

# The 'Express Train from Taiwan to Polynesia': on the congruence of proxy lines of evidence

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## Abstract

Renfrew's concept of an Indo-European expansion was carefully hedged with strict caveats to avoid earlier methodological and political pitfalls. His 'farming-language dispersal' hypothesis has inspired others to seek similar examples among other language families. This review argues that the model has gone awry in one of these, the 'Express Train from Taiwan to Polynesia' hypothesis. The persistence of the Austronesian language/rice-farming hypothesis results from a cluster of methodological errors that include an overall failure to heed Renfrew's caveats, over-reliance on a controversial putative linguistic homeland and failure to deal with parallel evidence impartially, resulting in unsupported claims of congruence.

## Keywords

Island Southeast Asia; Austronesian; genetics; physical anthropology; historical linguistics; migration.

## The origin of the farming-language dispersal hypothesis

After the Second World War, linguistic-racial migrationism fell into disrepute. In 1987 Renfrew (1989: 3–24) reconsidered Indo-European origins. Phylogeographic analysis of related languages was central to his model, but he warned against the pitfalls of 'linguistic palaeontology' (cultural reconstruction based on reconstructed proto-words for cultural items). He pointed out that language groups, human groups and pots do not necessarily equate with each other, and that individual cultural items can move independently of cultural packages or people. He also accepted Ammerman and Cavalli-Sforza's (1984) genetic 'wave-of-advance' model. The archetype of the farming-language dispersal model thus explicitly specified both genetic and cultural diffusion, rather than just population invasion and replacement.

Renfrew (1989) recognized the importance of dating language splits directly using linguistic evidence, rather than inferring them from archaeological evidence, to avoid circular arguments. The same applies to any proxy for the past, cultural or biological. Clearly the best proxy for charting population processes should be genetic, and again internal dating, however fraught with imprecision, is necessary to avoid circularity in arguments of congruence. Careful modelling and analysis of the dates for founding mitochondrial genetic lines in Europe by Richards (2003) have gone a long way to separate Neolithic expansions from the Near East from re-expansions of *in situ* Palaeolithic populations.

Debate will continue, but Renfrew's carefully argued caveats together with new methods of genetic phylogeography (Richards 2003) provide an objective framework for evaluating the fifteen other candidates for prehistoric farming-language dispersal events proposed by Diamond and Bellwood (2003). In August 2001 a multidisciplinary conference was convened by Renfrew and Bellwood to do just this. No cross-disciplinary consensus was reached at this conference on the Austronesian example (see Shouse 2001; Oppenheimer and Richards 2003).

### **Concordance in proxy evidence**

Diamond and Bellwood have argued that there are two uncomplicated examples of prehistoric farming-language dispersals, supported by 'clear concordance' between five separate lines of evidence. This changes the basic paradigm from Renfrew's 'wave-of-advance' to an explicit 'replacement' model. Their exemplars are the 'Bantu' farming expansions in Africa, and the 'Express Train from Taiwan to Polynesia' (ETTP). In their words:

The simplest form of the basic hypothesis... is that farmers and their culture replace neighbouring hunter-gatherers and the latter's culture. This hypothesis would be supported if all five independent types of evidence coincided in attesting the replacement of local hunter-gatherers by expanding farmers bearing their own archaeologically visible culture, domesticates, skeletal types, genes, and languages, and if all those indicators were traceable back to the farmers' homeland of origin. Our two clearest examples of such concordance of evidence are... Neolithic populations speaking Austronesian languages (Fig. 2, no. 8), and the expansion of farmers speaking Bantu languages.

(Diamond and Bellwood 2003: 598)

Their term 'replacement' clearly applies to the full extent of the ETTP hypothesis (trail 'no.8' as shown in their Fig. 2) although, strictly speaking, the final 'colonizations of previously uninhabited Polynesia and Micronesia' should not be called replacement. The Bantu example may be an excellent genetic and cultural case (Salas et al. 2002). The ETTP hypothesis is another matter.

The ETTP hypothesis is dependent on (a) rice agriculture driving a Mongoloid expansion into the Philippines and Southeast Asia that largely replaced indigenous

Australo-Melanesian hunter-gatherers (Bellwood 1997: 69–95); (b) the orthodox Austronesian language tree for geographic structure from Asia to the Pacific, and a Taiwanese origin (*ibid.*: 96–127); and (c) ceramics – red-slipped pottery in Southeast Asia from 2000 BC, and dentate-impressed red-slip Lapita pottery in the south-west Pacific from 1500 BC – as the proxy for dating the proposed migration stages (*ibid.*: 219–36).

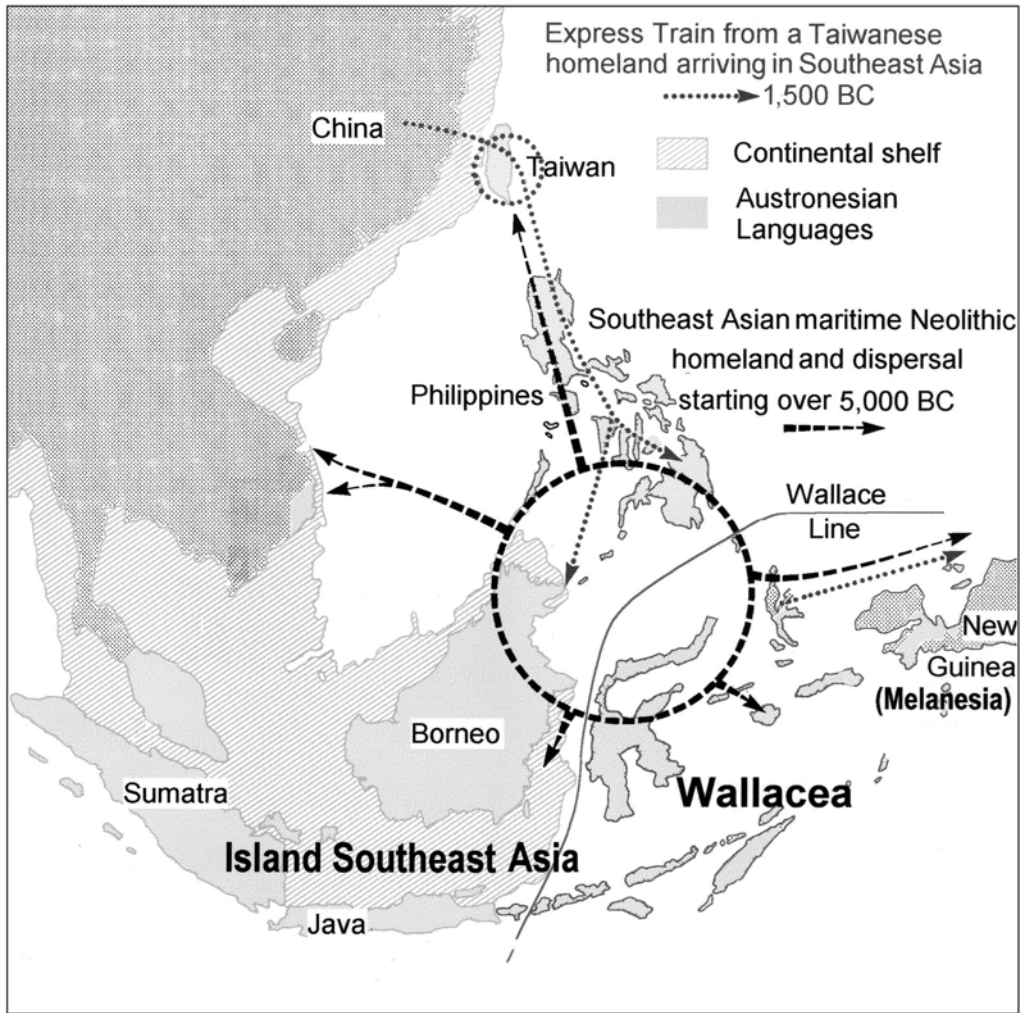
The chief point of agreement between dissenters and the ETTP hypothesis is the near congruence of disciplines on the furthest lap of the journey, namely the colonization of Polynesia. Dissenters argue that this eastern congruence should not be used in grand reconstruction to bolster the lack of congruence further west in Near Oceania, Wallacea and Southeast Asia, or the primacy of Taiwan as the migration source homeland.

Of the five lines of proxy evidence from Taiwan to Polynesia, archaeologically visible culture and domesticates are not the remit of this review; however a convincing archaeological rebuttal was available from the start by Meacham (1984–5) against the archaeological case made for the choice of Taiwan as the homeland. Terrell (1986: 59) and Solheim (1996) have also argued for island Southeast Asia (ISEA: Fig. 1) as the early Holocene homeland of these maritime Neolithic cultures. The hypothetical domesticate trail starts in Taiwan with rice, but rapidly shifts in island Southeast Asia (ISEA) and Near Oceania to other domesticates such as coconuts and other tree crops, bananas and root crops (Latinis 2000), which were already being exploited in Wallacea and/or New Guinea before the mid-Holocene. The ETTP rice trail from the Philippines into Wallacea and its putative association with red-slipped pottery has also been deconstructed (Paz 2002). Since archaeology, including the archaeology and biology of these domesticates, is being discussed by others in this issue, I shall focus here on the three other proxies.

## Language

The ETTP hypothesis uses language history reconstruction to identify Taiwan as the homeland of the Austronesian speakers. The evidence for Taiwan rather than the Philippines, the main alternative, is however 'controversial' (*sic*) (Pawley 2002: 260). Despite Renfrew's caveat against 'linguistic palaeontology', the latter is used explicitly in the Taiwan argument (Bellwood 1997: 96–127). This is surprising in view of the evidence: Blust's (1985) landmark paper shows that the Formosan languages have an impoverished set of reconstructed cognates covering little of the sailing technology, ceramics or animal and plant domesticates of the Austronesian dispersal regions. Terms for most domesticates are reconstructed instead to languages of island Southeast Asia (Blust 1985), which fits the biological and archaeological evidence for the likely sites of domestication (Latinis 2000). The only crops clearly reconstructing in Formosan Austronesian languages are rice and millet.

The ETTP hypothesis ignores Renfrew's caveats by using archaeological, not linguistic, dating for the putative language splits. Apart from circularity and the risk of choosing archaeological dates that fit a preferred linguistic narrative, this practice ignores language evidence that gives older dates. Even Blust's (1985) linguistic dates of around 3500 BC for the first split east of the Wallace Line (Fig. 1) are rejected. Archaeologically derived estimates are used instead (Bellwood 1997: 119).



*Figure 1* Two main alternative views of Polynesian origins, Asian mainland and offshore. The oldest view (interrupted solid black line and circle) argues for an Island Southeast Asian maritime Neolithic homeland ( $> 5,000$  BC) (Terrell 1986: fig. 19; Solheim 1996; Oppenheimer 1998: 78–112). The ‘out of Taiwan’ view of a recent rapid migration from China via Taiwan, spreading to replace the older populations of Indonesia after 2,000 BC, is shown as a dotted line.

Abandonment of linguistic dating removes much force from the linguistic argument. This is a pity, because the linguistic evidence clearly has something important to say. The distribution of the Oceanic branch of Austronesian suggests that its nine branches arose from a common source somewhere near New Guinea, but this does not preclude earlier Austronesian linguistic expansions, and evidence for a ‘pre-Proto-Oceanic’ substratum has in fact been pointed out in northern New Guinea (Ross 1988: 21); but this is not consistent with the tightly constrained dates and single rapid movement envisioned by the ETPP hypothesis (Bellwood 1997: 118).

## **Physical anthropology**

According to Diamond and Bellwood (2003: 598), human 'skeletal types' support the identification of Taiwan as the Austronesian biological 'homeland'. Elsewhere Bellwood (1997: 87) has argued that 'the most likely hypothesis is that Southern Mongoloid populations have entered the archipelago from the north, mainly via the Philippines as far as Austronesian expansion is concerned'. Thus 'replacement' explicitly replaces Renfrew's use of Ammerman and Cavalli-Sforza's 'wave of advance' model.

The published data in fact do not support the ETTP hypothesis of Neolithic racial/ethnic replacement. There is minimal evidence for it in the patchy skeletal record (Hanihara 1993). Craniometric evidence links modern Polynesians only remotely with China and Taiwan, showing instead closer links with island Southeast Asia, in particular the Sulu Sea (Pietrusewsky 1996). Some argue for a striking alternative. Building on work by Bulbeck (1982) and Hanihara (1993), Storm (1995) argues for local morphological evolution of 'Southern Mongoloid' types in Southeast Asia. Bellwood (1997: 91–2) uses archaeo-linguistic arguments to reject this skeletal argument.

The local morphological evolution model is however supported by Turner's work on dental evidence (Turner 1987, 1990; see also Rayner and Bulbeck 2001). Taiwanese teeth dated 4000–1500 BP group with China and Northeast Asia rather than Southeast Asia, tending to sinodont rather than sundadont in Turner's (1987) classification. Sundadonty characterizes 'Southern Mongoloids' of Indo-China, island Southeast Asia and Polynesia, and is regarded as ancestral to the sinodonty of 'Northern Mongoloids' of China, Northeast Asia and Native Americans (Turner 1990). Sundadont features characterize 'Aboriginal Malay' populations of the Malay Peninsula (Rayner and Bulbeck 2001), who have mitochondrial DNA lines ancestral to those of China and the Americas (Oppenheimer 2003: 229–35). Under the out-of-Taiwan hypothesis, Wallacea and Polynesia should have become more sinodont, while western Indonesia and Indo-China should have remained sundadont, resulting in an east–west cline – the opposite of what is actually found (Oppenheimer 2003: Fig 5.4; Rayner and Bulbeck 2001; Bulbeck 2000).

## **Genetic evidence**

Diamond and Bellwood (2003: 598) argue that genes coincide with the four other proxies in supporting the ETTP hypothesis. This claim is testable. The trail should be clear and proportional to the degree of migration. Wave of advance effects might be modest (e.g. < 20 per cent, Richards 2003), while replacement on the scale suggested by Diamond and Bellwood (2003) should involve over 50 per cent.

The time interval between the arrival of Asian immigrants in the Philippines and the later Lapita dispersal from the Bismarck Archipelago to Polynesia is said on archaeological evidence to be *c.* 1,000 years (Bellwood 1997: 118). If so, aboriginal Taiwanese, Philippine, Wallacean and Polynesian gene lines should all share specific

genetic innovations. But hypotheses of longer-term local evolution within island Southeast Asia would predict genetic innovations shared between island Southeast Asia and the Pacific, which should trace back to island Southeast Asia or Wallacea, but *not* to Taiwan (Fig. 1). These two predictions can be tested and compared.

The combination of detailed results from many genetic studies reveals a gross genetic dissimilarity between Taiwan and Polynesia at multiple loci, in type, specificity and proportion. There are insufficient genetic links to support even a small wave of advance from Taiwan. In contrast, Wallacea consistently supplies such links (reviewed in Oppenheimer 2004). Even as long ago as 1989, Hill and Serjeantson found no convincing specific links between Polynesians and Chinese, but found several between Pacific and Southeast Asian people. They concluded that 'Polynesians... are mainly derived from a Southeast Asian population prior to Mongoloid expansion' (1989: 286). Such intrusive genetic links from Southeast Asia to the Pacific, and many others noted since, may be discussed under the three categories: *autosomal* (derived from both parents), *maternal* (using mitochondrial DNA) and *paternal* (using the Y chromosome).

#### *Autosomal evidence*

Hill and Serjeantson (1989: 286–7) noted a triplicated gene for Zeta-globin found both in Southeast Asia and throughout lowland Oceania. This harmless gene triplication arose in Southeast Asia (*ibid.*), but, significantly, each Pacific population studied also has a subset carrying a further mutation between two of the triplicated genes, which is not present in Southeast Asia. This suggests a significant delay somewhere east of Southeast Asia, before dispersal into the Pacific.

Alpha globin gene haplotypes (mutations in the DNA region immediately flanking the genes for 'alpha globin') indicate that most of lowland Oceania is an area of Asian genetic intrusion ranging from 42 to 81 per cent, but the marker haplotypes are too widespread in Asia to identify a source and certainly do not point to Taiwan (Oppenheimer 2004). The Alpha globin genes themselves are normally duplicated on the same chromosome, but one of these twin genes may be deleted in some individuals. Two of these single-gene-deletions occur in *both* Southeast Asia *and* the Pacific. The flanking DNA alpha haplotype is typically Oceanic (type IIIa) for all the Oceanic deletion types and typically Southeast Asian (Ia & IIa) for the respective Southeast Asian deletion types. For the same two deletions to have acquired Oceanic flanking haplotypes as they moved out to the Pacific, the source of dispersal must have been an area that had significant admixture of both types of alpha deletions, and also both Asian and Pacific flanking alpha haplotypes respectively, over a sufficient period of time for *gene conversions* (Hill 1992: 218–22) to occur. The main region of admixture and transition between Southeast Asian and Melanesian genotypes (and phenotypes) is Wallacea (Fig. 1).

Mutational haplotypes have been worked out for the Beta-globin locus. One common variant-specific mutation of the Beta globin gene causing Beta thalassaemia has been shown to change its flanking DNA type between Indonesia and Near Oceania (Hill 1992: 222). This also suggests delay before the Pacific dispersal.

### *Mitochondrial DNA*

A 9-base-pair mtDNA deletion is commonly found throughout East Asia and lowland Oceania, but not at all in Australia or the New Guinea Highlands. This indicates Asian intrusions onto a blank Pleistocene Pacific genetic canvas, but not a specific link to Taiwan. The deletion defines the root of the Asian B haplogroup and is over 50,000 years old (Oppenheimer 2004). It occurs in East and Southeast Asian and most Native American populations, which eliminates it as a specific trail-marker: someone with this trait could equally have come from Taiwan, Tonkin, Timor or Texas, a point still not appreciated in some archaeological reviews.

However, the small branch of the Asian B haplogroup that dominates lowland Oceania has three further specific mutations (at nucleotides 16217, 16261 and 16247). This 'Polynesian Motif' (PM) is the commonest mtDNA type in Polynesia (75–90 per cent) and Micronesia (25–50 per cent). It is also found in substantial frequencies throughout island Melanesia, lowland New Guinea and the islands of Wallacea, but *not* in Taiwan or most of Southeast Asia. However, its immediate ancestor (with only two of the three mutations) is present in all those regions as well as in Oceania. The PM is rare west of the Wallace Line; exceptions include small pockets in S.E. Borneo just west of the Wallace Line, and famously Madagascar, whose inhabitants speak an Austronesian language derived mainly from S.E. Borneo. The distribution of the final PM genetic innovation places Wallacea as the likely source of the commonest maternal genotype in lowland Oceania.

The diversity in derivatives of the PM allows us to examine the delay in spreading from Wallacea. This shows that there was a succession of colonization events as the PM spread into the Pacific (Oppenheimer 2004). Due to founder effects (small groups of arrivals exaggerating the high frequency of the PM compared to its derivatives), each fresh colonization effectively sets the PM molecular clock back to zero. When the divergence times are calculated, the estimated colonization of western Polynesia (Samoa) and eastern Polynesia (Cook Islands) of 3,000 and 1,000 BP respectively, correspond fairly well with known archaeological dates (Oppenheimer and Richards 2003). Wallacea has the oldest estimate for the PM at 17,000 years, but this figure has a high standard error. Two independent estimates based on much larger data sets from New Guinea produce > 10,000 years (Oppenheimer 2004). While these may be overestimates due to diversity carried from Wallacea, it does support the great antiquity of the PM here and suggests an Asian crossing of the Wallace Line far earlier than the ETPP hypothesis predicts.

### *Intrusive Asian Y chromosome lineages in the Pacific*

M119 and M122 are the only two common Asian haplogroups that have spread to the Pacific. They present a different picture from other loci, indicating a relatively small intrusion with near absence in New Guinea. M119 is uncommon throughout Oceania, while M122 is especially so in Near Oceania, but reaches 30 per cent and 60 per cent respectively in Tahiti and Tonga. The Tahiti figure results from historic Chinese immigration, but Tonga does however appear to be a prehistoric founder

event. Analysis of detailed haplotypes indicates no matches with Taiwan (Oppenheimer 2004).

*An Oceanic Y sub-type to match the Polynesian Motif*

The apparently low Asian Y intrusion into the Pacific might reflect a predominantly ‘Melanesian’ origin of Polynesian Y chromosomes. However, this does not agree with the estimates for Asian autosomal or mtDNA intrusions (see above). On the other hand a Wallacean gene line fits better than any indigenous ‘Melanesian’ Y markers. The dominant Polynesian Y haplotype (50–80 per cent) belongs to a widespread ancient Asian ‘haplogroup 10’ (Hg10) defined by an RPS4Y marker. An early introduction to Asia and Australia in the Late Pleistocene (Oppenheimer 2003: 184–93), Hg10 is mainly found in those regions as locally mutated derivatives, although it is notably absent from Taiwan and the Philippines. The root ancestral form has been found only in India, Borneo and Wallacea – the latter a region where Hg 10 has acquired a new Oceanic mutation M38. M38 is the only Hg10 type found in the rest of the Pacific. This could be the male analogue of the Polynesian Motif: it is ultimately Asian, may originate in early Holocene Wallacea or north coastal New Guinea, is absent from the New Guinea highlands, and is common in Polynesia. Age estimates are *c.* 11,500 years for the western Pacific, with a later expansion signal dated *c.* 5,000 BP. In Polynesian groups a strong expansion signal appears dated to *c.* 2,200 BP, indicating multiple pulsed expansions at different times (Kayser et al. 2000). Once again the New Guinea lowlands or Wallacea are likely locations for the early Holocene delay before dispersal into the Pacific.

## Conclusions

None of Diamond and Bellwood’s five ‘lines of evidence’ confirms the ETTP hypothesis individually, let alone showing concordance. (1) Rooting the Austronesian language tree in Taiwan is still acknowledged to be controversial even by its adherents; (2) prehistoric rice agriculture has not been demonstrated in Wallacea or anywhere further east at the right dates, nor was it associated with red-slipped pottery; (3) the domesticates transported into the Pacific came from New Guinea, Wallacea and Southeast Asia, not China or Taiwan; (4) skeletal evidence has not demonstrated Neolithic replacement, and is ambivalent on local evolution in Southeast Asia *vs.* immigrant ‘southern Mongoloids’; and (5) genetic evidence shows Southeast Asian intrusions into the Pacific, but no specific Polynesian roots in Taiwan. In contradiction to the ‘Late Holocene Express Train’, prolonged delay of these intrusive lines is likely in Wallacea and/or lowland New Guinea before the Late Holocene expansion to Polynesia.

Renfrew hedged the farming-language dispersal hypothesis with methodological caveats, partly due to historic mistakes made regarding the Indo-European story. But the most important caveat was that each of the multiple lines of evidence requires its own dating method if self-fulfilling assertions and circularity are to be avoided.



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