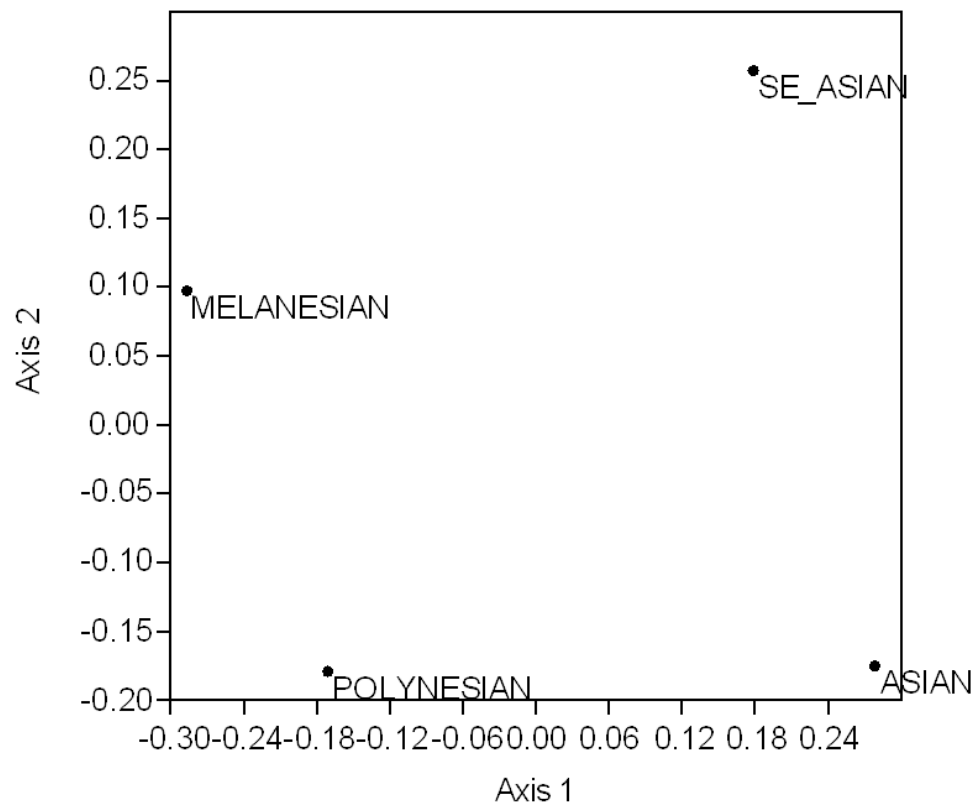


Figure 82: Correspondence analysis of the ANS for Asians, Southeast Asians, Melanesians, and Polynesians



The plot from the inferior nasal aperture is displayed here. Axis 1 presents a continuum from Asians to Melanesians with the Polynesians very close to the Melanesians and the Southeast Asians near the Asians. Axis 2 presents a continuum from Southeast Asians to Asians with the Melanesians near the Asians and the Polynesians intermediate.

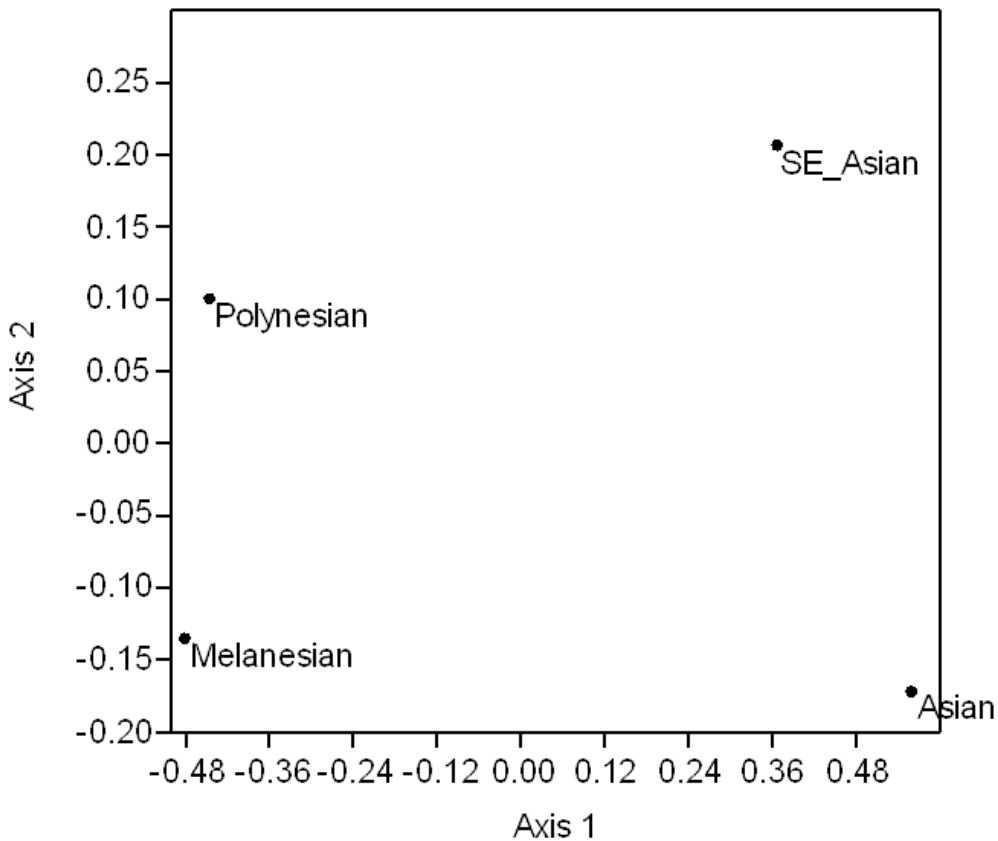


Figure 83: Correspondence analysis of the INA for Asians, Southeast Asians, Melanesians, and Polynesians

The plot from the interorbital breadth is displayed here. Axis 1 presents a continuum from Polynesians to Melanesians with the Asians near the Polynesians and the Southeast Asians near the Melanesians. Axis 2 presents a continuum from Polynesians to Asians with the other groups intermediate.

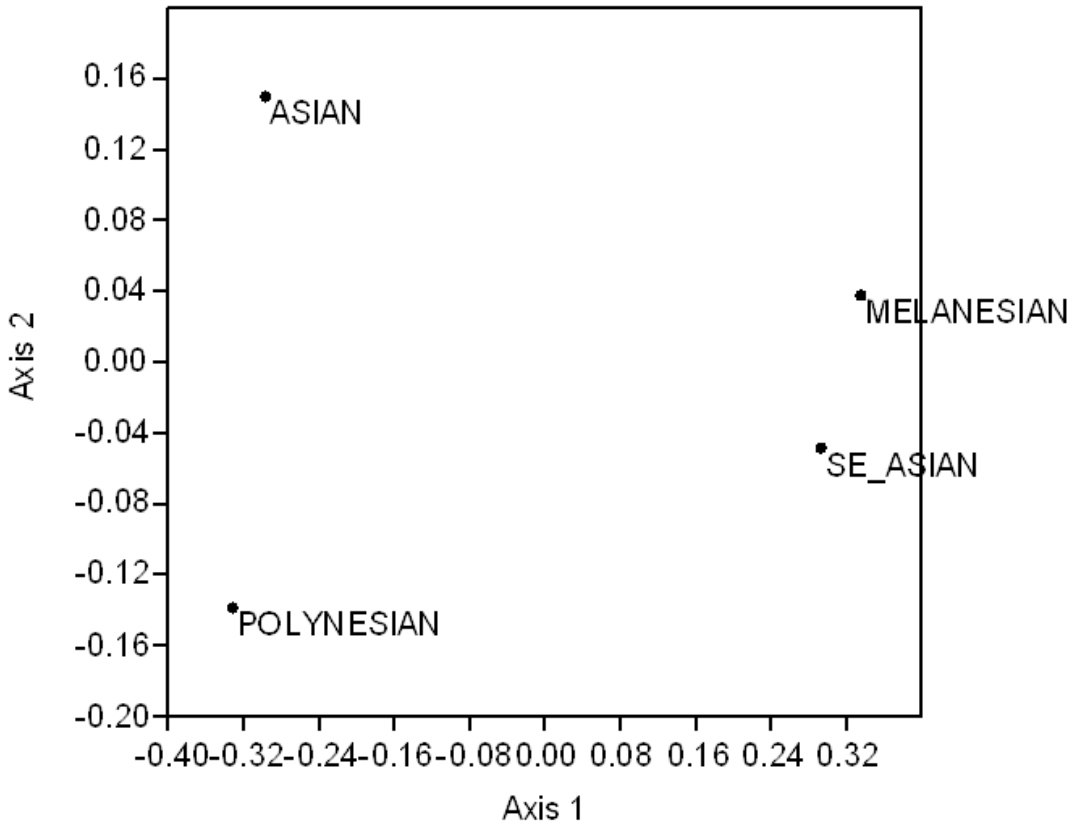


Figure 84: Correspondence analysis of the IOB for Asians, Southeast Asians, Melanesians, and Polynesians

The plot from the nasal aperture width is displayed here. Axis 1 presents a continuum from Polynesians to Asians with the other groups intermediate. Axis 2 presents a continuum from Polynesians to Southeast Asians with the other groups intermediate.

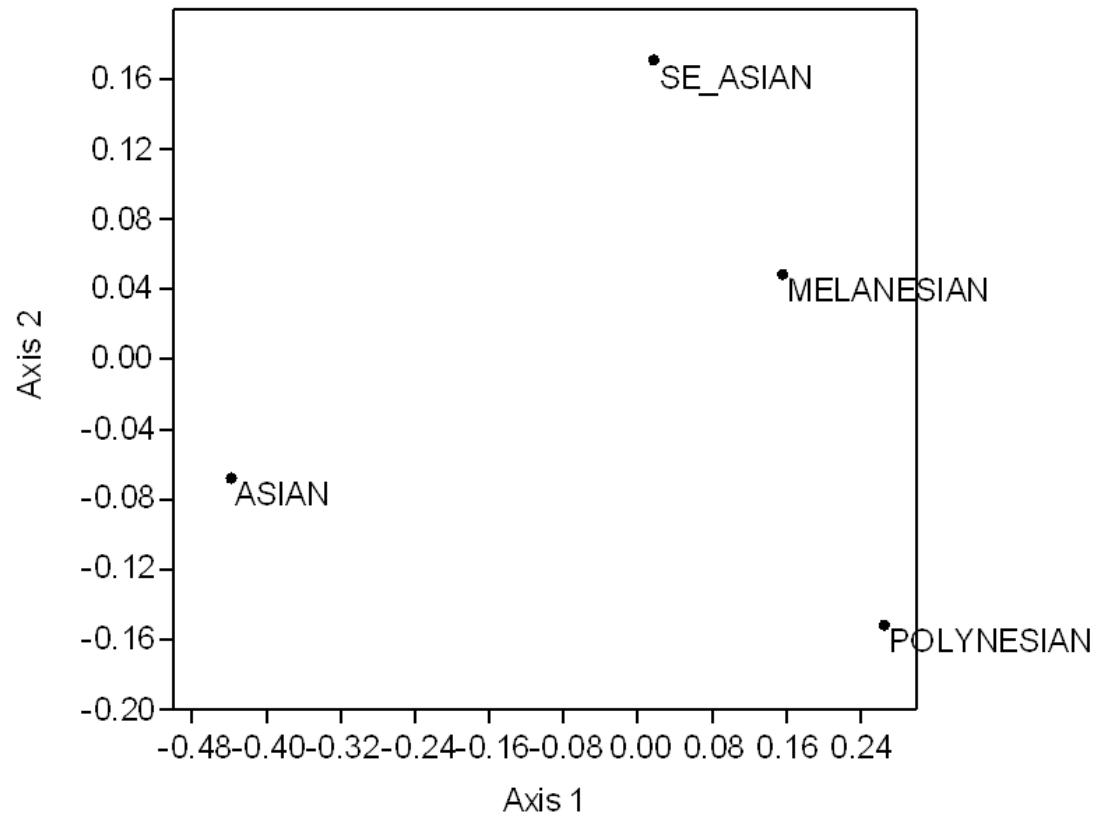


Figure 85: Correspondence analysis of the NAW for Asians, Southeast Asians, Melanesians, and Polynesians

The plot from the nasal bone contour is displayed here. Axis 1 presents a continuum from Polynesians to Asians with the other groups intermediate. Axis 2 presents a continuum from Polynesians to Southeast Asians with the Melanesians near the Southeast Asians and the Asians intermediate.

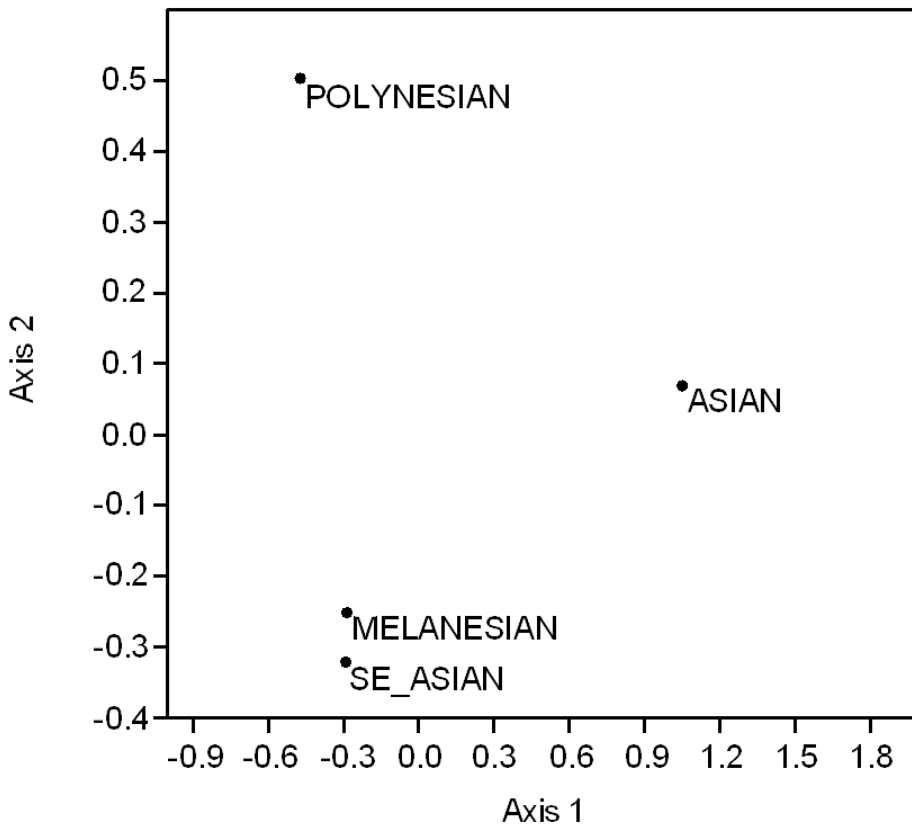


Figure 86: Correspondence analysis of the NBC for Asians, Southeast Asians, Melanesians, and Polynesians

The plot from the posterior zygomatic tubercle is displayed here. Axis 1 presents a continuum from Melanesians to Asians with the other groups intermediate. Axis 2 presents a continuum from Polynesians to Melanesians with the Southeast Asians near the Melanesians and the Asians intermediate.

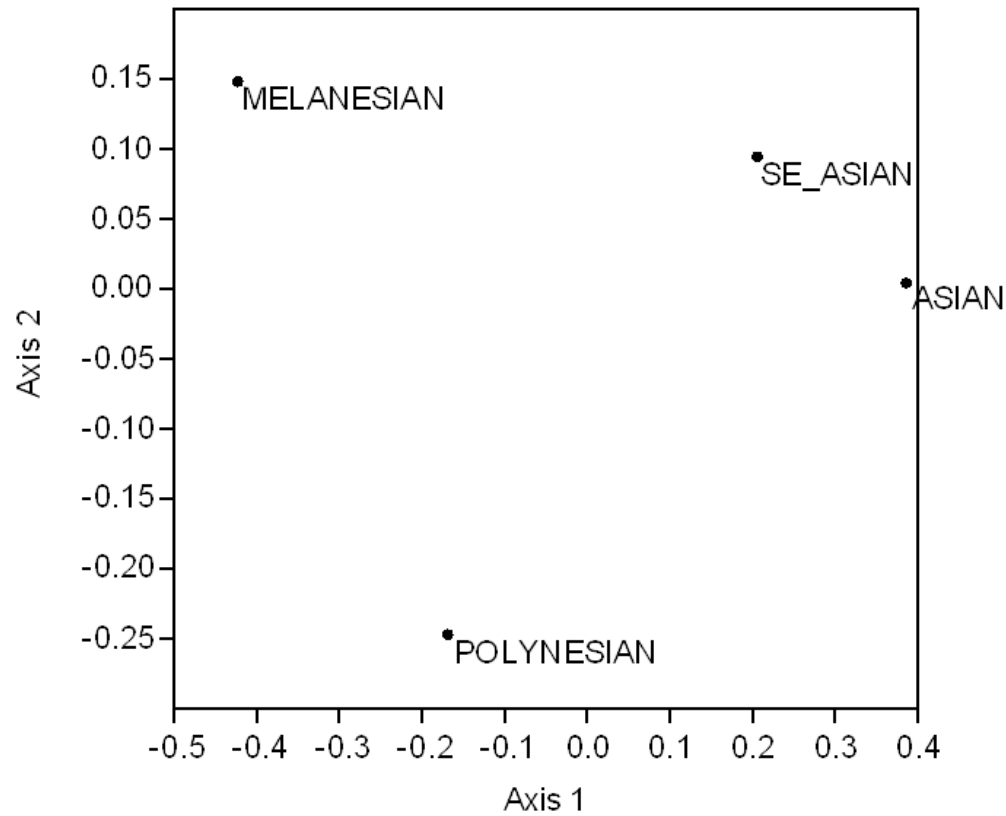


Figure 87: Correspondence analysis of the PZT for Asians, Southeast Asians, Melanesians, and Polynesians

The plot from the zygomaticomaxillary suture course is displayed here. Axis 1 presents a continuum from Asians to Melanesians with the other groups intermediate. Axis 2 presents a continuum from Polynesians to all of the other groups.

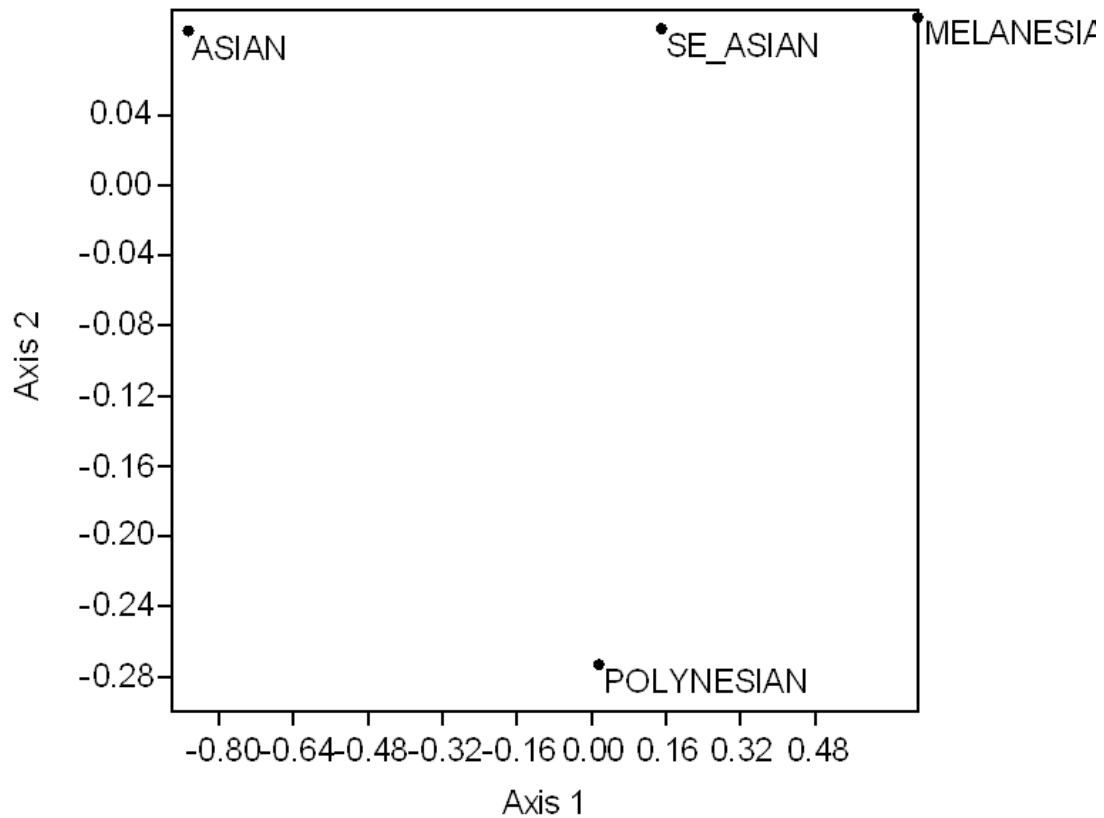


Figure 88: Correspondence analysis of the ZSC for Asians, Southeast Asians, Melanesians, and Polynesians

## Hierarchical Cluster Analysis Using Multiple Traits

### *Larger Groups of the World*

The following is the dendrogram produced from hierarchical cluster analysis using 5 traits (IOB, NAW, NBC, PZT, and ZSC) for large groups of the world and the Pacific. The Melanesians and the Southeast Asians cluster the most closely together out of all the groups. These groups cluster secondly with the Polynesians. All three groups are separated from the other groups of the world, including the Asians. The American Indians and Asians cluster closely with one another and cluster more loosely with the Eskimos. The American Indians and Asians cluster closely with one another and cluster more loosely with the Eskimos.

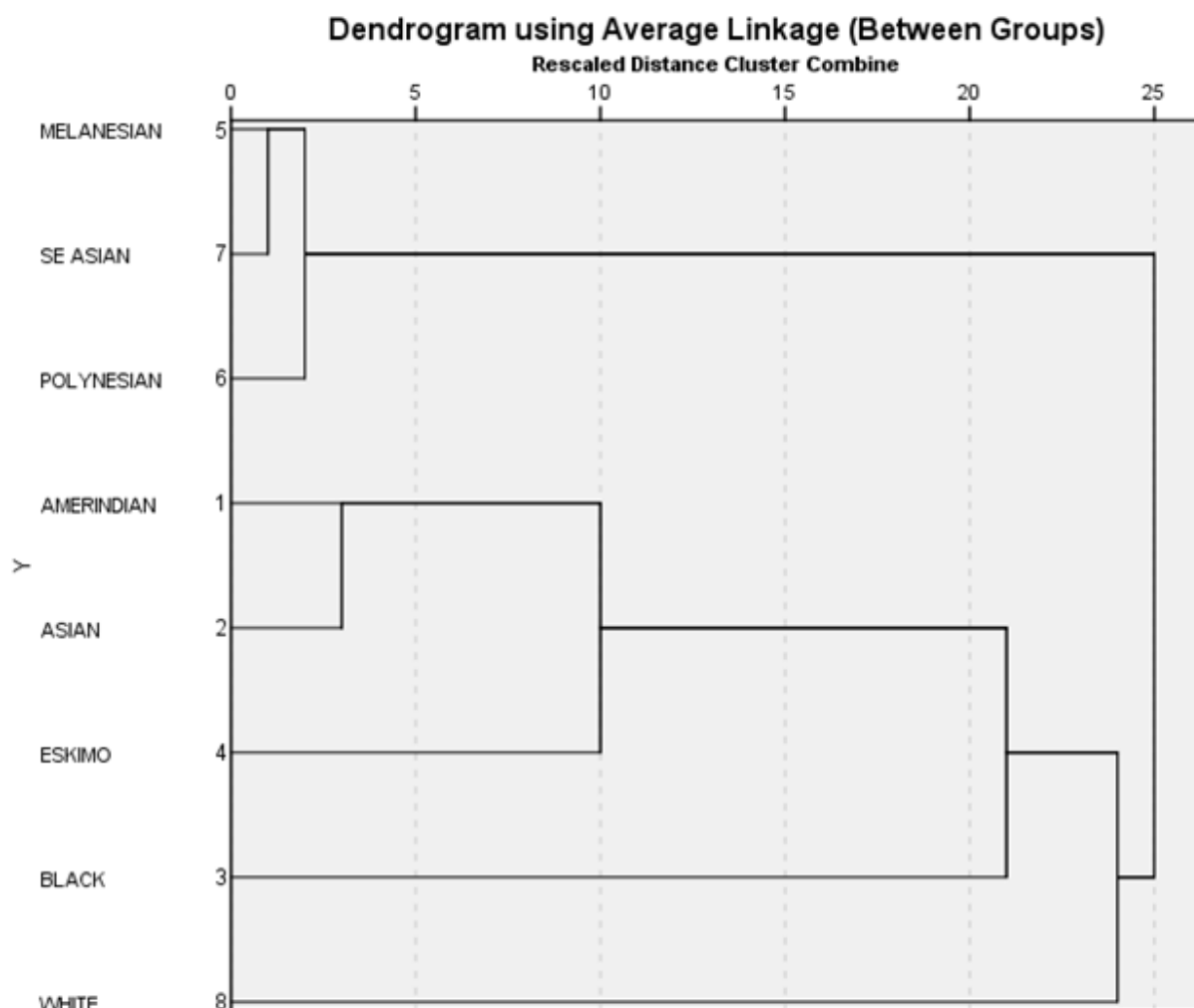


Figure 89: Dendrogram for large groups of the world and the Pacific using 5 traits

### *Mainland Asia, Southeast Asia, Melanesia, and Polynesia*

The following is the dendrogram produced from hierarchical cluster analysis using 9 traits (ANS, INA, IOB, NAW, NBC, NO, PBD, PZT, ZSC) for mainland Asia, Southeast Asia, Melanesia, and Polynesia. Once again, the Southeast Asians cluster closely with the Melanesians. The Polynesians cluster with these groups more loosely. The Melanesians, Polynesians, and Southeast Asians remain separated from the mainland Asians.

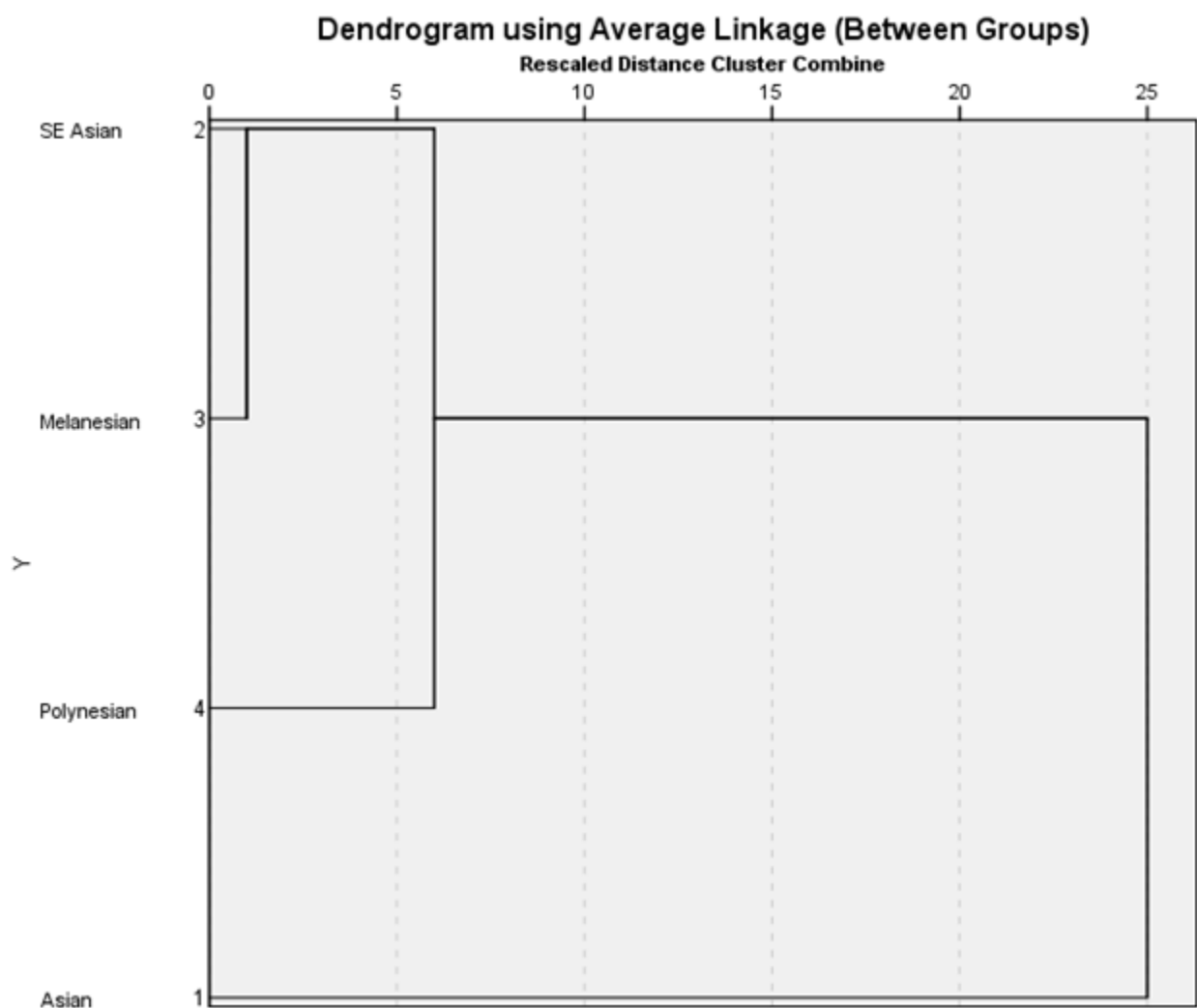


Figure 90: Dendrogram for mainland Asians, Southeast Asians, Melanesians, and Polynesians using 9 traits



## CHAPTER IV

### DISCUSSION

#### Frequency Comparison

For most traits, the frequencies of the character states of Southeast Asians and Pacific Islanders are not distinguishable (Tables 1, 3, 4, 5, 6, 7, 8, 9, & 10). In fact, this is true for all traits other than the inferior nasal aperture (Table 2). The Southeast Asian group (n=94) largely exhibits no ridge of bone and no sloping while the Pacific Island group (n=71) has a higher tendency toward a sloping inferior nasal region. When these two groups are combined into one 'Pacific' group (n=165), their character state frequencies are distinct from other groups of the world for most traits. This is especially true for the supranasal suture (Table 19), nasal bone contour (Table 16), and the malar tubercle (Table 14) which remain very distinctly different from the distributions of all world groups. Overall, the Pacific group exhibits higher frequencies of closed or obliterated supranasal sutures, a high and rounded nasal bone contour, and larger malar tubercles.

For some of these traits, this group distinction is still seen but is less clear. The Pacific group is distinct but has fairly comparable frequencies with that of the African group for the inferior nasal aperture (Table 12) with a high prevalence of a sloping inferior nasal region and fairly comparable frequencies with those of the African and Asian groups for the absence of a nasal overgrowth (Table 17). For the interorbital breadth (Table 13), the Pacific group has fairly comparable frequencies with that of the European group, exhibiting a high frequency of an intermediate interorbital breadth. For the nasal aperture width (Table 15), the Pacific group has

fairly comparable frequencies with that of the American Indian group, exhibiting a high frequency of an intermediate width.

For other traits, the Pacific group exhibits similar trait frequencies to other groups. This is true with the transverse palatine suture (Table 20), as both the Pacific and African groups exhibit higher frequencies an anterior bulging transverse palatine suture. For the anterior nasal spine, the Pacific group exhibits frequencies similar to those of African and American Indian groups, expressing a high prevalence of a small nasal spine (Table 11). The Pacific group exhibits frequencies similar to several other groups, most especially the European group, for the postbregmatic depression (Table 18).

### **Feature by Feature Comparisons between Regions**

When the Southeast Asian group and the Pacific Island group are compared, a few distinctions can be made, but the majority of the traits show no significant distinctions between the groups at the 95% level of confidence. The inferior nasal aperture is significantly different between the two groups at the ( $p < 0.001$ ) level. The Pacific Island groups have a much higher inclination toward a sloping inferior nasal region. The Southeast Asians possess high frequencies for a sloping inferior nasal region but also have high frequencies of no sloping with no ridge of bone as well. The posterior zygomatic tubercle is significantly different between the two groups at the ( $p < 0.01$ ) level. While both groups exhibit high frequencies of a small and moderate projection, the Southeast Asian group exhibits higher frequencies of a large projecting tubercle. The zygomaticomaxillary suture course is significantly different between the groups at the ( $p < 0.05$ ) level. The Southeast Asian individuals exhibit higher frequencies of a jagged or S-

shaped suture than the Pacific Islanders while both groups exhibit high frequencies of a straight suture. All other traits were not found to be significantly different between the Southeast Asians and the Pacific Islanders.

When compared with mainland Asia, the frequencies of the Pacific group are clearly distinct for most traits. The inferior nasal aperture, interorbital breadth, nasal aperture width, nasal bone contour, and zygomaticomaxillary suture course are all significantly different at the ( $p < 0.001$ ) level between the two groups. Populations of the Pacific have a higher frequency for inferior nasal aperture sloping while the mainland Asians have a higher frequency of no sloping and no ridge. While both groups have highest frequency for an intermediate interorbital breadth, populations of the Pacific have a higher frequency of a broad interorbital breadth and the mainland Asians have a higher frequency for a narrow interorbital breadth. Both groups have highest frequency for an intermediate nasal aperture width as well, but the populations of the Pacific have a higher inclination toward a wide nasal aperture width. The Pacific group has a much higher frequency for a high and rounded nasal bone contour. The mainland Asians exhibit higher levels of a low and rounded nasal bone contour as well as a contour with steep lateral walls and a broad plateau. The Pacific group has a much higher frequency for a straight zygomaticomaxillary suture while very little mainland Asians exhibit this character state, instead exhibiting a large frequency of jagged or S-shaped sutures. The anterior nasal spine is significantly different at the ( $p < 0.01$ ) level between the two groups. While both groups have highest frequencies for a minimal nasal spine, the populations of the Pacific exhibit a higher frequency for a moderate projection than the mainland Asians. The posterior zygomatic tubercle is significantly different at the ( $p < 0.05$ ) level between the two groups. The mainland Asians tend to have a higher frequency for larger protruding tubercles and a much lower frequency for no

projection while the Pacific group generally exhibits a smaller projecting tubercle. The mainland Asians and the Pacific group have very similar frequencies for the nasal overgrowth and the postbregmatic depression, exhibiting a high frequency for no overgrowth as well as no postbregmatic depression. These traits were not found to be significantly different.

When the groups of the Pacific are separated and compared with the mainland Asians, several distinctions can be made. The inferior nasal aperture, zygomaticomaxillary suture course, and nasal bone contour are all significantly different between the groups at the ( $p < 0.001$ ) level. The Melanesians and Polynesians exhibit highest frequencies for a slightly sloping inferior nasal region and second highest frequencies for a heavy sloping inferior nasal region. The Asians and Southeast Asians exhibit highest frequencies for an inferior nasal region with no sloping and no ridge of bone. However, the Southeast Asians have a relatively high frequency of a slightly sloping inferior nasal region. This is possibly indicative of a clinal pattern from an inferior nasal aperture with no sloping in the west to a more sloping inferior nasal aperture as you move east across the geography. The Asian group exhibits highest frequencies for a jagged or S-shaped zygomaticomaxillary suture course while the Southeast Asians and Melanesians exhibit highest frequencies for a straight suture. The Polynesians fall intermediate to these two extremes, exhibiting an equal percentage of straight and jagged sutures. This is the only trait that appears to vary so significantly between the groups of the Pacific and mainland Asia. The groups of the Pacific all exhibit high frequencies for a high and rounded nasal bone contour while the Asians exhibit high frequencies for a contour with steep lateral walls and a broad plateau. The Polynesians exhibit extreme frequencies for this trait that is likely the result of small sample size. When groups of the Pacific are separated, the Polynesian sample drops to ( $n=11$ ). When examining nasal bone features, this number drops even further due to the fragile

nature of the nasal bones. Because of this, caution should be taken when interpreting these results. With this in mind, the Polynesian group does appear to have relatively similar frequencies to those of the other groups of the Pacific. The anterior nasal spine, interorbital breadth, nasal aperture width, and posterior zygomatic tubercle are all significantly different between the groups at the ( $p < 0.01$ ) level. All four groups have highest frequency for a minimally projecting anterior nasal spine however the Southeast Asian group has a higher frequency for a projecting nasal spine than the other groups. All of the groups express highest frequencies for an intermediate interorbital breadth however the Asians and Polynesians both have relatively high frequencies of a narrow interorbital breadth while the Melanesians and Southeast Asians both have relatively high frequencies of a broad interorbital breadth. All groups express highest frequencies for an intermediate nasal aperture width as well. However, the three groups of the Pacific exhibit higher frequencies for a wide nasal aperture than the Asian group. The Asian, Southeast Asian, and Polynesian groups all exhibit highest frequencies for a moderately projecting posterior zygomatic tubercle. The Melanesians differ from this in that they express highest frequency for a weak projecting tubercle. The nasal overgrowth and postbregmatic depression traits were not found to be significantly different between the groups.

When the groups of the world are compared with the Pacific group, all traits examined were found to be significantly different at the ( $p < 0.001$ ) level. The Pacific group exhibits a high frequency of an intermediate breadth, similar to the distribution of the European American group. For the nasal aperture width, the Pacific group exhibits a high frequency of an intermediate width, not closely comparable with any other group. The Pacific group exhibits a high frequency of a high and rounded nasal bone contour, unlike any other group. The Pacific group exhibits high frequencies of a slightly projecting and moderately projecting posterior

zygomatic tubercle and low frequencies of no projection. The Pacific group has the highest inclination of all of the groups toward a larger and more projecting posterior zygomatic tubercle. The high frequency of a straight zygomaticomaxillary suture course is most notably distinct in the Pacific group as no other group has high frequencies of this character state.

### **Correlations between Traits**

The correlation coefficient table (Table 21) reveals that the postbregmatic depression (PBD) was the only trait that did not present a significant correlation with any of the other traits. The inferior nasal aperture (INA) and the nasal bone contour (NBC) correlated with four of the other traits while the inter-orbital breadth (IOB) and the Zygomaticomaxillary suture course (ZSC) both correlated with three of the other traits. This is in concordance with Hefner (2009) who noted that most of the midfacial traits were strongly correlated. This indicates that an idea of independence among morphoscopic traits is incorrect and that these traits should instead be taken in conjunction with one another when assessing biological affinity to an individual.

### **Geographic Distributions of Traits and Clinality**

Looking at the geographic distribution maps for China, Japan, Southeast Asia, Melanesia, and Polynesia, three traits show possible clinality across the geography. The frequency for a large nasal spine is low but more prevalent in China, Japan, and Southeast Asia but this character state disappears as you move eastward (Figure 62). A higher frequency for a slight nasal spine increases as you move eastward as well. In mainland Asia, the inferior nasal aperture presents a

high frequency of no sloping and no ridge of bone but there is an inclination toward a sloping inferior nasal aperture as you move eastward into the Pacific (Figure 63). The projection of the posterior zygomatic tubercle decreases as you move eastward across the geography (Figure 69). While the regions of the Pacific still have a high frequency of slight to moderate tubercle projections, the largest projection of this trait is seen in mainland Asia. Other traits, such as the zygomaticomaxillary suture course, show why separating the groups can sometimes bring to light variability that is lost when they are grouped together (Figure 70). The Japanese exhibit very different frequencies from the Chinese for this trait, falling more closely with the distributions of the Pacific than with the rest of mainland Asia. These groups exhibit high frequencies of a straight suture and a midline projection while the Chinese exhibit a high frequency of a jagged or S-shaped suture.

When looking at the geographic distribution for traits only within the Pacific, three traits show possible clinality across the geography. The frequency for an open and unfused supranasal suture is slightly higher in Polynesians suggesting a higher inclination toward an open suture and away from a closed suture as you move eastward across the geography (Figure 72). This could be genetic, environmental, or possibly even a result of differential masticatory processes. It has been suggested that this trait develops over top of the metopic suture to help with the strong forces of mastication. While this frequency difference is slight, if this assumption is true, it could be said that the Polynesians may have a diet that requires stronger masticatory processes due to their prevalence of an open and unfused supranasal suture. The prevalence of a more pinched nasal bone shape is seen in the west (Figure 74) with Southeast Asia while a higher frequency of individuals have no or minimal nasal bone pinching in regions of the east like Polynesia. A higher frequency of a large malar tubercle can be seen with the Southeast Asian

group and a higher frequency for no tubercle or a smaller malar tubercle in Polynesia (Figure 75).

### **Clustering of Populations on Single-Trait Correspondence Analysis Axes**

Examining the plots of the first two correspondence analysis axes for all world groups, it can be seen that the Melanesians, Polynesians, and Southeast Asians cluster together for the nasal aperture width (Figure 79) and zygomaticomaxillary suture course (Figure 82). The Melanesians and Southeast Asians cluster together for the interorbital breadth (Figure 78) and nasal bone contour (Figure 80). The Asians are loosely clustered with the Melanesians and Southeast Asians for the interorbital breadth but does not tightly cluster with these groups for any other traits. The Asians, Eskimos, and American Indians cluster together for the nasal aperture width while the Eskimos and American Indians cluster together for the posterior zygomatic tubercle (Figure 81). Interestingly, the European Americans and Polynesians cluster together for the interorbital breadth, the Eskimos, African Americans, and American Indians cluster together for the zygomaticomaxillary suture course, and the Asians and African Americans cluster together for the nasal bone contour.

Examining the plots of the first two correspondence analysis axes for groups of the Pacific, it is noted that for the anterior nasal spine (Figure 83), inferior nasal aperture (Figure 84), interorbital breadth (Figure 85) and nasal aperture width (Figure 86) the groups do not cluster together, remaining far removed from one another. With this being said, the Southeast Asians and Melanesians were located slightly closer to one another than the other groups for the interorbital breadth and nasal aperture width. The Southeast Asians and Melanesians clustered



very close together for the nasal bone contour (Figure 87) and were loosely clustered together for the zygomaticomaxillary suture course (Figure 89). The Southeast Asians and mainland Asians clustered together for the posterior zygomatic tubercle (Figure 88).

### **Clustering of Populations by Hierarchical Cluster Analysis**

As seen in Figure 90, the Melanesians, Polynesians, and Southeast Asians group very close to one another, however they remain far removed from the American Indians, African Americans, European Americans, Asians, and Eskimos. This is surprising as I would expect these three groups to distantly cluster with the Asian group, similar to how the Eskimo and American Indian groups cluster with the Asians, because of shared ancestral linkages with Asian groups as well as the often misrepresentation of individuals from the Pacific as “Asian” individuals in forensic ancestry estimation due to their relative physical similarities as mentioned in the introduction. This could possibly be indicative of truly different morphoscopic trait expression between groups of the Pacific and other groups of the world but this could also be indicative of inter-observer error. The Melanesian, Polynesian, and Southeast Asian data were all collected by the author with moderate experience with morphoscopic trait assessment while all of the other groups were collected by a different and more experienced observer. This possible error should be noted and taken into consideration when closely examining morphoscopic data of large world groups taken by different observers of different experience levels. As seen in Figure 91, the Southeast Asians and Melanesians group closely with one another. The Polynesians also group with these two, though more remotely. The Asian group remains the outgroup.

## **Suggestions for Future Research**

Significant progress has been made toward the standardization of morphoscopic assessments through the Osteoware (2011) program, however there is still room for improvement. Hefner (2009) mentioned that the further refinement of the morphoscopic method and trait definition will help to reduce error in the future. I feel future researchers and program creators can work together to call attention to issues that are found to make future programs and consequently data collection more scientific and accurate when comparing with multiple observers. Working with and learning from anthropologists who have had great experience in the assessment of morphoscopic traits will, I believe, help to cut down on inter-observer error as well. I will discuss areas of improvement I noticed throughout the data collection process of this project.

For the assessment of the malar tubercle, a note on Osteoware (2011) and in the Osteoware Manual (Hefner, 2011) states that a “completely absent malar tubercle is rare.” However, referring back to Hefner (2009), all geographic groups examined (Africans, Europeans, Asians, and Native Americans) expressed a high percentage of an absent malar tubercle, between 41%-51%, which in my understanding is not considered rare. I feel that my data was likely biased by this notation in the program and thus caused me to be much more likely to give an assessment of a trace malar tubercle to an unconfident absent malar tubercle. I only assessed a cranium as having no malar tubercle if I was absolutely positive there was no trace of any tubercle, any slight uncertainty was assessed as a trace malar tubercle.

For the assessment of the zygomaticomaxillary suture course, character states include a straight-lined suture with no protrusion, a suture with a protrusion at the midline, or a suture with two or more angles making it jagged or S-shaped. In many of the crania I observed, the zygomaticomaxillary suture course exhibited a single projection but this projection was almost never found at the midline. In many cases, this single projection was found 2/3 of the way down the zygomatic bone which often made my decision of the assessment seem unconfident. If clarification were to be made, future observers may avoid inaccurately assessing this feature.

Another issue that occurs when assessing morphoscopic traits is what one would assume after reading the introduction of this thesis. Clinal distributions best display human variability and because of this, division of groups becomes ambiguous and often arbitrary. The same can be said for many morphoscopic traits. While some crania and traits are easily divisible into a score, there are also traits that tend to fall somewhere in-between scores. As Rhine (1990) points out, trait definition is always difficult because at what point on a continuum of variability does one assessment become another? I have no suggestions for this issue at this time as it has been a long-standing concern in this area of research that I believe is just part of the clinal variability of human biology. I do urge future researchers to take time and look closely at traits to make an assessment while also maintaining observer consistency in the assessments throughout the data collection process. I also encourage researchers conducting morphoscopic trait research to communicate between one another and discuss ideas of assessments to make more uniform assessments.

While assessing the morphoscopic traits listed in the Osteoware (2011) program, I noticed several other persistent traits within particular groups though they were not recorded or analyzed for this research. One of these noticeable traits included significant sagittal keeling in

individuals from Papua New Guinea and Fiji, both Melanesian populations. I assume this may be due to differential diet that requires more labored masticatory processes or it could possibly be the result of genetic influences. Another noted trait is that of inca bones, particularly found within individuals from Fiji. These would be interesting matters to research further for populations of the Pacific.

Concerning this region of the world, I feel that a better understanding of local variability could result from examining the morphoscopic trait distribution of individuals from Micronesia, mainland Southeast Asia, Taiwan, Australia, and New Zealand. These groups were not included in this research because of previous repatriation or a lack of crania from these regions within the collections used. If access were able to be gained by future researchers, a better understanding of relationships between these regions of the Pacific could be learned.

## CHAPTER V

### CONCLUSIONS

All but one of the morphoscopic traits examined were found to be correlated with one another. The postbregmatic depression (PBD) was the only trait found not to correlate with any of the other traits. The inferior nasal aperture (INA) and the nasal bone contour (NBC) were found to correlate the most often with other traits, both traits of the facial region. These noted correlations between morphoscopic traits, especially those of the facial region, indicate these traits should be analyzed in conjunction with the other traits and not analyzed independently when estimating the biological affinity of an individual.

Hierarchical clustering using larger groups of the world revealed that the Melanesians, Polynesians, and Southeast Asians all grouped very closely together as expected. This suggests a close association for the trait expressions for the groups of the Pacific when compared to all world groups. However, their degree of separation from other groups, especially mainland Asians, was unexpected. Because of their ancestral background, it was expected that these groups would cluster with each other first and with the Asian group second. The results from this cluster analysis could be indicative of either inter-observer error or truly significantly different morphoscopic trait distributions between the Pacific and the rest of the world. Hierarchical clustering using only the Asians and groups of the Pacific showed that the Melanesians and Southeast Asians share the most similarity between morphoscopic traits.

When groups of the Pacific (Southeast Asia, Melanesia, and Polynesia) are compared with groups of mainland Asia (China and Japan), a few distinguishable morphoscopic differences are noted. Seven out of nine traits examined were found to be statistically

significantly different between the mainland Asian groups and the populations of the Pacific. Only the nasal overgrowth and postbregmatic depression were found to not be significantly different between the groups. From this, hypothesis #1 can be accepted which states that many of the trait frequencies of Southeast Asians and Pacific Islanders will vary significantly from those of mainland Asian trait frequencies. Overall, the groups of the Pacific exhibit a higher prevalence for a more sloping inferior nasal aperture, a slightly more broad inter-orbital breadth, a slightly wider nasal aperture width, a more oval contour of the nasal bones, smaller posterior zygomatic tubercles, and a straight zygomaticomaxillary suture course when compared to mainland Asian groups.

Within separated groups of the Pacific, seven out of nine traits examined were found to be significantly different. Once again, the nasal overgrowth and the postbregmatic depression were found to not be significantly different between the groups. Clinality across the geography of the Pacific was noticed for six traits: inferior nasal aperture, anterior nasal spine, supranasal suture, malar tubercle, posterior zygomatic tubercle, and nasal bone shape. A clinal pattern was noted from a non-sloping inferior nasal aperture in the west and a more sloping inferior nasal aperture in the east. The presence of a projecting anterior nasal spine is more prevalent in the west but disappears as you move eastward. The presence of an open and unfused supranasal suture is slightly more prevalent in the east but diminishes in the west. The projection of the malar tubercles diminishes in the east in comparison with the west. The presence of larger protruding posterior zygomatic tubercles is prevalent in the west and the presence of smaller tubercles can be found in the east. The presence of a more pinched nasal bone shape is more prevalent in the west but diminished in the east. From the observation of clinality in these six

traits, I accept hypothesis #2 which states that the trait frequencies of this region will show a clinal pattern across the geography.

In comparison with the other groups of the Pacific, the Melanesians were found, on average, to have a higher prevalence of a heavy sloping inferior nasal aperture, a wider inter-orbital breadth, and an anterior bulging transverse palatine suture. In comparison with the other groups of the Pacific, the Polynesians were found, on average, to have a higher prevalence for a low and rounded nasal bone contour, minimal to no superior nasal bone pinching, and absent malar tubercles. In comparison with the other groups of the Pacific, the Southeast Asians were found to have a higher prevalence for large posterior zygomatic tubercles, a moderate degree of superior nasal bone pinching, and an anterior bulging transverse palatine suture.

Within the Pacific, the Melanesians and Southeast Asians correlated closely with their respective trait frequency distributions most often, sharing similar distributions for 4 of the traits. The correspondence analyses clustered the Melanesians and Southeast Asians together in 8 different instances. The hierarchical clustering analysis also grouped these two populations closer than any of the other groups. This close association is most likely due to the geographic proximity of these groups and gene flow occurring between them. From this, I can reject hypothesis #3 which states the trait frequencies of Melanesians will show the greatest dissimilarity in comparison with the mainland Asian, Southeast Asian, and Polynesian groups. In fact, it was found with this research that the mainland Asian group shows the greatest dissimilarity with these groups. With this same information, I can accept hypothesis #4 which states that the Melanesians will be more similar to the Southeast Asians than the Polynesians or the mainland Asians.

The Southeast Asians and Polynesians correlated closely with 3 of their respective trait distributions. This is not surprising considering that Southeast Asia is the likely ancestral homeland of the Polynesians. The Melanesians and Polynesians also correlated closely with 3 of their respective trait distributions. This could be due to admixture in recent times, however, this could also provide some support for the slow boat model which holds that Polynesian migrants moved slowly through Melanesia allowing sufficient time for excessive admixture before arriving in the islands in the east. The mainland Asian group did not correlate a significant amount with the Southeast Asian, Melanesian, or Polynesian groups.

When compared with larger groups of the world, the Pacific group did not correspond with any of the other groups for all five traits examined. All five traits were found to be statistically significantly different among the groups. Overall, the Pacific group had a higher inclination for a larger posterior zygomatic tubercle and a much higher prevalence of a straight zygomaticomaxillary suture than other groups of the world examined. The expression of these traits, especially the zygomaticomaxillary suture course, should be kept in mind when estimating the biological affinity of an individual.



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## APPENDIX

ANS cross tab table and chi-square probability for Mainland Asia and the Pacific

### ANS \* OVERALLREGION

Crosstab

		OVERALLREGION		Total
		Mainland Asia	Pacific	
ANS	1.0	Count	60	84
		% within OVERALLREGION	81.1%	61.8%
	2.0	Count	8	41
		% within OVERALLREGION	10.8%	30.1%
	3.0	Count	6	11
		% within OVERALLREGION	8.1%	8.1%
Total		Count	74	136
		% within OVERALLREGION	100.0%	100.0%

#### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	10.287 <sup>a</sup>	2	.006
Likelihood Ratio	11.245	2	.004
N of Valid Cases	210		



INA cross tab table and chi-square probability for Mainland Asia and the Pacific

## INA \* OVERALLREGION

Crosstab

		OVERALLREGION		Total
		Mainland Asia	Pacific	
INA	Count	9	24	33
	1.0			
	% within OVERALLREGION	12.2%	15.7%	14.5%
	Count	13	65	78
	2.0			
	% within OVERALLREGION	17.6%	42.5%	34.4%
	Count	47	55	102
	3.0			
	% within OVERALLREGION	63.5%	35.9%	44.9%
	Count	3	6	9
	4.0			
	% within OVERALLREGION	4.1%	3.9%	4.0%
Total	Count	2	3	5
	5.0			
	% within OVERALLREGION	2.7%	2.0%	2.2%
	Count	74	153	227
Total				
% within OVERALLREGION		100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	17.999 <sup>a</sup>	4	.001
Likelihood Ratio	18.690	4	.001
N of Valid Cases	227		

IOB cross tab table and chi-square probability for Mainland Asia and the Pacific

## IOB \* OVERALLREGION

Crosstab

		OVERALLREGION		Total	
		Mainland Asia	Pacific		
IOB	1.0	Count	31	29	60
		% within OVERALLREGION	41.9%	19.1%	26.5%
	2.0	Count	39	95	134
		% within OVERALLREGION	52.7%	62.5%	59.3%
	3.0	Count	4	28	32
		% within OVERALLREGION	5.4%	18.4%	14.2%
Total		Count	74	152	226
		% within OVERALLREGION	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	16.517 <sup>a</sup>	2	.000
Likelihood Ratio	16.970	2	.000
N of Valid Cases	226		

NAW cross tab table and chi-square probability for Mainland Asia and the Pacific

## NAW \* OVERALLREGION

Crosstab

		OVERALLREGION		Total
		Mainland Asia	Pacific	
NAW	1.0	Count	1	16
		% within OVERALLREGION	1.4%	7.5%
	2.0	Count	66	163
		% within OVERALLREGION	89.2%	72.1%
	3.0	Count	7	46
		% within OVERALLREGION	9.5%	20.4%
Total		Count	74	226
		% within OVERALLREGION	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	16.428 <sup>a</sup>	2	.000
Likelihood Ratio	18.945	2	.000
N of Valid Cases	226		

NBC cross tab table and chi-square probability for Mainland Asia and the Pacific

## NBC \* OVERALLREGION

Crosstab

		OVERALLREGION		Total	
		Mainland Asia	Pacific		
NBC	.0	Count	17	16	33
		% within OVERALLREGION	23.6%	11.7%	15.8%
	1.0	Count	17	104	121
		% within OVERALLREGION	23.6%	75.9%	57.9%
	2.0	Count	28	2	30
		% within OVERALLREGION	38.9%	1.5%	14.4%
	3.0	Count	9	11	20
		% within OVERALLREGION	12.5%	8.0%	9.6%
	4.0	Count	1	4	5
		% within OVERALLREGION	1.4%	2.9%	2.4%
	Total	Count	72	137	209
		% within OVERALLREGION	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	74.066 <sup>a</sup>	4	.000
Likelihood Ratio	78.019	4	.000
N of Valid Cases	209		

NO cross tab table and chi-square probability for Mainland Asia and the Pacific

## NO \* OVERALLREGION

Crosstab

		OVERALLREGION		Total
		Mainland Asia	Pacific	
NO	Count	50	89	139
	% within OVERALLREGION	72.5%	78.1%	76.0%
	Count	19	25	44
	% within OVERALLREGION	27.5%	21.9%	24.0%
Total	Count	69	114	183
	% within OVERALLREGION	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.740 <sup>a</sup>	1	.390	.476	.247
Continuity Correction <sup>b</sup>	.465	1	.495		
Likelihood Ratio	.732	1	.392		
Fisher's Exact Test					
N of Valid Cases	183				

PBD cross tab table and chi-square probability for Mainland Asia and the Pacific

## PBD \* OVERALLREGION

Crosstab

		OVERALLREGION		Total
		Mainland Asia	Pacific	
PBD	.0	Count	62	138
		% within OVERALLREGION	88.6%	84.1%
	1.0	Count	8	26
		% within OVERALLREGION	11.4%	15.9%
Total		Count	70	164
		% within OVERALLREGION	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.774 <sup>a</sup>	1	.379		
Continuity Correction <sup>b</sup>	.458	1	.498		
Likelihood Ratio	.804	1	.370		
Fisher's Exact Test				.425	.253
N of Valid Cases	234				

PZT cross tab table and chi-square probability for Mainland Asia and the Pacific

## PZT \* OVERALLREGION

Crosstab

		OVERALLREGION		Total
		Mainland Asia	Pacific	
PZT	.0	Count	0	8
		% within OVERALLREGION	0.0%	3.6%
	1.0	Count	18	84
		% within OVERALLREGION	28.1%	37.7%
	2.0	Count	29	90
		% within OVERALLREGION	45.3%	40.4%
	3.0	Count	17	41
		% within OVERALLREGION	26.6%	18.4%
Total		Count	64	223
		% within OVERALLREGION	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	9.200 <sup>a</sup>	3	.027
Likelihood Ratio	11.288	3	.010
N of Valid Cases	223		

ZSC cross tab table and chi-square probability for Mainland Asia and the Pacific

## ZSC \* OVERALLREGION

Crosstab

		OVERALLREGION		Total
		Mainland Asia	Pacific	
ZSC	.0	Count	3	93
		% within OVERALLREGION	4.8%	44.7%
	1.0	Count	21	54
		% within OVERALLREGION	33.9%	25.1%
	2.0	Count	38	65
		% within OVERALLREGION	61.3%	30.2%
	Total	Count	62	215
		% within OVERALLREGION	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	61.384 <sup>a</sup>	2	.000
Likelihood Ratio	71.187	2	.000
N of Valid Cases	215		



ANS cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

## ANS \* LARGEGROUPS

Crosstab

		LARGEGROUPS		Total
		Pacific Islands	SE Asia	
ANS	1.0	Count	36	48
		% within LARGEGROUPS	63.2%	60.8%
	2.0	Count	20	41
		% within LARGEGROUPS	35.1%	26.6%
	3.0	Count	1	11
		% within LARGEGROUPS	1.8%	12.7%
Total	Count		57	79
	% within LARGEGROUPS		100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	5.692 <sup>a</sup>	2	.058
Likelihood Ratio	6.717	2	.035
N of Valid Cases	136		

INA cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

## INA \* LARGEGROUPS

Crosstab

		LARGEGROUPS		Total	
		Pacific Islands	SE Asia		
INA	1.0	Count	18	6	24
		% within LARGEGROUPS	28.6%	6.7%	15.7%
	2.0	Count	33	32	65
		% within LARGEGROUPS	52.4%	35.6%	42.5%
	3.0	Count	12	43	55
		% within LARGEGROUPS	19.0%	47.8%	35.9%
	4.0	Count	0	6	6
		% within LARGEGROUPS	0.0%	6.7%	3.9%
	5.0	Count	0	3	3
		% within LARGEGROUPS	0.0%	3.3%	2.0%
Total		Count	63	90	153
		% within LARGEGROUPS	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	28.615 <sup>a</sup>	4	.000
Likelihood Ratio	32.522	4	.000
N of Valid Cases	153		

IOB cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

## IOB \* LARGEGROUPS

Crosstab

		LARGEGROUPS		Total
		Pacific Islands	SE Asia	
IOB	1.0	Count	13	16
		% within LARGEGROUPS	21.3%	17.6%
	2.0	Count	37	58
		% within LARGEGROUPS	60.7%	63.7%
	3.0	Count	11	17
		% within LARGEGROUPS	18.0%	18.7%
Total	Count		61	91
	% within LARGEGROUPS		100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	.330 <sup>a</sup>	2	.848
Likelihood Ratio	.327	2	.849
N of Valid Cases	152		

NAW cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

## NAW \* LARGEGROUPS

Crosstab

		LARGEGROUPS		Total
		Pacific Islands	SE Asia	
NAW	1.0	Count	9	7
		% within LARGEGROUPS	14.5%	7.8%
	2.0	Count	38	59
		% within LARGEGROUPS	61.3%	65.6%
	3.0	Count	15	24
		% within LARGEGROUPS	24.2%	26.7%
Total	Count		62	90
	% within LARGEGROUPS		100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	1.776 <sup>a</sup>	2	.412
Likelihood Ratio	1.742	2	.419
N of Valid Cases	152		

NBC cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

### NBC \* LARGEGROUPS

#### Crosstab

			LARGEGROUPS		Total
			Pacific Islands	SE Asia	
NBC	.0	Count	6	10	16
		% within LARGEGROUPS	11.1%	12.0%	11.7%
	1.0	Count	42	62	104
		% within LARGEGROUPS	77.8%	74.7%	75.9%
	2.0	Count	1	1	2
		% within LARGEGROUPS	1.9%	1.2%	1.5%
	3.0	Count	5	6	11
		% within LARGEGROUPS	9.3%	7.2%	8.0%
	4.0	Count	0	4	4
		% within LARGEGROUPS	0.0%	4.8%	2.9%
	Total	Count	54	83	137
		% within LARGEGROUPS	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.930 <sup>a</sup>	4	.570
Likelihood Ratio	4.332	4	.363
N of Valid Cases	137		

NO cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

## NO \* LARGEGROUPS

Crosstab

		LARGEGROUPS		Total
		Pacific Islands	SE Asia	
NO	Count	37	52	89
	% within LARGEGROUPS	80.4%	76.5%	78.1%
	Count	9	16	25
	% within LARGEGROUPS	19.6%	23.5%	21.9%
Total	Count	46	68	114
	% within LARGEGROUPS	100.0%	100.0%	100.0%

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	.252 <sup>a</sup>	1	.616		
Continuity Correction <sup>b</sup>	.074	1	.786		
Likelihood Ratio	.254	1	.614		
Fisher's Exact Test				.652	.396
N of Valid Cases	114				

PBD cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

## PBD \* LARGEGROUPS

Crosstab

		LARGEGROUPS		Total	
		Pacific Islands	SE Asia		
PBD	.0	Count	63	75	138
		% within LARGEGROUPS	90.0%	79.8%	84.1%
	1.0	Count	7	19	26
		% within LARGEGROUPS	10.0%	20.2%	15.9%
Total		Count	70	94	164
		% within LARGEGROUPS	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)	Exact Sig. (2-sided)	Exact Sig. (1-sided)
Pearson Chi-Square	3.137 <sup>a</sup>	1	.077		
Continuity Correction <sup>b</sup>	2.418	1	.120		
Likelihood Ratio	3.274	1	.070		
Fisher's Exact Test				.087	.058
N of Valid Cases	164				

PZT cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

### PZT \* LARGEGROUPS

#### Crosstab

		LARGEGROUPS		Total	
		Pacific Islands	SE Asia		
PZT	.0	Count	6	2	8
		% within LARGEGROUPS	9.0%	2.2%	5.0%
	1.0	Count	33	33	66
		% within LARGEGROUPS	49.3%	35.9%	41.5%
	2.0	Count	25	36	61
		% within LARGEGROUPS	37.3%	39.1%	38.4%
	3.0	Count	3	21	24
		% within LARGEGROUPS	4.5%	22.8%	15.1%
Total		Count	67	92	159
		% within LARGEGROUPS	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	13.896 <sup>a</sup>	3	.003
Likelihood Ratio	15.326	3	.002
N of Valid Cases	159		

ZSC cross tab table and chi-square probability for the Pacific Islands and Southeast Asia

## ZSC \* LARGEGROUPS

Crosstab

		LARGEGROUPS		Total	
		Pacific Islands	SE Asia		
ZSC	.0	Count	47	46	93
		% within LARGEGROUPS	72.3%	52.3%	60.8%
	1.0	Count	13	20	33
		% within LARGEGROUPS	20.0%	22.7%	21.6%
	2.0	Count	5	22	27
		% within LARGEGROUPS	7.7%	25.0%	17.6%
Total	Count	65	88	153	
	% within LARGEGROUPS	100.0%	100.0%	100.0%	

Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	8.944 <sup>a</sup>	2	.011
Likelihood Ratio	9.591	2	.008
N of Valid Cases	153		

ANS Cross tab table and chi-square probability for separated groups

## ANS \* GROUP

Crosstab							
		GROUP				Total	
		Asian	Melanesia	Polynesia	SE Asian		
ANS	1.0	Count	60	30	6	48	144
		% within GROUP	81.1%	61.2%	75.0%	60.8%	68.6%
	2.0	Count	8	18	2	21	49
		% within GROUP	10.8%	36.7%	25.0%	26.6%	23.3%
	3.0	Count	6	1	0	10	17
		% within GROUP	8.1%	2.0%	0.0%	12.7%	8.1%
Total		Count	74	49	8	79	210
		% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	16.836 <sup>a</sup>	6	.010
Likelihood Ratio	18.757	6	.005
N of Valid Cases	210		



INA Cross tab table and chi-square probability for separated groups

## INA \* GROUP

		Crosstab				
		GROUP				Total
		Asian	Melanesia	Polynesia	SE Asian	
INA	Count	9	16	2	6	33
	1.0 % within GROUP	12.2%	30.2%	20.0%	6.7%	14.5%
	Count	13	27	6	32	78
	2.0 % within GROUP	17.6%	50.9%	60.0%	35.6%	34.4%
	Count	47	10	2	43	102
	3.0 % within GROUP	63.5%	18.9%	20.0%	47.8%	44.9%
	Count	3	0	0	6	9
	4.0 % within GROUP	4.1%	0.0%	0.0%	6.7%	4.0%
	Count	2	0	0	3	5
	5.0 % within GROUP	2.7%	0.0%	0.0%	3.3%	2.2%
Total	Count	74	53	10	90	227
	% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	46.919 <sup>a</sup>	12	.000
Likelihood Ratio	51.679	12	.000
N of Valid Cases	227		

IOB Cross tab table and chi-square probability for separated groups

## IOB \* GROUP

Crosstab							
		GROUP				Total	
		Asian	Melanesia	Polynesia	SE Asian		
IOB	1.0	Count	31	10	3	16	60
		% within GROUP	41.9%	19.2%	33.3%	17.6%	26.5%
	2.0	Count	39	31	6	58	134
		% within GROUP	52.7%	59.6%	66.7%	63.7%	59.3%
	3.0	Count	4	11	0	17	32
		% within GROUP	5.4%	21.2%	0.0%	18.7%	14.2%
Total		Count	74	52	9	91	226
		% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	19.841 <sup>a</sup>	6	.003
Likelihood Ratio	21.499	6	.001
N of Valid Cases	226		

NAW Cross tab table and chi-square probability for separated groups

## NAW \* GROUP

		Crosstab					
		GROUP				Total	
		Asian	Melanesia	Polynesia	SE Asian		
NAW	1.0	Count	1	7	2	7	17
		% within GROUP	1.4%	13.5%	20.0%	7.8%	7.5%
	2.0	Count	66	32	6	59	163
		% within GROUP	89.2%	61.5%	60.0%	65.6%	72.1%
	3.0	Count	7	13	2	24	46
		% within GROUP	9.5%	25.0%	20.0%	26.7%	20.4%
Total		Count	74	52	10	90	226
		% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	19.430 <sup>a</sup>	6	.003
Likelihood Ratio	21.007	6	.002
N of Valid Cases	226		

NBC Cross tab table and chi-square probability for separated groups

## NBC \* GROUP

Crosstab							
		GROUP				Total	
		Asian	Melanesia	Polynesia	SE Asian		
NBC	.0	Count	17	6	0	10	33
		% within GROUP	23.6%	12.5%	0.0%	12.0%	15.8%
	1.0	Count	17	38	4	62	121
		% within GROUP	23.6%	79.2%	66.7%	74.7%	57.9%
	2.0	Count	28	1	0	1	30
		% within GROUP	38.9%	2.1%	0.0%	1.2%	14.4%
	3.0	Count	9	3	2	6	20
		% within GROUP	12.5%	6.3%	33.3%	7.2%	9.6%
	4.0	Count	1	0	0	4	5
		% within GROUP	1.4%	0.0%	0.0%	4.8%	2.4%
Total	Count	72	48	6	83	209	
	% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%	

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	82.240 <sup>a</sup>	12	.000
Likelihood Ratio	86.878	12	.000
N of Valid Cases	209		

NO Cross tab table and chi-square probability for separated groups

## NO \* GROUP

Crosstab						
		GROUP				Total
		Asian	Melanesia	Polynesia	SE Asian	
NO	Count	50	32	5	52	139
	.0 % within GROUP	72.5%	78.0%	100.0%	76.5%	76.0%
	Count	19	9	0	16	44
	1.0 % within GROUP	27.5%	22.0%	0.0%	23.5%	24.0%
Total	Count	69	41	5	68	183
	% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	2.152 <sup>a</sup>	3	.542
Likelihood Ratio	3.307	3	.347
N of Valid Cases	183		

PBD Cross tab table and chi-square probability for separated groups

## PBD \* GROUP

Crosstab						
		GROUP				Total
		Asian	Melanesia	Polynesia	SE Asian	
PBD	Count	62	54	9	75	200
	% within GROUP	88.6%	90.0%	90.0%	79.8%	85.5%
	Count	8	6	1	19	34
	% within GROUP	11.4%	10.0%	10.0%	20.2%	14.5%
Total	Count	70	60	10	94	234
	% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	4.143 <sup>a</sup>	3	.246
Likelihood Ratio	4.078	3	.253
N of Valid Cases	234		

PZT Cross tab table and chi-square probability for separated groups

### PZT \* GROUP

#### Crosstab

		GROUP				Total
		Asian	Melanesia	Polynesia	SE Asian	
PZT	Count	0	5	1	2	8
	.0					
	% within GROUP	0.0%	8.8%	10.0%	2.2%	3.6%
	Count	18	30	3	33	84
	1.0					
	% within GROUP	28.1%	52.6%	30.0%	35.9%	37.7%
	Count	29	20	5	36	90
	2.0					
	% within GROUP	45.3%	35.1%	50.0%	39.1%	40.4%
	Count	17	2	1	21	41
	3.0					
	% within GROUP	26.6%	3.5%	10.0%	22.8%	18.4%
Total	Count	64	57	10	92	223
	% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	25.000 <sup>a</sup>	9	.003
Likelihood Ratio	28.731	9	.001
N of Valid Cases	223		

ZSC Cross tab table and chi-square probability for separated groups

## ZSC \* GROUP

Crosstab							
		GROUP				Total	
		Asian	Melanesia	Polynesia	SE Asian		
ZSC	.0	Count	3	43	4	46	96
		% within GROUP	4.8%	78.2%	40.0%	52.3%	44.7%
	1.0	Count	21	9	4	20	54
		% within GROUP	33.9%	16.4%	40.0%	22.7%	25.1%
	2.0	Count	38	3	2	22	65
		% within GROUP	61.3%	5.5%	20.0%	25.0%	30.2%
Total		Count	62	55	10	88	215
		% within GROUP	100.0%	100.0%	100.0%	100.0%	100.0%

### Chi-Square Tests

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	73.796 <sup>a</sup>	6	.000
Likelihood Ratio	86.451	6	.000
N of Valid Cases	215		

IOB cross tab table and chi-square probability for major groups of the world

**Crosstab**

			ANCLARGE						Total
			Amerindian	Asian	Black - Am	Eskimo	Pacific	White - Am	
IOB	1.0	Count	27	21	4	18	29	9	108
		% within ANCLARGE	62.8%	43.8%	6.6%	85.7%	19.1%	18.0%	28.8%
	2.0	Count	15	24	26	3	95	38	201
		% within ANCLARGE	34.9%	50.0%	42.6%	14.3%	62.5%	76.0%	53.6%
	3.0	Count	1	3	31	0	28	3	66
		% within ANCLARGE	2.3%	6.3%	50.8%	0.0%	18.4%	6.0%	17.6%
Total	Count	43	48	61	21	152	50	375	
	% within ANCLARGE	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	

**Chi-Square Tests**

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	134.404 <sup>a</sup>	10	.000
Likelihood Ratio	125.964	10	.000
N of Valid Cases	375		

NAW cross tab table and chi-square probability for major groups of the world

**Crosstab**

			ANCLARGE						Total
			Amerindian	Asian	Black - Am	Eskimo	Pacific	White - Am	
NAW	1.0	Count	3	2	2	1	16	32	56
		% within ANCLARGE	7.0%	4.2%	3.3%	4.8%	10.5%	64.0%	14.9%
	2.0	Count	38	41	30	20	97	13	239
		% within ANCLARGE	88.4%	85.4%	49.2%	95.2%	63.8%	26.0%	63.7%
	3.0	Count	2	5	29	0	39	5	80
		% within ANCLARGE	4.7%	10.4%	47.5%	0.0%	25.7%	10.0%	21.3%
Total	Count	43	48	61	21	152	50	375	
	% within ANCLARGE	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	

**Chi-Square Tests**

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	155.996 <sup>a</sup>	10	.000
Likelihood Ratio	130.267	10	.000
N of Valid Cases	375		



NBC (also labelled NBS in Hefner 2009) cross tab table and chi-square probability for major groups of the world

**Crosstab**

			ANCLARGE						Total
			Amerindian	Asian	Black - Am	Eskimo	Pacific	White - Am	
NBS	.0	Count	4	11	26	0	16	3	60
		% within ANCLARGE	9.3%	23.9%	42.6%	0.0%	11.7%	6.0%	16.8%
	1.0	Count	18	13	15	9	104	4	163
		% within ANCLARGE	41.9%	28.3%	24.6%	45.0%	75.9%	8.0%	45.7%
	2.0	Count	16	16	11	0	2	9	54
		% within ANCLARGE	37.2%	34.8%	18.0%	0.0%	1.5%	18.0%	15.1%
	3.0	Count	5	5	6	9	11	17	53
		% within ANCLARGE	11.6%	10.9%	9.8%	45.0%	8.0%	34.0%	14.8%
	4.0	Count	0	1	3	2	4	17	27
		% within ANCLARGE	0.0%	2.2%	4.9%	10.0%	2.9%	34.0%	7.6%
	Total	Count	43	46	61	20	137	50	357
		% within ANCLARGE	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%

**Chi-Square Tests**

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	220.838 <sup>a</sup>	20	.000
Likelihood Ratio	207.717	20	.000
N of Valid Cases	357		

PZT cross tab table and chi-square probability for major groups of the world

**Crosstab**

			ANCLARGE						Total
			Amerindian	Asian	Black - Am	Eskimo	Pacific	White - Am	
PZT	.0	Count	23	14	18	10	8	25	98
		% within ANCLARGE	53.5%	29.2%	29.5%	47.6%	5.0%	50.0%	25.7%
	1.0	Count	18	19	19	10	66	20	152
		% within ANCLARGE	41.9%	39.6%	31.1%	47.6%	41.5%	40.0%	39.8%
	2.0	Count	2	10	14	1	61	3	91
		% within ANCLARGE	4.7%	20.8%	23.0%	4.8%	38.4%	6.0%	23.8%
	3.0	Count	0	5	10	0	24	2	41
		% within ANCLARGE	0.0%	10.4%	16.4%	0.0%	15.1%	4.0%	10.7%
	Total	Count	43	48	61	21	159	50	382
		% within ANCLARGE	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%

**Chi-Square Tests**

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	101.507 <sup>a</sup>	15	.000
Likelihood Ratio	120.784	15	.000
N of Valid Cases	382		

ZSC cross tab table and chi-square probability for major groups of the world

**Crosstab**

			ANCLARGE						Total
			Amerindian	Asian	Black - Am	Eskimo	Pacific	White - Am	
ZS	.0	Count	0	2	4	0	93	0	99
		% within ANCLARGE	0.0%	5.4%	7.5%	0.0%	60.8%	0.0%	28.9%
	1.0	Count	13	15	16	7	33	17	101
		% within ANCLARGE	31.0%	40.5%	30.2%	33.3%	21.6%	47.2%	29.5%
	2.0	Count	29	20	33	14	27	19	142
		% within ANCLARGE	69.0%	54.1%	62.3%	66.7%	17.6%	52.8%	41.5%
Total	Count	42	37	53	21	153	36	342	
	% within ANCLARGE	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	

**Chi-Square Tests**

	Value	df	Asymp. Sig. (2-sided)
Pearson Chi-Square	146.314 <sup>a</sup>	10	.000
Likelihood Ratio	171.828	10	.000
N of Valid Cases	342		