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# MULTIDISCIPLINARY PERSPECTIVES ON THE AUSTRONESIAN HOMELAND: A CRITIQUE<sup>1</sup>

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Linguistics, archaeology, and genetics have been used to reconstruct the past. Where findings differ, there is a tendency to rely on a hierarchy of reliability in the sciences. With regard to the Austronesian homeland, it has been asserted that linguistics and archaeology rely on each other's evidence for postulating an Out-of-Taiwan hypothesis. This paper examines the arguments that use individual lines of evidence. Whereas evidence from linguistics and archaeology support an Out-of-Taiwan hypothesis, genetics does not provide a coherent scenario for or against such a hypothesis. Issues of dating, sampling, and non-paternity should be addressed before genetics can be reliably used in conjunction with linguistics and archaeology.

**1. INTRODUCTION.** The notion that linguistics, archaeology, and genetics can be used to reconstruct the past is not new. Based on a large study of gene frequencies for non-DNA polymorphisms in world populations, Cavalli-Sforza et al. (1988) noted that average genetic distances between the most important clusters found are proportional to archaeological separation time. In addition, these geneticists also declared that “[l]inguistic superfamilies show remarkable correspondence with the two major clusters, indicating considerable parallelism between genetic and linguistic evolution,” the two superclusters being the (i) Caucasoids and the (ii) Northeast Asians and Amerindians. (Cavalli-Sforza et al. 1988:6002). While new techniques and genetic data constantly necessitate new perspectives on genetic classification (see Jorde and Wooding 2004,<sup>2</sup> for example), it becomes necessary to relate these findings to those in archaeology and linguistics (see Blench and MacDonald 2000 and Sanchez-Mazas et al. 2008<sup>3</sup> for more recent examples). Naturally, observations are made about whether the findings in these different fields corroborate, complement, or even contradict one other.

In the case of establishing the Austronesian homeland, the disciplines of archaeology and linguistics seem to be mostly congruent in supporting an Out-of-Taiwan hypothesis, while there are more conflicting views within the field of genetics itself. Where findings differ between genetics and archaeology/linguistics, there is a tendency to rely on a hierarchy of reliability in the sciences. In this hierarchy, genetics and linguistics are ranked at opposite ends of the spectrum—genetics as a biological science is ranked at the top of this hierarchy while linguistics (or more specifically, the comparative method) has been criticized by the geneticists for being “not quite as powerful as often assumed” (Hill et al. 2007:30). In addition, a serious claim has been leveled at researchers who support the Out-of-Taiwan hypothesis. It has been asserted that linguistics and archaeology rely on one another's evidence for postulating the

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<sup>2</sup> Jorde and Wooding (2004) reviewed the results of genetic analyses that show that genetic similarity can be established among individuals better than populations, and that while the clustering of individuals is correlated with geographic origin, ancestry, or even with some traditional concepts of race, these correlations are not perfect, because genetic variation tends to be distributed in a continuous, overlapping fashion among populations.

<sup>3</sup> Blench and MacDonald (2000) focused on the past movement of African livestock, while Sanchez-Mazas et al. (2008) discussed past human migrations in East Asia.

hypothesis. Oppenheimer (2004a) accused Diamond and Bellwood (2003) of using the different lines of evidence incorrectly, these different lines being archaeology, biology of domesticates, language, physical anthropology, and genetic evidence. He stated in particular that archaeological, and not linguistic, dates had been used for the putative language splits, thus running the risks of circularity and of choosing archaeological dates that fit a preferred linguistic narrative (Oppenheimer 2004a). In a reverse scenario, Szabó and O’Connor (2010) criticized the over-reliance of archaeology on linguistics in constructing the Out-of-Taiwan hypothesis. That one discipline relies on the evidence of another for establishing a core argument is a serious indictment, and the charge has to be carefully evaluated. It is the goal of this paper to examine the arguments constructed, using the individual lines of evidence from linguistics, archaeology, and genetics with regard to postulating the Austronesian homeland.

**2. LINGUISTICS.** The Austronesian language family is exceptional for having no fewer than ten primary branches (Blust 1999), and for its geographical span that ranges 26,000 km from Madagascar in the west to Easter Island in the east (Diamond 2000). The Austronesian languages include the Formosan languages spoken in Taiwan, which constitute primary branches of the tree, together with the Malayo-Polynesian languages, which are spoken outside Taiwan. Western Malayo-Polynesian languages are found in the Philippines and western Indonesia, including Palauan and Chamorro of western Micronesia, the Chamic languages of mainland Southeast Asia, and Malagasy. Central-Eastern Malayo-Polynesian languages refer to all other Malayo-Polynesian languages. These extend into places such as Western New Guinea and include the Oceanic languages, which are spoken in Melanesia, Micronesia, and Polynesia (Blust 1985).

There are two main means by which the homeland of the Austronesian language family has been located: linguistic paleontology and migration theory. The first of these is an approach to culture history that was pioneered by Pictet (Saussure 1915/1959, Blust 1985). Also known as the *Wörter und Sachen* ‘words and things’ technique, linguistic paleontology uses reconstructed words as a basis for making inferences about the culture and environment of prehistoric language communities. With regard to linguistic migration theory, Sapir (1916/1968) noted that the area of highest linguistic diversity is the most likely center of dispersal of a language family or linguistic subgroup. In pursuing these methods, both the comparative method and lexicostatistics have been used. Arguably, the comparative method is more rigorous and hence more reliable than the other. This issue will be revisited at the end of this section.

With regard to the Austronesian homeland, linguistic paleontology has been carried out by Blust (1985, 1995) by using the comparative method. As elaborated by Blust (1995:455), the comparative method is based on two well-tested claims about the nature of language—that the relationship between sound and meaning is largely arbitrary (Saussure 1915/1959) and that sound change is largely regular (Osthoff and Brugmann 1878). As the sound changes are regular, the original forms can be rigorously reconstructed. Linguistic paleontology then relies on these reconstructed proto-forms to make cultural and environmental inferences about the “codified experience of its speakers” (Blust 1995:456). Campbell (2000) noted that reconstructed vocabulary can also provide chronological information, since it can be concluded that items named by terms which are reliably reconstructed to the proto-language were already known at the time when the proto-language was spoken.

Reconstructed forms for Proto-Austronesian include words for plants such as three different types of bamboo, the areca palm and nut, two types of fern, sword grass, three words for millet, stinging nettle, pandanus, derris root, rattan, five words associated with rice, sugarcane, elephant ear taro (*Alocasia* spp.) (but not the banana, breadfruit, coconut, cucumber, ginger, hibiscus, indigo, jackfruit, kapok, mango, mangrove, cordyline, ramie, sago, *Colocasia* taro, turmeric yam, and other trees that feature in Proto-Malayo-Polynesian), and animals such as deer, dog, some type of dove, freshwater eels, at least one type of monkey, the pangolin, wild and domesticated pigs, and some kind of large ruminant that may have been distinct from the deer (but not the civet cat, chicken, crocodile, flying fox, or python, for which widespread cognate sets are found outside Taiwan) (Blust 1985:52). The reconstructions also point to a tectonically unstable area (\*linuR ‘earthquake’) with hills or mountains, lakes, marginal possible influence from the monsoons, a distinct cold season, and periodic typhoons. Crucially, the reconstructions

also include Proto-Austronesian \*qamiS(-san) ‘north wind, cold weather’, which means ‘winter’ in the Formosan languages spoken in the mountainous areas of Taiwan, but the ‘north’ or ‘north wind’ in areas where seasonal variations of temperature are less extreme (Blust 1985:54). Blust (1985) noted this to be incompatible with the hypothesis of an equatorial or a near-equatorial homeland. In addition, the reflexes of \*baRiuS mean ‘typhoon’ in southern Taiwan, the Philippines, and the Marianas. These point to the possibility that the Austronesian homeland is within the typhoon belt of the northern hemisphere.<sup>4</sup> In addition, Blust’s reconstructions associated with marine life or a marine environment also support a previous conclusion drawn by Kern (1889), that the Austronesian homeland was near the sea. Finally, it is crucial to note that there is widespread evidence for an outrigger-canoe complex outside Taiwan, but not among Formosan aborigines.

Where linguistic migration theory is concerned, both the comparative method and lexicostatistics have been utilized. Using the comparative method, the Austronesian languages can be subgrouped based on shared innovations found between members of the same group. The primary subgroups established through the comparative method are the different Formosan language groups (some of which contain one member) and the Malayo-Polynesian languages. The Malayo-Polynesian languages have been split into Western Malayo-Polynesian (Blust 1977) and Central-Eastern Malayo-Polynesian groups, and the latter in turn split into Central Malayo-Polynesian and Eastern Malayo-Polynesian, which can be further split into the South Halmahera-West New Guinea group and the Oceanic group (Blust 1978, 1982, 1983, 1993). Within the framework of linguistic migration theory, the Austronesian homeland is most likely to be the area of greatest diversity. This does not necessarily correlate with the area where the greatest number of languages is found (Blust 1995). Based on the principle of least moves, the Austronesian homeland is thus identified by Blust (1985, 1995) as Taiwan, which has the greatest number of primary branches, and hence the greatest degree of linguistic diversity. Notably, these results contradict those established by lexicostatistics (Dyen 1965). Using lexicostatistical methods, Dyen (1965) concluded that the Austronesian homeland was in the area of New Guinea and the Bismarck Archipelago. However, lexicostatistics has been highly disputed, since it measures gross lexical similarities without reference to shared innovations, which are the basis for subgrouping.<sup>5</sup> Lexicostatistics also lacks rigor, as it has no explanation for the regularity of sound changes found within linguistic subgroups. Hence, the dominant view in linguistics, based on application of the comparative method, would be that the Austronesian language speakers originated from Taiwan.

Finally, it must be noted that while linguistics is able to provide information on relative chronology based on subgrouping, the time depth of proto-languages must be based on archaeological dates.<sup>6</sup> Even so, absolute dating is clearly secondary to the linguistic argument, and none of the evidence used above in the core arguments for the Out-of-Taiwan hypothesis relies on the evidence of another field.

**3. ARCHAEOLOGY.** The mainstream view in archaeology is that there was a Neolithic dispersal that took place from Taiwan into the northern Philippines about 4,000 years ago (Bellwood 1997, Bellwood and Dizon 2008), after which there was a movement onwards to Eastern Indonesia and the Bismarcks, and on to Sāmoa by 800 BC (Bellwood 1997, 2005, Bellwood and Dizon 2008). The main evidence for this line of argument comes from Lapita pottery and its associated cultural complex. The Torongan and Reranum Caves in the Batanes Islands have been found to contain red-slipped pottery that resembles the pottery

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<sup>4</sup> This differs from Kern’s conclusions that the AN homeland was within the tropics or not far outside them. Kern’s conclusion was not founded on a well-established subgrouping of the Austronesian languages and was influenced by claims about a possible external relationship with other languages of southern China, northern Vietnam, and Hainan Island. Haudricourt (1954) believed that the AN homeland should be in the coastal areas of mainland Asia, but further north than Kern had considered, between the islands of Hainan and Taiwan. These views were, however, formed when the subgroupings had not been firmly established, due to lack of data, and hence have been superseded by the view expressed in Blust 1985, 1995.

<sup>5</sup> See the contributions of Robert Blust, James Matisoff, Christopher Ehret and Aharon Dolgopolsky in Renfrew et al. 2000.

<sup>6</sup> See Blust 1986/1987.

from Chaolaiqiao in southeastern Taiwan. This red-slipped pottery that is otherwise undecorated shares similar everted and slightly concave rim forms and is dated to cal. 2,000 BC in the Torongan and Rerantum Caves, and cal. 2,200 BC in southeastern Taiwan (Bellwood and Dizon 2008). Besides red-slipped pottery, cord-marked sherds were also found in the Rerantum Cave (Bellwood and Dizon 2008), cord-marked pottery having been earlier associated with archaeological assemblages in Taiwan (Bellwood 1995). With regard to domesticates, Bellwood and Dizon (2008) stated that bones of domesticated pigs from at least 3,000 BP have been found in Sunget, noting that the Batanes Islands have no evidence for a pre-human wild pig population, and that the wild pig of Luzon was never domesticated (Groves 1997). The implication appears to be that these had been introduced by an external population.

In New Britain, Lapita sherds had first been reported by Father Otto Meyer in 1909, although their significance for Polynesian origins was not known until Gifford’s and Shutler’s excavation at Lapita on the west coast of New Caledonia in 1952<sup>7</sup> (Kirch 1989, Gifford and Shutler 1956). Elsewhere, the Lapita cultural complex began to emerge during the late 1980s (see Kirch 2000 for examples). Besides the red-slipped pottery, excavations in sites ranging from the Mussau Islands and Ambitle, to New Ireland, to the Arawe group off the southern coast of New Britain, and on to Nissan and Buka in the northern Solomons have resulted in the unearthing of red-slipped globular jars with out-turned rims, as well as decorated pottery that was covered in “finely executed motifs, many representing human faces, made by pressing small toothed (‘dentate’) stamps onto the leather-hard clay before firing” (Kirch 2000:90). Radiocarbon dates for the dentate-stamped pottery range between 1,500 and 1,400 BC. The earliest dates for similar sites at Fiji come in only at about 1,100–900 BC (Anderson and Clark 1999). These dates point to a movement from Near Oceania to Remote Oceania. Ultimately, the Lapita sites are emblematic of a shared culture. The red-slipped and decorated pottery was usually found in settlements situated on coastal beach terraces, or built over shallow lagoons as clusters of stilt-houses in Near Oceania (Kirch 2000). Other evidence unearthed shows that the occupants utilized all tree crops that had been locally domesticated, as well as pigs, dogs, and chickens. They also were seafarers, as evidenced by the movement of items such as pottery and obsidian, and their material culture included items such as stone and shell adzes, flaked tools of obsidian and chert, shell scrapers and peeling knives, as well as fishhooks, among other things. The pottery style of the Lapita complex (especially that of the red-slipped pottery), as well as the stone adzes, fishhooks, and other ornaments, can apparently be linked to the Ta-p’en-k’eng culture of Taiwan, which has been dated to about 3,000 BC (Kirch 1995). From the above, it is clear, that based on the archaeological evidence alone, archaeologists are able to postulate an extremely rapid Neolithic movement out of Taiwan around 3,000 BC. Hence, there is no need for the archaeologists to rely on linguistic data.

It is possible to see why the archaeology that supports the Out-of-Taiwan hypothesis has been subjected to criticisms about over-reliance on linguistics. With the individual lines of evidence from both fields pointing to the same conclusions, the occupants who had once resided at Lapita sites, and the people who came before and after them are recognized to be Austronesians. The historical developments that led to the movement of the Austronesians are then conceived as a process whereby demographically-expanding populations moved outwards from primary agricultural homeland regions due to population pressure (Bellwood 1995). Known as the farming/language dispersal hypothesis, the identification of the expansion relied on the correlations between early centers of agriculture and major language family homelands (Renfrew 1992, 2000). Bellwood (1995:104) claimed that the areas of agricultural origin show a “larger-than-average” number of different languages as well as high levels of internal family diversity. He cited Blust 1985, pointing out that Taiwan is the home to the primary branches of the Austronesian languages, including Proto-Austronesian, and suggested that the Neolithic archaeological assemblages in Taiwan can be understood to be an extension of the archaeological assemblages found in mainland China, such as that of Hemudu. Other Austronesian-associated sites, such as the Lapita sites in Near Oceania mentioned above, show evidence of having once been occupied by agriculturalists who had adjusted to living near the coast. Without having examined the primary evidence that had been used to postulate a

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<sup>7</sup> This site gave rise to the name of the distinctive pottery style.

Neolithic expansion from Taiwan, one might assume that archaeology had made generalizations about the Austronesian movement based on the linguistic evidence.

Szabó and O'Connor (2010) criticized the over-reliance of archaeology on linguistics in the construction of the Out-Of-Taiwan hypothesis. They pointed out potential problems with individual items in the Neolithic package. For example, Bellwood's description of "shell ornaments" (2002) is "broad and nebulous, making it entirely possible that diversity is being glossed over"<sup>8</sup> (Szabó and O'Connor 2010:623). In addition, they questioned whether transmission could have taken place horizontally rather than vertically. They also made the claim that there is really no consistent expression of the polythetic Neolithic cultural complex, and that at some sites, red-slipped pottery by itself is the only means of assessing the Austronesian connection (as with the Dimolit, Rabel Cave, Laurente Cave, and Musang Cave sites in northern Luzon).<sup>9</sup> In addition, they stated that the Arku Cave in northern Luzon, Bukit Tengkorak in Sabah, and Uattamdi in the Northern Moluccas are contemporaneous with the emergence of the Lapita culture complex. Finally, they emphasized the difficulty of associating languages and a "silent archaeological record" (Szabó and O'Connor 2010:625), stating that the Austronesian-speaking population had knowledge of potting, agriculture, fishing, and polished stone-adze making, based on reconstructed terms in the proto-language, but so did other linguistic/cultural groups in mainland Southeast Asia (Higham 2002). The authors thus urged paying close attention to spatial and temporal complexities.

It is clear that more precise descriptions would enable a more specific understanding of the past. But while Szabó and O'Connor were right in urging archaeologists to pay close attention to complexities, the issues they raised do not amount to a falsification of the Out-Of-Taiwan claim. As they had correctly pointed out, the Neolithic package comprises more than a single item (as with red-slipped pottery), hence rejecting a single item in the Neolithic package (shell beads) as evidence for cultural identity is not enough to weaken the view that Neolithic expansion took place. The question may then be, how many items must there be from the package to clearly indicate the same Neolithic complex? Here, there may be a need to claim that the strengths of the different individual elements are not the same, and that pottery in a distinctive style is indicative enough of a specific culture. Therein also lies a possible strength in using evidence from more than one discipline. It is possible not to conflate the products of this Neolithic culture with horizontal transmission rather than vertical transmission, if one notes that the migration pathway is similar to the development of Austronesian languages.<sup>10</sup> If there had been much cultural exchange between Austronesian and non-Austronesian groups, surely there would be much more evidence of language contact. As for the close dates of the Arku Cave in northern Luzon, Bukit Tengkorak in Sabah, and Uattamdi with that of the Lapita culture complex, Bellwood and Dizon (2008) explained that expansion took place very rapidly from the Philippines to Sāmoa. Recent dating of the Batanes Islands has also shown that the dates should be pushed back (Bellwood and Dizon 2008), so that the Neolithic movement from the Philippines to Sāmoa occurred over an estimated 1,200 years. Finally, the claim that mainland Southeast Asian groups also have reconstructed words for items within the Neolithic package does not mean that they were involved in this specific archaeological history, unless one finds, for example, red-slipped or dentate-stamped pottery in these areas. Crucially, Szabó and O'Connor (2010) provided no viable alternative to understanding these artefacts.

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<sup>8</sup> The authors then contrasted shell beads from the Neolithic sites of Palawan with those from the Uattamdi site in the northern Moluccas. These differ in terms of raw materials used, morphologies, and manufacturing techniques. For example, holes were drilled rather than ground into the shell beads in the Moluccas. The "monolithic category" of "shell beads" as a marker of migrating Austronesian-speaking populations is hence inadequate, according to Szabó and O'Connor (2010:624).

<sup>9</sup> See Bellwood 1997.

<sup>10</sup> See the following section.

Terrell (2010) attempted to provide an alternative view in the form of the “sleeping giant” hypothesis. He was against the idea that prehistory in the Pacific could be framed as two waves of migration.<sup>11</sup> Terrell questioned what had stopped the first migration, and what had made the second migration so influential. In his hypothesis, Terrell (2010) alluded to the Late Pleistocene and early Holocene era, during which New Guinea was still connected with Australia via a land bridge. He stated that via this land bridge, people arrived in New Guinea, and that even if it would “undoubtedly be an exaggeration,” “people moved inland and lost all touch with the outside world” (Terrell 2010:605). The rest of the island groups to both sides of New Guinea must still have had been populated, and “it is probable that the arts of sailing and island survival were still being cultivated during the Pleistocene by people living in these enduring island realms” (Terrell 2010:605). However, since New Guinea formed a barrier between these ancient archipelagos of Sunda and Sahul, “conditions clearly favoured divergence among Pleistocene Pacific Islanders in customs, speech and physical appearance” (Terrell 2010:605). The situation then only began to change by 6,000 BP, when the earth’s seas approached current levels. With the evolution of floodplains, river deltas, and lagoons, the settlers could then grow sago palms, exploit the lagoons, and travel and trade with one another, and with islanders in Indonesia and the Bismarck Archipelago (Terrell 2004). There is hence no need, according to Terrell, for people in the south-western Pacific to “wait for the invention of ‘agriculture’ in China to start looking for new places to live” (Terrell 2010:606).

While Terrell (2010) attempted to infer what had happened in the past, what he said about human migration appears to be completely unfalsifiable. Even though there was a land bridge in the past, there is no way of providing evidence that people did not move inland and that they did not lose touch with the outside world. There is hence no clear scientific basis to this approach, and it should be abandoned in favor of a strong claim that is still clearly falsifiable. Hence, the view from archaeology that has to be considered is that a Neolithic expansion had indeed taken place, and that the homeland of expansion is Taiwan or South China (Bellwood 1995, 1996, 1997, 2002, 2005, Bellwood and Dizon 2008, Kirch 2000). Again, the archaeologists’ postulation of a Neolithic movement out of Taiwan is first and foremost based on archaeological evidence, and not on linguistic evidence.

There is no doubt that while linguistics can establish relative dating, archaeology is far stronger in determining the absolute age of cultural artefacts. However, determining the relationship between these artefacts and a particular culture is not straightforward. It is also disputed whether a historical connection can be posited between a living group and the archaeology of an antecedent culture (Trigger 1989). This is problematic because of the “flat view” of prehistory that has to be assumed, in which traditional societies remained static (Earle 2007). There is thus a particular need for understanding continuity through other means, such as linguistics and genetics.

**4. GENETICS.** While there is an overall agreement on an Out-of-Taiwan Austronesian migration among linguists and archaeologists, there is a lack of consensus on the issue among geneticists. In general, to understand the past, geneticists use three different types of evidence. These are biparental evidence (such as autosomal evidence); mitochondrial (mtDNA) evidence, which is maternally inherited; and Y-chromosomal evidence, which is paternally inherited. Hence, one attractive supposition might be that the conclusions drawn by the geneticists depend on the type of evidence that is used. For example, mtDNA data might point to an Out-of-Taiwan Austronesian migration, while Y-chromosomal data might not. However, a quick survey of genetic studies shows that this simple explanation does not work.

Where biparental evidence is concerned, Chang et al. (2002) examined eight mutations and one polymorphism of the fucosyltransferase (*FUT2*) gene using blood samples from 140 Han Taiwanese, 60 from northern and 77 from southern mainland China, 54 Japanese, 265 Thai, 117 Filipinos, 135 Indonesians, 53 Caucasians, and from a total of 798 unrelated individuals from ten tribes of Taiwan aborigines (141 Yami, 132 Atayal, 66 Saisiyat, 51 Tsou, 38 Rukai, 115 Bunun, 118 Amis, 75 Paiwan, 37

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<sup>11</sup> The first wave that supposedly took place 40,000 years ago involved the dark-skinned people who were hunter-gatherers, and the second wave involved agriculturalists (Austronesians) much later on during the Holocene period (Pawley 2002).

Puyuma, and 25 Pepo).<sup>12</sup> This study show that the highest frequencies of Austronesian-specific mutations (C571T, G849A, C628T, and the 3-pd deletion) are found among Taiwan aborigines, and all of the Austronesian-specific mutations can be found in this region, too. Other studies that connect Austronesian speakers with an origin in Taiwan include that of Kimura et al. (2002), who demonstrated similar *SDF1-3'* *A* allele<sup>13</sup> distribution in Southeast Asia and Melanesia, Ohashi et al. (2006), who demonstrated continuity in the polymorphisms of the *ABO* blood group gene in three populations within the New Georgia group of the Solomon Islands, and Regueiro et al. (2008), who drew links between Austronesian speakers in Madagascar and Polynesia based on the genetic profile of 15 autosomal STR (short tandem repeat) loci. The inferences drawn in these studies, however, conflict with those of other studies based on biparental evidence.

In Oppenheimer's rejection of the converging lines of linguistic, archaeological, and sometimes genetic evidence that support the Out-of-Taiwan hypothesis, he alluded to three different types of autosomal evidence. The first of these is a triplicated gene for Zeta-globin<sup>14</sup> that has been found in Southeast Asia and throughout lowland Oceania (Hill and Serjeantson 1989). Each Pacific population studied also appeared to be carrying a further mutation between two of the triplicated genes. This was not found to be present in Southeast Asia. Oppenheimer (2004a:569) suggested that this indicates "a significant delay somewhere east of Southeast Asia, before dispersal into the Pacific." This is incompatible with the mainstream archaeological view that Neolithic expansion took place very rapidly out of Taiwan. The other two types of autosomal evidence focus on Alpha globin gene<sup>15</sup> haplotypes<sup>16</sup> and Beta-globin gene haplotypes. Concerning the Alpha globin gene haplotypes, the haplotypes that show Asian genetic intrusion in lowland Oceania, which range from 42 to 81 percent, are too widespread in Asia to identify Taiwan as a source. In addition, while Alpha globin genes are normally duplicated, one of these genes may be deleted in some individuals. Oppenheimer stated that two types of deletion can be found in Southeast Asia and the Pacific, and that sufficient time must be given for the observed admixture of both deletions to take place. He identified the main region of admixture between Southeast Asian and Melanesian genotypes to be Wallacea. The implication here appears to be that Wallacea was the center of diversity, and hence the source of movement. Third, Oppenheimer cited Hill (1992), who identified a mutational haplotype of the Beta globin gene that is connected with Beta thalassemia. This mutational haplotype is associated with the region between Indonesia and Near Oceania, and Oppenheimer suggested that this indicates a delay before the Pacific dispersal or gene flow between Austronesian and non-Austronesian populations in eastern Indonesia. Hence, based on studies such as that of Chang et al. (2002) and Oppenheimer (2004a), biparental data both support and contradict the Out-of-Taiwan hypothesis.

Similar observations can be made of mtDNA data. A 9-base pair<sup>17</sup> mtDNA deletion is said to be commonly found throughout East Asia and lowland Oceania, but not in Australia or in the New Guinea Highlands. In phylogenetic terms, Oppenheimer stated that this deletion delineates the root of a haplogroup<sup>18</sup> known as the Asian B haplogroup, and is over 50,000 years old (Oppenheimer 2004b). This

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<sup>12</sup> The plains tribes in Taiwan are also known as Pepo. They include the Katagalan, Kavalan, Taokas, Pazeh, Papora, Babuza, Hoanya, Thao, Siraya, and Qauqaut people (Li 1997).

<sup>13</sup> DNA sequences

<sup>14</sup> Zeta-globin genes are formed from the duplication of the alpha gene into theta and zeta globin genes. While zeta-globin is synthesized in the yolk sac of the early embryo, alpha globin is produced throughout life. See Bruno et al. 1995.

<sup>15</sup> The Alpha globin gene encodes the alpha chain of the hemoglobin protein, which together with the beta gene and the beta globin chain, joins with two others to form the tetrameric adult hemoglobin protein, hemoglobin being the material in the bloodstream that is used to transport oxygen from the lungs to the rest of the body and carbon dioxide back up to the lungs. See Guyton and Hall 2006.

<sup>16</sup> A haplotype is a combination of DNA sequences or alleles at different locus/loci on the chromosome that are transmitted together. See The International HapMap Consortium 2005.

<sup>17</sup> A base pair is formed by two nucleotides or molecules on opposite and complementary DNA strands that are connected by hydrogen bonds. See Scott et al. 2004.

<sup>18</sup> A haplogroup is a group of similar haplotypes that share a common ancestor with a single mutation.

deletion also occurs in East and Southeast Asian and most Native American populations, thus eliminating the notion that it can be directly traced back to Taiwan. In addition, the branch of Asian B haplogroup that is found in lowland Oceania has three more specific mutations at nucleotides 16217, 16261, and 16247. Referred to as the “Polynesian Motif,” this group of specific mutations is said to be found in Polynesia, Micronesia, island Melanesia, lowland New Guinea, and the islands of Wallacea, but not in Taiwan or most of Southeast Asia (Oppenheimer 2004a). It is notable that the immediate ancestor of the Polynesian Motif, which incorporates two of the three mutations, is also found in these regions, and that exceptions include parts of Southeast Borneo just West of the Wallace Line and in Madagascar, wherein an Austronesian language derived from Southeast Borneo is spoken. Oppenheimer then proposed a system of calculating divergence times for the Polynesian Motif molecular clock, which supports the antiquity of the Polynesian Motif, suggesting that an Asian crossing of the Wallace Line took place more than 10,000 years ago, far earlier than the “Express Train from Taiwan to Polynesia” hypothesis predicts.

In a separate mtDNA study by Hill et al. (2007), 929 anonymous, unlinked DNA samples from across various locations in Island Southeast Asia and Taiwan were sampled. The breakdown of this sample includes 170 Sumatrans (42 from Medan, 24 from Padang, 52 from Pekanbaru, 28 from Palembang and 24 from Bangka), 46 Javanese (36 from Tengger, 1 from Yogyakarta, 1 from Banjumas, 1 from Garut, 1 from Jakarta, 1 from Probolinggo, 1 from Semarang, 3 from Solo, and 1 from Wonogiri), 157 people from Borneo (68 from Kota Kinabalu and 89 from Banjarmasin), 2 individuals from Bajawa in Flores, 80 Balinese (including 67 from Denpasar, 3 from Gianyar, 1 from Nusa Dua, 1 from Semarapura, 4 from Singaraja, 2 from Tabanan, and 2 from Ubud), 44 individuals from Mataram in Lombok, 237 individuals from Sulawesi (46 from Ujung Pandang, 38 from Palu, 89 from Manado, and 64 from Toraja), 50 individuals from Waingapu in Sumba, 43 individuals from Ambon, 45 individuals from Alor,<sup>19</sup> 61 Filipinos, and 78 Taiwanese aboriginals (21 Amis, 18 Atayal, 18 Bunun, and 21 Paiwan). Findings were that almost 14 percent of individuals have mtDNA haplotypes that belong to a haplogroup that cannot be found outside Island Southeast Asia (ISEA), and that dates back to ~40,000–70,000 years ago. In addition, even though Hill et al. recognized that the haplogroup associated with the Polynesian Motif is highly diverse in both China and Thailand, and is most common in Taiwan and the Philippines, they dated the mutation to the late Pleistocene. Finally, they identified M7c1c as a plausible mtDNA marker that may potentially indicate a mid-Holocene Out-of-Taiwan dispersal. They stated that this particular mutation, which is very common in China, accounts for about eight percent of the ISEA sample. However, the single mtDNA for M7c1c dates back to ~8,000 years ago, which is older than what would have been expected from the traditional Out-of-Taiwan model. Hill et al. concluded that evidence of dispersals reflects heterogeneity rather than an abrupt transition throughout the early to mid-Holocene, that the strongest trends in the genetic data appear to result from “the movement and expansion of indigenous, rather than introgressive, mtDNA lineages, dating to between ~15,000 and ~5,000 years ago”, and that these lineages relate more closely to those of the Southeast Asian mainland than to those of modern aboriginal Australians and New Guineans (2007:40).

Again, there is also disagreement among the geneticists who are using mtDNA data. Trejaut et al. (2007) identified 96 distinct haplotypes at 81 variable sites of the mtDNA control region in 640 Taiwanese aboriginal samples representing all nine mountain tribes. While they showed that Taiwanese aboriginals share their maternal ancestry with other East Asian populations via haplogroups B, R9, and M7, a separation time of 13,000 to 3,800 years can be obtained from the phylogenetic construction of B4a1a sequences, which points to interaction periods in Indonesia and finally in Melanesia where the complete motif specific to Polynesian B4a1a1 sequences (the Polynesian motif) was developed. Thus, it seems to be the case that there are two possible interpretations with the same type of mtDNA evidence. While Oppenheimer (2004a) focused on divergence time for developing the whole Polynesian motif, suggesting that the Out-of-Taiwan hypothesis is incorrect, since Asian populations must have crossed the Wallace Line more than 10,000 years ago, Trejaut et al. (2007) recognized a more inclusive time period

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<sup>19</sup> Note that most of the languages of Alor are Papuan.

that may be consistent with the picture provided by the archaeological evidence, and focused on the notion that the B4a1a sequences in Taiwan are connected to the B4a1a1 Polynesian sequences.

While both biparental and mtDNA data can be used either to support or to refute the Out-of-Taiwan hypothesis, the Y-chromosomal evidence has been used mainly to oppose the Out-of-Taiwan hypothesis. Oppenheimer (2004b), for instance, indicated that M119 and M122 are the only two common Asian haplogroups that have spread to the Pacific. M119 is uncommon in Oceania, and so is M122, except that the latter reaches 30 to 60 percent in Tahiti and Tonga respectively. Oppenheimer dismissed the Tahiti figure as resulting from historic Chinese migration, and stated that the Tonga figure appears to be a prehistoric founder event, but he did not provide further elaboration, except to say that the analysis of detailed haplotypes indicates no matches with any group from Taiwan (Oppenheimer 2004b). Also in relation to Y chromosomal evidence, Oppenheimer stated that there is a dominant Polynesian Y haplotype that belongs to a widespread ancient Asian “haplogroup 10.” Although found in areas such as India, Borneo, and Wallacea, wherein a new mutation M38 has been identified, this haplotype is significantly absent from Taiwan, as well as from the Philippines. Oppenheimer declared that this may be the male analogue of the Polynesian Motif, and may have originated in early Holocene Wallacea or north coastal New Guinea, and that age estimates posit these areas as locations wherein there could have been early Holocene delay before dispersal into the Pacific. Other studies, such as that Kayser et al. (2000), Gibbons (2001), and Hurler et al. (2002), have suggested the lack of a common specific Y chromosomal element shared by the Taiwanese aboriginals and the Polynesians. However, before it can be concluded that the Y chromosomal evidence shows that there was no migration of Austronesian men out of Taiwan, the caveats with which Y chromosomal data should be used must be understood. As compared to biparental or mtDNA data, Y chromosomal data has been shown to be a less reliable way of understanding genealogy. While the sequences of mtDNA data are clearer, Y chromosomes have unique properties that make them more difficult to prepare (Jobling et al. 1997). Y chromosomes are large, susceptible to a high frequency of parallel substitution, and bear many different types of polymorphisms, as opposed to mtDNA or autosomal evidence. Jobling et al. (1997) stated that the Y chromosome tree’s resolution is low, but will improve as more markers are discovered. Inferences made using Y chromosomal data may thus have to be taken with a grain of salt.

The overall picture provided by geneticists is far from clear. It is important to note that human diversity is apportioned in such a way that various populations differ from each other by less than 7 percent (Lewontin 1972), which is an extremely small target to hit. In addition, there is a range of uncontrolled factors at work, from dating to sampling to non-paternity. Dating methods have always been a concern for researchers interested in examining the past (Renfrew 1989, Oppenheimer 2004a). While linguistics is able to provide relative dating based on the sequences of putative splits within a language family, archaeological events give absolute dates to these prehistoric linguistic events (Pawley and Ross 1995). This view is not shared by Oppenheimer, who suggested that “the best proxy for charting population processes should be genetic” (2004a:592). However, some caveats are needed about the use of genetic dating. In genetics, absolute dates for population divergence are usually built on molecular phylogeny, and “a molecular ‘clock’ measuring a constant speed of genetic divergence is accepted a priori” (Blench et al. 2008). There are five problems that Blench et al. (2008) identified in relation to carrying out genetic dating, since molecular clocks are normally calibrated against absolute dates for the common ancestors of humans as well as chimpanzees based on the fossil record. First, there is a lack of well-documented paleontological evidence for these dates (Stauffer et al. 2001), and second, the arbitrary choice of the outgroup also causes problems, as apes exhibit a much higher level of intra-specific genetic divergence than humans (Gagneux et al. 1999). Third, Blench et al. stated that “genetic dates are usually inferred with such large confidence intervals that they can easily match multiple historical or cultural events and thus satisfy any hypothesis defended *a priori* by the researcher” (2008:8). Fourth, Blench et al. stated that “genes are not people and there is no reason for the nodes of a phylogenetic tree (the MRCA) to correspond to identifiable events in population history, such as migrations or differentiations” and that “[i]n reality, genetic tree nodes are usually older than population events” (2008:8). Finally, it cannot be assumed that the rate of evolution of gene frequency is constant. Small populations tend to see a faster

rate of evolution, while larger populations tend to experience a slower rate of evolution. Thus, based on this appraisal, the claim by Oppenheimer (2004a) that genetic dating is the best proxy for charting population processes is clearly problematic. Instead, a multidisciplinary approach combining the resources of linguistics, archaeology, and genetics should be preferred.

Next, with regard to sampling, one of the dangers in population genetics is that of sample size. Blench et al. stated, “DNA typing technologies allow us to define haplotypes at a much more precise level than before, such that the number of detectable haplotypes is always higher than the number of individuals sampled (which was not the case with studies based on blood groups or proteins)” (2008:13). This means that sampling should be done even more carefully than ever, and that the number of samples involved has the potential to affect the results of the genetic studies itself. In this regard, it needs to be recognized that there are studies that do not mention how sampling sizes are managed. For example, Oppenheimer (2004a) did not indicate sample sizes in the studies he cited. It is also clear that the sampling numbers were not the same across these studies. In discussing the Polynesian Motif, he alluded to having used drastically different sample sizes. He stated that the New Guinea data sets used in Oppenheimer (2004b) for the mtDNA study were “much larger” than the ones used for Wallacea (Oppenheimer 2004a:597). His use of data sets of varying sizes thus has repercussions for the quality of the genetic dating he suggested. Similarly, in Hill et al. 2007, sample size ranged from one sample from Yogyakarta to 89 samples from Manado. Sample sizes are said to affect genetic dating—larger populations usually result in a slower rate of evolution being calculated and vice versa (Blench et al. 2008).

Also, with regard to sampling frames, most of the studies cited in this paper do not provide information on how the population groups are delineated. For example, although Hill et al. attempted to be as comprehensive as possible by including a large number of samples from varied sources, it is unclear as to whether these groups are defined in terms of ethnolinguistic or geographical characteristics. Selecting a sample from Jakarta, for example, is not the same as selecting a sample from Bunun. While the former may not necessarily correlate with a viable ethnolinguistic group, the latter does. This begs the question of how representative the study can be if there are no clear guidelines established for which samples are to be used. Targeted sampling that is ethnolinguistically viable is required in order to establish genetic profiles that are as reflective of distinctive groups of people as possible.

Also related to sampling, it is important to note that non-paternity is a problem when people self-report their parentage (Anderson 2006). Figures usually cited for non-paternity are 9 percent (Baker and Bellis 1995) or 10 percent or greater (Alfred 2002, Cervino and Hill 2000). These no doubt affect interpretations of genetic evidence. In a comparison of mitochondrial and autosomal STR genetic distances among 28 Pacific Island and Asian populations, substantial affinities were observed in the autosomal STR data between Remote Oceanic Islanders and Near Oceanic populations from highland Papua New Guinea and Australia, as opposed to mtDNA data, even though the samples were taken from the same populations (Lum et al. 1998). This led Lum et al. to suggest that “dispersal events that resulted in successful colonization differed in sex ratio from those involved in trading, warfare, and perhaps exploration” (1998:621). Statements such as these provide an interesting perspective on migration if non-paternity can be ruled out.

Finally, where genetic data are concerned, it is important to note that the interpretation of genetic results is no more or less scientific than the interpretation of linguistic or archaeological evidence. While Oppenheimer (2004a) should be commended for presenting data that oppose the mainstream view of linguists and archaeologists, he still showed a blatant disregard for what is not explainable. For example, with regard to the intrusive Asian Y-chromosomal lineages in the Pacific, Oppenheimer admitted that evidence of the M122 Asian haplogroup shows that while there had been historic Chinese immigration in Tahiti, the migration to Tonga appears to have been a prehistoric event. However, instead of explaining why there should have been a Chinese Y-chromosomal lineage in the Pacific, Oppenheimer dismissed this simply by stating that the detailed haplotypes indicate no matches with Taiwan (2004b).

In that last regard, multiple proxy lines of evidence are more valuable than ever, for two reasons. First, that there are more stakeholders invested in an overarching goal means that there can potentially be a more stringent system of checks and balances involved in the process of research itself. Next, arguments

are made stronger when findings from different disciplines corroborate or complement one another. It is however perhaps necessary to add another caveat here—that it may be dangerous and inaccurate to say that a finding is weak when it conflicts with the findings from a separate discipline, especially when researchers from one field do not understand the assumptions and methods that have been employed in another field. For example, Renfrew's (1989) and Oppenheimer's (2004a) caveat<sup>20</sup> against linguistic palaeontology reveal a lack of understanding of what linguistic palaeontology is and the significance of its contributions. In relation to this, it is also inaccurate to say that a particular finding from one field is weak because it conflicts with the findings from more than one other field. Thus, although it may be easier to find congruence between archaeology and linguistics than between archaeology/linguistics and genetics (Blench et al. 2008), it does not mean that the role of genetics is not valuable. In fact, genetics can be regarded as a line of evidence that is used to dismiss alternative hypotheses. For example, due to the lack of genetic evidence, the homeland of the Austronesians cannot be Siberia, Japan, Tibet, India, and certainly not South America.

**5. CONCLUSION.** Contrary to Oppenheimer's (2004a) assumptions that interdisciplinary research should be corroboratory—that the lines of evidence are meant to run parallel to one another without affecting each other, this paper argues that the true nature of interdisciplinary research should allow for complementary and contradictory inferences to be made across the disciplines. Complementary inferences are especially important when one discipline can shed light on an area that another discipline is unable to explain. For example, linguistics can provide a fuller perspective on perishable material items or even a non-material cultural past (Blust 1996), where it would be difficult for archaeologists to unearth evidence. In addition, where archaeologists may be reluctant to infer that archaeological cultures were ancestral to modern populations in the same areas, continuity may be found in genetic or linguistic evidence. Similarly, for those who view languages as a single meme, archaeology and genetics can provide other cultural and genetic links. Besides complementary inferences, contradictory inferences are also important, because they can highlight potentially problematic assumptions and gaps that have to be addressed. For example, the contrast in dating between genetics and archaeology (archaeological dates of 3,000–4,000 BC versus mtDNA dates of 13,000 to 3,800 years ago for the Austronesian expansion) tell us that more can possibly be done in terms of strengthening genetic dating.

With regard to the roles of linguistics, archaeology, and genetics in establishing the Austronesian homeland, this paper shows that whereas the individual lines of evidence from linguistics and archaeology support an Out-of-Taiwan hypothesis, genetics does not provide a coherent scenario for or against the Out-of-Taiwan hypothesis. While genetics may be used to dismiss alternative hypotheses, issues of dating, sampling, and non-paternity have to be addressed before it can truly be used in conjunction with linguistics and archaeology.

Finally, the mistaken assumptions made about archaeology and linguistics in studies such as those of Oppenheimer (2004a) and Hill et al. (2007) show that cross-disciplinary communication is important and necessary. In order for a discipline such as genetics to be viable in reconstructing the past, it must learn from the lessons of other disciplines as well.

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<sup>20</sup> Both Renfrew (1989) and Oppenheimer (2004a) suggested that linguistics and archaeology should not rely on each other's evidence for proposing arguments crucial to their own fields, while Oppenheimer (2004a) was of the view that linguistic palaeontology should not be used in reconstructing the Austronesian homeland.

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