

# Reconnecting Genes, Languages and Material Culture in Island Southeast Asia: Aphorisms on Geography and History

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## Abstract

The Holocene history of Island Southeast Asia (ISEA) is dominated by the ‘Out-of-Taiwan’ hypothesis and derivatives, such as the spread of the Island Southeast Asian Neolithic. According to these ideas, approximately 4500–4000 years ago, farmer-voyagers from Taiwan migrated southward into ISEA to subsequently acculturate, assimilate or displace pre-existing inhabitants. These processes are considered to have produced a consilience between human genetics, Austronesian languages and the archaeological record within ISEA, although recurrent critiques have questioned these putative correspondences. These critiques have proposed that each line of evidence should be independently evaluated and considered, rather than assumed to correspond.

In this paper, the authors advocate a fuller engagement with and a deeper understanding of the spatial and temporal processes that structure archaeological, genetic and linguistic distributions within Island Southeast Asia. Geography and history are often marginalized in discussions of the Holocene history of ISEA, yet both are fundamental to the interpretation and reconciliation of multidisciplinary data within the region. These themes are discussed using aphorisms that are designed to be illustrative, namely to promote thought and reflection, rather than to be comprehensive.

## Keywords

Austronesian; archaeology; genetics; areality; phylogeny; Island Southeast Asia

## 1. Introduction

In this discursive and intentionally provocative paper, a series of propositions are advanced to account for observed distributions and historical interpretations of genes, languages and material culture in Island Southeast Asia (ISEA). These propositions are intended to illustrate some fundamental problems with the nature of existing historical interpretations within the region. The observations made in this paper are not intended to be comprehensive; rather, they are

designed to promote reflection and reassessment of the region's multidisciplinary history. While we do not believe that the same problems necessarily pertain to other regions, we are confident that the methodological lessons learned for ISEA are relevant for attempts to construct metahistorical interpretations, or historical metanarratives, using multidisciplinary data in other parts of the world.

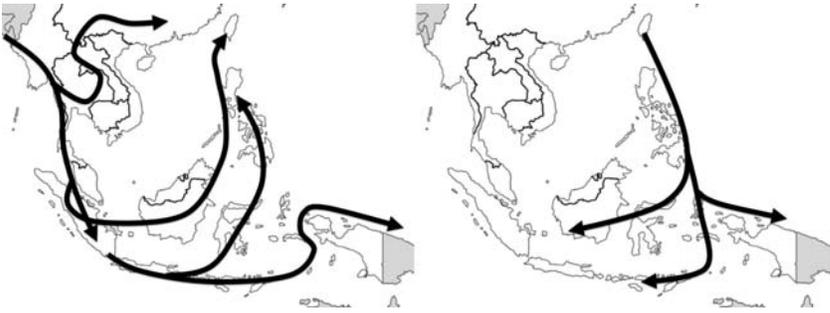
We begin by discussing discordances between genetic, linguistic and archaeological data using case studies at multiple spatial scales within ISEA. Following this, several emergent themes are raised that need to be more fully considered in the long-term multidisciplinary histories of ISEA. We conclude with a set of working principles that should be employed when considering the interpretation of data, whether from a single discipline or from a range of disciplinary sources; these emphasize the complex nature of human societies and their social histories.

## **2. Evidential Considerations: From the Comparative to the Contextual**

A key aspect of historical research is to understand the indeterminate relations between more abstract structural concerns and the more empirical level of individual human agency (from Marx, 1987 [1852] to Braudel, 1972, to Giddens, 1984; see Hodder, 1999). Indeed, understanding the role of economic, political and social structures with respect to the role of individual and group choice in determining historical processes is central to most disciplines within the humanities. Indeterminacy is often marked by a dynamic tension between comparative and contextual approaches, which often characterize historical investigations at the macro- and micro-scales, respectively (Denham, 2011). These issues are discussed here with respect to case studies at different analytical scales within ISEA.

### *2.1. Macro-scale 1: Comparative Study of Autosomal Genetic Phylogeny and Austronesian Language Dispersal across ISEA*

The HUGO Pan-Asian single-nucleotide polymorphism (SNP) consortium (2009) provides a robust human genetic phylogeny for large parts of mainland South East Asia (mSEA) and ISEA, including Taiwan, the Philippines, Indonesia and Malaysia. Autosomal DNA variation indicates primary directions of human movement from west to east and from south to north, movements which seemingly accord with the original colonization of Southeast Asia by modern humans during the Late Pleistocene (Fig. 1; cf., e.g., Macaulay et al., 2005). The directionality of language spread inferred is almost consistently opposite to that inferred from historical linguistics using the comparative method (e.g., Blust, 2009, for Austronesian languages). HUGO (2009: 1543) suggests the discrepancies between genetic clades and linguistic affiliation are 'consistent either with substantial recent admixture among the populations [...], a history of language replace-



**Figure 1.** The non-concidence of genetic and linguistic flows (from Donohue and Denham, 2011: Fig. 2). The maps indicate the spread of two different phylogenies, inferred using normal phylogeographic principles (e.g., Avise, 2000, and see also Blust, 2009). The map on the left shows the spread of the autosomal DNA reported in HUGO (2009). The map on the right indicates the (approximate) spread of Austronesian languages, following Blust's subgrouping (note that it would be equally probable, reading Blust, to have an additional branch joining the Philippines directly to Borneo).

ment [...] or uncertainties in the linguistic classifications themselves [...]. In short, the authors of HUGO are unable to account for the gene-language discrepancies, which also occur in studies of mtDNA and Y-chromosome data (Capelli et al., 2001; Hurles et al., 2005; Kayser et al., 2008; Li et al., 2008; Soares et al., 2011), whenever a large sample of Asian populations is included.

The autosomal DNA distribution is surprising given the near-wholesale replacement of pre-existing languages by Austronesian languages within ISEA during the Holocene. Consequently, the spread of contemporary language families was not associated with a significant transformation in the genetic composition of human populations within ISEA, as often claimed (e.g., Diamond and Bellwood, 2003; Bellwood, 2005). However, this does not deny that there are contributions from Taiwan within ISEA, as well as from other regions (e.g., Xu et al., 2012); but these contributions do not represent the wholesale replacement or even absorption of pre-existing populations (following Oppenheimer and Richards, 2001). Rather, they account for maximally 20% of Y chromosome variation (Capelli et al., 2001) and at most 20% of mitochondrial DNA (mtDNA) variation (Hill et al., 2007).

Instead of linking genetic and linguistic dispersals within ISEA, the generally contiguous distribution of linguistic subgroups in space correlates with the prehistoric population divergence of genetic markers (HUGO, 2009: 1544). Nichols and Peterson (1998: 612) note in a different context that 'biological genetic features have geographically based rather than linguistically based

distributions.’ We concur and add that genetic groupings within ISEA correlate with linguistic classifications only in those circumstances in which the phylogeny of the linguistic family spreads out across contiguous regions in space (see Donohue et al., in press). These findings indicate the primacy of social geography in unraveling the historical processes that account for the gross distributions of genetic and linguistic attributes at the comparative level within ISEA.

## 2.2. Macro-scale 2: *Decoupling the Language/Farming Dispersal within ISEA*

The idea of genetic and linguistic concordance within ISEA is predicated on the Out-of-Taiwan dispersal of Austronesian language speaking farmer-voyagers (Bellwood, 1995, 2002, 2005, 2007; Diamond and Bellwood, 2003). The demic expansion from Taiwan into ISEA is considered to have been facilitated by the competitive advantage derived from agriculture of these migrants with respect to pre-existing populations of hunter-gatherers or neonate horticulturalists (Bellwood, 2007). Consequently, it has been repeatedly argued—and asserted—that the expansion from Taiwan consisted of people, languages and farming that all left concordant genetic, linguistic and archaeological signatures (e.g., Diamond and Bellwood, 2003; Xu et al., 2012). Such propositions consistently underpin multidisciplinary research on the long-term history of ISEA.

However, such interpretations are unfounded because there is scant archaeological evidence for the dispersal of agriculture into ISEA from Taiwan or East Asia beyond the introduction of pigs into northern Luzon around 4500–4000 years ago (Piper et al., 2009; see Donohue and Denham, 2010, for a review). There is limited reliable evidence for the contemporary introduction of rice into ISEA (see Paz, 2002, 2005), although finds include rice at Andarayan in northern Luzon dating to c. 3500 years ago (Bellwood, 2004). Most early rice is associated with pottery, including often as impressions or inclusions, suggesting to Paz (2002) that it was potentially derived from extralocal trade.<sup>1</sup> Claims for earlier introductions to Borneo (i.e., Datan, 1993; Barker et al., 2011b) should be

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<sup>1</sup>) This interpretation does not deny the linguistic evidence for rice, other crops and associated technology (summarized in Pawley, 2007). We note the absence of robust archaeological support for an early (c. 4000-year-old) dispersal of these crops, and the fact that these new crops did not supplant earlier subsistence practices. These considerations, combined with the well-documented possibility of languages ‘repairing’ sound correspondences in neologisms (e.g., Weinreich, 1953 and others), suggest that the historical processes involved in the dispersal of rice, other crops and associated technologies are uncertain and need not be contemporaneous with the spread of Austronesian languages, or of other traces in the archaeological record.

treated cautiously, as they are uncertain in terms of domestication status and species identification. Furthermore, there is no reliable archaeological evidence dating to c. 4000 years ago for the introduction into ISEA of any agricultural technology or other cultivated plant from Taiwan or East Asia. Indeed, the existing evidence seems to suggest that agricultural practices within ISEA that likely facilitated the expansion of Austronesian languages there and in the Pacific were indigenous or derived from New Guinea (Denham, in press).

Early agricultural practices in ISEA, Melanesia and the Pacific were (and remain) radically different to those in East Asia, including Taiwan. The former comprised the polyculture of vegetatively propagated plants in plots; vegetative propagation and transplantation occurred for trees (e.g., breadfruit), shrubs (e.g., *aibika*, *Abelmoschus manihot*), herbs (e.g., bananas), grasses (e.g., sugarcane) and root crops (e.g., taro and yams) (Denham, 2004, 2011). By contrast, East Asian agriculture tended towards monoculture of sexually reproduced plants in fields; cultivation from seed is characteristic of rice, millets, other cereals, legumes and tree crops. These agronomic differences are partly biogeographical: vegetative propagation tends to predominate in wet tropical locales (Barton, 2012), although it can be a minor component elsewhere (Weiss et al., 2006); they also reflect, and perpetuate, long-standing cultural traditions and orientations (Barton and Denham, 2011).

Based on these observations, as well as the types of archaeobotanical materials recovered at archaeological sites within ISEA (Paz, 2002, 2005; Donohue and Denham, 2010; Barton and Denham, 2011; see papers in Barker and Janowski, 2011; Oliveira, 2012), it seems likely that vegeticultural practices predominated within ISEA until the last 2000 years. Vegeticulture refers to an orientation to plant exploitation, including cultivation, based upon the vegetative reproductive capacity of plants, e.g., underground storage organs, suckers, cuttings and so on, rather than based on the sexual reproductive capacity of plants, e.g., seeds (Barton and Denham, submitted). There is no strong archaeological or palaeoecological evidence to indicate that wet-field or open-field rice monoculture was practiced within ISEA until, at most, the last 2000 years (Anshari et al., 2001, 2004). Until this time, seed-based crops such as rice were likely to have been minor components of subsistence, with several authors pointing to its cultivation being more important as a symbol of status (e.g., Hayden, 2011; Barton, 2012). Prior to the adoption of rice agriculture, vegeticultural practices most probably predominated in ISEA and facilitated the westward dispersal of plants, such as bananas (Perrier et al., 2011) and sugarcane (Grivet et al., 2004), that were initially domesticated in the New Guinea region. The antiquity and nature of these practices are uncertain (although see Denham et al., 2003), and it has been proposed that plant exploitation mosaics existed across ISEA during the mid-Holocene (Denham, 2011; Barton and Denham, 2011).

Certainly, the expansion of Austronesian-speaking people into the Pacific was based on a crop suite and cultivation practices derived from the ISEA and New Guinea region. None of the major plants of traditional agriculture in the Pacific were domesticated in Taiwan or East Asia. In this regard, Bellwood (2005: 145) has identified New Guinea as the ‘powerhouse’ underpinning Pacific agriculture.

In contrast, the animal domesticates incorporated into traditional practices within ISEA, New Guinea and the Pacific were all domesticated on mainland Asia. The chicken (*Gallus gallus*), dog (*Canis familiaris*) and pig (*Sus scrofa*) seemingly dispersed rapidly across ISEA and Melanesia from c. 4000 to 3000 years ago (Larson et al., 2007; Piper et al., 2009) and subsequently became entwined in the long-term history of agriculture in New Guinea and the Pacific from c. 3250–3100 cal BP (Denham et al., 2012). Significantly, archaeological evidence in ISEA is almost non-existent for chicken and sparse for dog before c. 3500 years ago. The different origins, dispersals and adoptions of animal husbandry and plant cultivation, respectively, in ISEA and Melanesia before integration into Pacific production systems remain to be unraveled. However, the predominant Asian origin for domesticated animals and the predominant New Guinea origin for domesticated plants suggest that the ISEA region hosted many complex histories of agricultural transformation during the Holocene that currently lack archaeological visibility (Barker et al., 2011a).

### *2.3. Meso-scale: Genetic Admixture Represents Social Space, Not Language Dispersal in Eastern Indonesia*

Xu et al. (2012) argue that a west-east cline of Asian-Papuan genetic admixture across eastern Indonesia ‘is in excellent agreement with inferences based on Austronesian languages’ (p. 4574), referring to the expansion of Austronesian languages from Taiwan across ISEA (from c. 4000 years ago). The logic of their argument is based on several premises, including: the genetic composition of modern ISEA populations can be traced to Asian or Papuan sources; the dates of genetic admixture and Austronesian language dispersal are contemporary; the spatio-temporal trajectories of both dispersals are comparable; and the Austronesian language expansion is the only historical event that could account for the observed genetic distribution (see Denham and Donohue, 2012; Xu and Stoneking, 2012).

Xu et al. identify two genetic populations within eastern Indonesia, Asian and Papuan. ‘Asian’ is asserted to derive from Austronesian language expansion into ISEA and ‘Papuan’ is inferred to represent genetic influences ‘related to New Guinea’ (2012: 4574), although the term is also, confusingly, used to refer to pre-existing inhabitants of eastern Indonesia (2012: 4578). Subsequent publications make it clear that the original authors intended to propose the latter meaning

for Papuan (Denham and Donohue, 2012; Xu and Stoneking, 2012). As a result, the somewhat ambiguous term ‘Papuan’ refers to the pre-existing populations of both ISEA and New Guinea, without differentiation. Consequently, Xu et al.’s (2012) results would merely demonstrate a west to east cline of Asian characteristics, which originate in the west (namely, Asia), with Papuan characteristics correspondingly increasing eastward (namely, to New Guinea). Such a result is hardly surprising: the genetic cline represents distance decay effects of Asian genetic characteristics originating in the west overlain onto Papuan characteristics originating from the earlier dispersal of modern humans eastward. Indeed, and as will be discussed further below, the spatial character of their data opens up questions of spatial autocorrelation.

Whichever scenario for the meaning of ‘Papuan’ is adopted, both scenarios require unpacking of the Asian genetic signal, part of which appears to originate on the continental shelf of Sunda, which formed a contiguous landmass until post-glacial sea level rise, rather than on Taiwan. To resolve uncertainties of what the ‘Asian’ component actually represents, comparable datasets from mainland Southeast Asia need to be included to disentangle mSEA and ISEA contributions to ‘Asian’ genetic ancestry (HUGO, 2009; Jinam et al., 2012). For example, the Jinam et al. (2012) study clearly shows that the ‘Asian’ genetic component in present-day ISEA has two discrete origins: one potentially from mainland Asia, which is dominant on present-day islands that formed part of the formerly contiguous land mass of Sahul during times of lower sea level (west of Wallace’s Line in Xu et al.’s study); and the other potentially including a Taiwanese component characteristic of island groups (Taiwan, Philippines and Wallacea) that were not joined to the Asian continent or, largely, to each other since human colonization (including the area east of Wallace’s Line in Xu et al.’s study).

The apparent synchronicity of the chronologies for genetic admixture and linguistic dispersal is questionable. Based on their own data, Xu et al. infer genetic admixture beginning about 5000 years ago for the Toraja highlands on Sulawesi, with successively later admixture eastwards (Xu et al., 2012: Fig. 1E). Consequently, the beginning of purported genetic admixture significantly predates the earliest appearance of Austronesian-associated and Taiwanese-derived material culture in any part of ISEA, which has been radiocarbon-dated to around 4500–4000 years ago in northern Luzon (Piper et al., 2009). Thus, even according to Xu et al.’s own data, there is a major chronological (as well as geographic) disparity between the beginning of genetic admixture in eastern Indonesia and the archaeologically verified appearance of Taiwanese influences, presumably including Austronesian languages, in ISEA.

The west-to-east genetic admixture cline in eastern Indonesia runs in the opposite direction to the inferred dispersal of Austronesian languages in this region (Donohue and Denham, 2011; see Fig. 1). Xu et al. consider genetic admixture

to be earliest in the west and successively later further east, and to be most recent in the northern Moluccas. In contrast, and based on authoritative linguistic research, Blust (2009) infers Austronesian languages dispersed southwards from Taiwan, first appeared in Indonesia in the vicinity of the Moluccas, and subsequently dispersed southwest across eastern Indonesia. Furthermore, Xu et al.'s research lacks the critical north-south dimension needed for comparison with Austronesian language dispersal in ISEA and only documents a west-east genetic cline within a restricted region, eastern Indonesia. In sum, the trajectories of Asian-Papuan genetic admixture and of Austronesian language dispersal are precisely opposite in eastern Indonesia; the two diffusionary processes, of genes and of languages, represent different historico-geographic phenomena.

If there is no chronological or directional reason to associate the Asian-Papuan genetic admixture cline with the dispersal of Austronesian languages, can we identify alternative historical processes to account for Xu et al.'s results? The genetic cline is most parsimoniously interpreted with reference to two sets of processes, biogeographical and social.

Foremost, the islands west of Wallace's Line were connected to each other and to mainland Southeast Asia until c. 13,000 years ago (Bulbeck, 2008). In contrast, the islands of Wallacea, which lie between the formerly contiguous land masses of Sahul (Australia and New Guinea) and Sunda (mSEA, Java, Sumatra, Borneo), were not connected to the extended Asian land mass, to New Guinea, or, in large part, to each other at any point since colonization by modern humans. From a biogeographical perspective, Wallacea represents a maritime bottleneck to east-west gene flow. Greater genetic homogenization to the west of Wallace's line seemingly reflects older processes of genetic admixture across the formerly contiguous land mass. Therefore, the genetic homogeneity west of Wallace's line and heterogeneity to the east likely reflect biogeographical processes of greater antiquity than proposed in Xu et al.'s paper.

Gradients of social interaction between Southeast Asia and New Guinea continued across Wallacea at points throughout the Holocene (Bulbeck, 2008; Donohue and Denham, 2010). Rather than a single dominant migration, there were multiple processes of genetic admixture before and after the advent of Austronesian languages, which continue to the present day. Multidisciplinary evidence supporting this historical interpretation includes genetic markers, such as the Polynesian motif (Soares et al., 2011), and potentially material-cultural influences, including pigs and a paddle-impressed pottery tradition (Larson et al., 2007; Donohue and Denham, 2010), that exhibit eastward directionalities in southern ISEA and predate Taiwanese influences (including Austronesian languages). Other dispersals occurred westward into ISEA from New Guinea, such as the aforementioned banana (*Musa* sp.; Perrier et al., 2011). These interactions, whether direct or indirect, have continued over the last 3000 years; for example,

archaeological evidence on New Guinea of items of ultimate mSEA origin dated to c. 3000–2000 years ago include Dong-Son bronzes (Golson, 1972), the wax gourd (*Benincasa hispida*; Matthews, 2003) and most probably the bottle gourd (*Lagenaria siceraria*; Golson, 2002). The cumulative effects of these interactions, which are structured in social space, are conflated in the genetic admixture cline that notably shows its most ‘significant [statistical] correlation between geographic and genetic distances’ (Xu et al., 2012: 4577), rather than with language.

In sum, the west-to-east cline documented by Xu et al. represents the genetic conflation of multiple periods of social admixture or interaction before and during the Holocene that enabled the multi-directional diffusion of genes, languages and material culture across southern ISEA.

#### *2.4. Micro-scale: A Contextual Study of Discordance between Languages and Genes on Sumba*

Lansing et al. (2007) have claimed that it is possible to detect, at a local level, the congruence of genetic and linguistic data on the island of Sumba, in central Indonesia. Their claim is based on the correspondence between the distribution of reflexes of Proto-Austronesian etyma and the distribution of Y-chromosome haplotype O, for which they note: ‘[a]lthough there is controversy about the geographic origins of haplogroup O, there is general agreement that it is associated with the Late Holocene expansion of Austronesian-speaking farmers from southeast Asia to Indonesia and Oceania’ (Lansing et al., 2007: 16024). Despite the claims for congruence, we argue that Lansing et al.’s data can better be interpreted as showing the discordance between linguistic and genetic data at this local level. We will demonstrate that their proposed model of ‘Austronesianization,’ conceived as a single demic diffusionary process that brought with it both linguistic and genetic material, is unsustainable and unparsimonious. The reasoning behind these assertions can be explained in depth for Sumba because the genetics of local populations are well-described and very basic linguistic data is available for a good sample of the villages.

Lansing et al. (2007: 16022) describe Sumba as an island ‘where Neolithic Austronesian farming communities settled and began interacting with aboriginal foraging societies.’ As mentioned above, haplotype O is taken to be indicative of Austronesian farming influence in the past. Today, the greatest concentrations of haplotype O are found in the center of the island, and overall the distribution ‘exhibits a decreasing gradient from east to west, becoming rare in the western end of the island’ (Lansing et al., 2007: 16024). If this haplotype is to be associated with a demic Austronesian expansion, then the model has to allow for a strongest Austronesian presence in the center; and this is what Lansing et al.

conclude. Other aspects of their data show spatial autocorrelation: Lansing et al. (2007: 16024) note that they ‘found a strong positive correlation between linguistic and geographic distances, which becomes stronger when controlling for genetic variation ( $r = 0.716$ ,  $P 0.001$ )’; and while overall there was ‘no correlation between genetic and geographic distances,’ they observe that if they focus on the ‘Austronesian component of genetic variation’ (presumably haplotype O, found in only 16% of the sampled population in eight villages) there is a significant correlation ( $r = 0.627$ ) with the number of retained Proto-Austronesian etyma.

Can these results be interpreted to represent common ancestry for genes and language on Sumba? A fundamental methodological error is to measure haplotype O frequencies against the retention of Proto-Austronesian words: effectively Lansing et al. treat the retained lexicon as indicative of age, in keeping with glottochronological principles (though see, e.g., Bergsland and Vogt, 1962, and many others). This conclusion flies in the face of what is known about how prone lexical material is to diffusion (e.g., Meillet, 1908; Séguy, 1971; Goebel, 1984; Cavalli-Sforza and Wang, 1986; Thomason and Kaufman, 1988; Comrie, 2000; Kessler, 2001; McMahon and McMahon, 2005; and many others, though see the results of Holman et al., 2008, with respect to a more selective wordlist) and effectively treats Sumba as a closed system, incapable of accepting loans from outside. There is good evidence that Sumba was an active participant within inter-island trade networks within this part of the Indo-Malaysian archipelago in the distant (e.g., Bulbeck, 2008) and recent pasts; for example, Sumba was previously known as *Sandalwood Island*, a reference to the important role it played in the trade of sandalwood (*Santalum* spp.), and cloth from Sumba has historically been valued as far east as New Guinea (Schoorl, 1979). Most importantly, the reliance on retained lexicon ignores the evidence of Lansing et al.’s own analysis, which was based on ‘traditional comparative linguistic approaches’ and which places the center of higher-level diversity for the languages of Sumba in the west of the island, not the center: they note that ‘the main subgroups distributed across the island from west to east.’ Finally, Lansing et al. (2007: 16024) state that the ‘divergence time between the two most geographically distant communities’ is ‘4,875 years, which is consistent with the timing of the Austronesian expansion,’ despite all evidence suggesting that Austronesian expansion into *northern* ISEA did not take place until 500 years after this date and was presumably later, c. 3500 cal BP, in Sumba at the extreme south of ISEA.

In effect, Lansing et al. (2007) recycle the purported correspondence between genetics and languages in ISEA to interpret their multidisciplinary data and to infer historical processes on Sumba. At the same time, they then seek to develop a regionally applicable model from their case study:

Whether the processes integrated in this model can explain patterns observed at continental scales remains an open question. However, a link can be postulated because large-scale patterns are contingent on processes occurring at local scales.

(Lansing et al., 2007: 16025)

They fail to fully acknowledge that a pattern between language and a genetic marker on one island cannot be extrapolated to be symptomatic of a whole region. Furthermore, their own data from Sumba exhibits a dramatic discordance between linguistic and genetic data sets for the island, with the linguistic “homeland” of Austronesian language dispersal on the island showing the lowest rates of occurrence of the Y chromosome haplogroup (O) that is claimed to be diagnostic of Austronesian farmers. In the absence of any significant archaeological data from the island, it is similarly unfounded to claim that, prior to the use of Austronesian languages, Sumba’s people were distributed in ‘aboriginal foraging societies.’

### *2.5. Multidisciplinary Discordance in ISEA: Cutting the Gordian Knot*

These case studies clearly show the lack of agreement between genetic distributions, linguistic subgroupings and the history of agriculture at different spatial scales within ISEA. There are not only discordances between different lines of evidence, but even within lines of evidence, as witnessed for the origins and dispersals of animal and plant domesticates within ISEA. Against this backdrop, the evidential basis for the demic expansion of Austronesian-speaking farmer-voyagers from Taiwan into ISEA is far from compelling. Although Austronesian language expansion is widely acknowledged to have originated on Taiwan, there is no evidence for the concomitant dispersal of agriculture into ISEA beyond northern Luzon or for the large-scale movements of people into ISEA from Taiwan around 4000–3500 years ago.

The lack of consilience requires researchers within each field of study to evaluate the presuppositions from other disciplines that they rely upon in order to contextualize or legitimate their work. Multidisciplinary discordance militates against using one line of evidence to act as a cipher for another; each needs to be considered on its own terms before they can be linked together (Donohue and Denham, 2010). The breaking of circular reasoning within the study of the Holocene history of ISEA is akin to cutting the Gordian knot. The long-term history of the region needs to be rebuilt from the bottom up, with due consideration to several methodological issues that can guide better multidisciplinary practice. These are presented as aphorisms below.

### 3. The ‘Historical’ Interpretation of Phylogenies Is Often Ahistorical

Genetic and linguistic phylogenies are based on modern-day distributions and can be used to infer processes in the past. Ancient DNA offers potential for verification of historical interpretations of modern phylogenies through the identification of the genetic characteristics of ancient populations. There is a presumption in the way that phylogenies are interpreted that diffusion—represented by gene flow, language shift or cultural interaction—can be distinguished from inheritance from initial dispersal of a population, language or culture. However, these two processes—inheritance from initial dispersal and subsequent diffusion—nearly always co-occur, are conflated and are cumulative through time. Hence, to varying degrees, they cannot be readily disentangled. Although the two components, phylogeny and reticulation, are often contrasted (Bellwood, 1996), this is largely heuristic, since they are not so readily differentiated either conceptually or in terms of a specific substantive distribution.

Within ISEAn research, genetic and linguistic phylogenies are often portrayed as representing inheritance derived from an original dispersal (Gray et al., 2009; Moodley et al., 2009; Xu et al., 2012). In these types of study, the two lines of evidence are compared and woven together, often using highly selective archaeological findings to provide a chronological framework, in order to generate an inclusive metanarrative for demic dispersal. Foremost within ISEA, genetic and linguistic phylogenies are linked to the putative dispersal of Austronesian-speaking farmers from Taiwan 4500–4000 years ago.

However, genetic and linguistic phylogenies within ISEA do not just represent inheritance derived from an initial dispersal; rather, the two sets of processes are nearly always entwined. Most phylogenies represent a mixture of inheritance derived from initial dispersals and subsequent diffusionary processes; metaphorically speaking, they constitute historical palimpsests. That is, each distribution and the resultant phylogeny conflates the ebbs and flows of multiple historical processes, from the deep past to ongoing processes. Therefore, the phylogenies should not be directly equated with inheritance that is somehow derived from an original dispersal event; rather, they represent a history of multiple processes of different ages to the present (Lansing et al., 2011).

For example, Xu et al. (2012) infer genetic admixture to correspond to a single historical event, namely, Austronesian dispersal. Their methods make a series of assumptions regarding the absence of earlier or later admixture processes, which they recognize could severely alter the age of their genetic admixture cline across eastern Indonesia. Rather than representing a single historical event, the ages of their admixture cline represent cumulative and conflated historical palimpsests of admixture through all time periods from original colonization by modern humans to the modern day. The admixture cline is an average that collapses history.

In essence, these types of study interpret phylogenies ahistorically. Namely, they flatten history, and there is almost no attempt to engage with the range of historical processes that led to the development of a particular distribution and phylogeny. Instead, phylogenies are interpreted to primarily reflect a single historical event in the past, with blurring around the edges from subsequent processes. However, this is a fundamental misapprehension regarding the nature of the distributions and phylogenies under construction. As will be discussed further below, archaeology and history are not limited to one major historical event within ISEA, or most other regions; rather, they document multiple interactions, both within this island world and with neighboring regions, throughout the Holocene that plausibly intensified within the last 2000 years.

We can summarize our position on the interpretation of the interdisciplinary data as it is relevant for our understanding of social histories as follows:

- a) Phylogeny  $\neq$  a single historical event/process
- b) Phylogeny = historical palimpsest
- c) Phylogeny =  $\sum_{t=1}^{t=\text{present}}$  ([Original dispersal + subsequent mutations/trans-formations]  $\pm$  [subsequent diffusion])

#### 4. Fractal Phylogenies

For the Holocene history of ISEA, there has been, and often continues to be, a general presumption that genetic, linguistic and material-cultural phylogenies, as well as domesticated animal/plant phylogenies, should coincide with each other (Bellwood, 1997, 2005; Diamond and Bellwood, 2003). However, the consilience of different phylogenies has been hard to establish within the region (discussed in the case studies above), except for geographically structured gradients and distance decay effects (see argument below). In part, this is limited by discrepancies between sampling points (compare Gray et al., 2009, and Moodley et al., 2009), but actually reflects more fundamental disjunctures and asynchronies.

The case studies discussed above clearly demonstrate the lack of consilience between genetic, linguistic and archaeological records at different spatial scales within ISEA. Furthermore, divergent interpretations have been inferred for language (compare Gray et al., 2009, with Donohue et al., in press), material culture (compare Bellwood, 1997, with Bulbeck, 2008), and animal and plant domesticates (compare Bellwood, 2005, with Donohue and Denham, 2010). In sum, there is often a lack of consilience among multiple lines of evidence within each discipline, not to mention between disciplines.

Different genetic markers—whether Y chromosome, mitochondrial DNA, autosomal and, potentially, genomic—exhibit different distributions and imply

different directions of movement for human gene flow within ISEA. Although some variations between the sexes would be expected, depending upon human movement, migrations and marriage (and extramarital) practices, some consistency in genetic signals should coalesce around a single historical interpretation. However, this is not the case either in terms of establishing associations between genetic markers and evidence from other disciplines, or in terms of geography. Often, different islands, island groups and regions within ISEA yield variable genetic signals that suggest different histories of population movements during the Holocene (Oppenheimer and Richards, 2001; Hill et al., 2007; Lansing et al., 2007; Mona et al., 2009; Kayser et al., 2008; Soares et al., 2008, 2011; HUGO, 2009; Karafet et al., 2010; Xu et al., 2012), as well as in terms of correspondences between genes and languages (Lansing et al., 2007; Donohue and Denham, 2010). As Spriggs (2010: 245) succinctly observes, the genetic support for Austronesian language dispersal is ‘fickle.’

Similarly, different linguistic markers—whether based in the lexicon, the phonology, the morphology or the syntax—exhibit variable geographies among Austronesian languages in the region (e.g., Reid, 1994). Donohue and Denham (2010) offer a synthesis of much earlier work, but it suffices to note that proposed divisions of the Austronesian languages of ISEA into subgroups repeatedly fail to mark the same divisions of languages when different methods are used. If we compare the results of the comparative method (Blust, 2009), early lexical methods (Dyen, 1962) and later ones (e.g., Gray et al., 2009), and clustering-by-morphology (Gosling, 2012), we find that the languages form congruent clusters across the different methods only when geography mediates the distribution of these subgroups.

Similarly, different ancient material-cultural traits—whether pottery, shell fishhooks, shell ornaments and stone axe/adzes—exhibit variable archaeological geographies, antiquities of occurrence and directionalities of dispersal (Szabo, 2004; Bulbeck, 2008; Donohue and Denham, 2010; O’Connor et al., 2011). The different historico-geographic expressions of each material-cultural trait suggest that they did not disperse across ISEA as part of a unitary ‘package’ (Denham, 2004; Donohue and Denham, 2010). Instead, different material-cultural items were developed within ISEA or were introduced to places within it at different times; they followed different historic-geographical pathways.

Lastly, and to reiterate previous discussions, different domesticated animals and plants exhibit markedly different distributions, phylogenies and inferred processes of dispersal across ISEA. In gross terms, domesticated rice (*Oryza sativa*) is generally considered to have been domesticated in China with subsequent dispersal southward into ISEA through either Taiwan (Bellwood, 2005) or Borneo (Barker, 2006). In contrast, bananas (*Musa* spp.) were initially domesticated in New Guinea with subsequent dispersal westward into ISEA, where

subsequent intraspecific and interspecific hybridization and further domestication occurred (Perrier et al., 2011). In contrast, again, taro (*Colocasia esculenta*) suggests multiple domestication events, with prolonged maintenance of geographically separate gene pools (Denham, 2010). As for animal domesticates, domesticated pigs (*Sus scrofa*) within ISEA suggest an eastward spread from mainland Asia that yielded populations in southern ISEA, New Guinea and the Pacific (Larson et al., 2007). These different historical dispersals do not reflect the dispersal of East Asian agriculture southward from Taiwan across ISEA, as conceived by Bellwood (1997, 2005). Certainly, there were strong regional connections between Taiwan and northern Luzon, including the introduction of domestic pigs and rice, but taken as a whole, ISEA was a ‘melting pot’ in which indigenous people adventitiously incorporated domesticated animals and plants that had been introduced from surrounding regions (Denham, 2010, 2011; Barker et al., 2011a).

Against this fractal backdrop, how is it possible to reconcile phylogenies from various disciplines, namely, to align them and account for them in terms of a single historical narrative, when they cannot be reconciled with each other or within each discipline? Although the lack of resolution may indicate current deficiencies of data, analysis and interpretation, it seems more likely that it reflects multiple historical processes. These are just examples designed to illuminate our argument, rather than to be comprehensive. However, they illustrate the fundamental point: multiple phylogenies derived from genes, languages, material culture and domesticates reflect multiple historical processes, most probably of very different antiquity and cultural association.

## 5. Spatial Autocorrelation

Processes of genetic and linguistic spread are socio-spatial processes, that is, they occur as a result of the movements and interactions of people living in places. Thus, geography is the common factor that links and structures genetic and linguistic distributions, and putative associations between genetic and linguistic distributions are more than likely to reflect respective spatial dependency or spatial autocorrelation (Cliff and Ord, 1970). In other words, rather than genes and languages being correlated with each other, they *appear* to be correlated because both of them co-vary and are structured by space. Indeed, the covariance of two variables (genes and languages) with a third (geography) compromises the application of standard statistical tests, such as parametric tests for correlation, which are often predicated on independence between variables.

The problem of spatial autocorrelation can be clearly demonstrated for comparisons of genetic and linguistic datasets within ISEA. Xu et al. (2012) find the strongest statistical correlation between genetic distributions and geography,

rather than with language. Given that Xu et al. (2012) rely on the linguistic dataset from Gray et al. (2009), which is also a geographically structured dataset (Gray et al., 2009; cf. Donohue et al., in press), any resultant correlation between genetic and linguistic distributions would appear spurious and likely be an effect of spatial autocorrelation among the datasets analyzed. However, the investigation of spatial relationships within and between datasets is not routinely conducted as part of genetic or linguistic investigations within ISEA, nor is the spatial character of the processes that created these distributions usually taken into account (see Terrell and Schechter, 2007, and Donohue et al., in press, as exceptions).

As a result of this missing spatial dimension, correlations and topological similarities between phylogenies can be misinterpreted and misattributed to the same historical process or set of processes in the past—such as the dispersal of Austronesian-speaking populations from Taiwan across ISEA. Without this spatial dimension, the various phylogenies appear to represent similar processes because they are both structured similarly in space.

For example, the phylogenetic topologies of Austronesian languages (Gray et al., 2009) and *Helicobacter* genetics (Moodley et al., 2009) are similar because both chart eastward diffusion to Oceania from Asia. There is nothing other than geography that fundamentally connects these datasets; indeed, the sampling points for the *Helicobacter* study are woeful for ISEA, representing the region with a concentration of samples from Taiwan, a single point from the northern Philippines, and nothing for ISEA (insular Malaysia, Indonesia, East Timor) or western New Guinea, thereby preventing any attempt to track the directionality of dispersal across the region. Consequently, it is not possible to see whether the dispersals of languages and bacteria across ISEA are consistent; rather, we are left merely with the impression that the two phylogenies show ‘Asian’ origins with subsequent eastward dispersals to Oceania. Based on this simple trend, Renfrew notes ‘the topology and detail of the two trees are genuinely independent’ (Renfrew, 2009: 468). This line of reasoning is, at best, problematic.

Foremost, given that both distributions are structured in social space—effectively beginning in Asia and ending in Oceania—they both exhibit geographical attenuation and transformation of attributes from the source region. Austronesian languages undergo attenuation eastward since only one language left Taiwan, (pre-)proto-Malayo-Polynesian, with subsequently only a sample of original Austronesian proto-language diversity forming the basis for sequentially derived subgroupings in ISEA, Melanesia and eventually remote Eastern Polynesia. Additionally, as the language family dispersed, its constituent subgroups and individual languages were transformed in terms of lexicon, phonology, morphology and syntax; these transformations were due to processes of internal change

as well as extrinsic processes, resulting from contact with different peoples speaking different languages in the regions in which Austronesians found themselves. Similarly, as people and bacteria have moved eastwards, the genetic composition of sequentially derivative populations has changed through a variety of processes, including bottlenecks, reproduction, mutation and so on.

In both cases, sequential dispersals have led to an accumulation of differences from the source population. Given that these dispersals both occurred from ‘Asia’ to Oceania, or from west-to-east in highly approximate terms, the phylogenies (which essentially reflect groupings of accumulated changes) share similar spatial structures and directionalities. As a result, the modern-day distributions of both populations are geographically correlated, but need not be ‘correlated’ to each other.

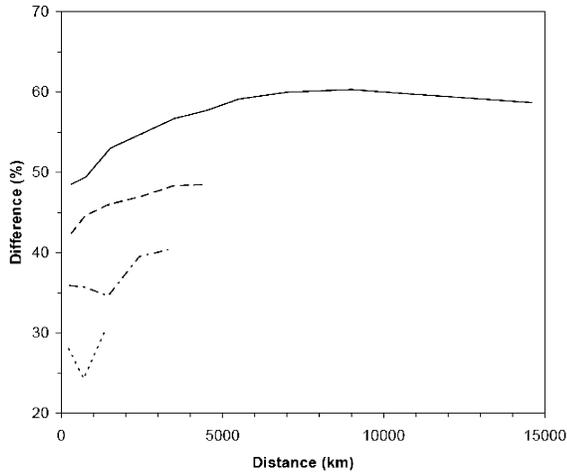
Irrespective of the implications of distance-decay effects, the correlation of two attributes need not indicate association or causality (Gould, 1970). Rather, association and causal relationships in the past have to be inferred through an understanding of historical processes operating in time and space. Without any geographical or historical understanding, the comparison and correlation of datasets, as witnessed in the discussion above, can yield spurious correspondences and interpretations between things that may be completely unconnected. To pursue this further, there are no grounds upon which to determine that the two dispersal events—of Austronesian languages and of *Helicobacter* genes—occurred at the same time or are in any way chronologically related.

There are numerous biological distributions that can be assembled into phylogenies that show clines or gradients between the Asian mainland and Oceania. For example, the phylogeny of wild *Musa acuminata* banana populations shows a similar west-to-east topology, representing genetic transformation and attenuation (excluding anthropically generated and translocated cultivars in Perrier et al., 2011: S2). Such clines represent biogeographical processes operating across past and current landscapes. Although animal dispersals are severely disrupted by Wallace’s Line, this biological boundary was less significant for plant dispersals (Sniderman and Jordan, 2011), although fewer plants and less genetic diversity traversed eastward of this maritime obstacle to gene flow. For example, multiple banana species and subspecies are present west of Wallace’s Line, with only a few wild species and subspecies being present in Wallacea, the New Guinea region and northern Australia (Daniells et al., 2001). The existence, and temporal persistence, of these clines is suggestive of a very significant geographical phenomenon, which is often overlooked in multidisciplinary studies within ISEA and elsewhere: distance decay effects.

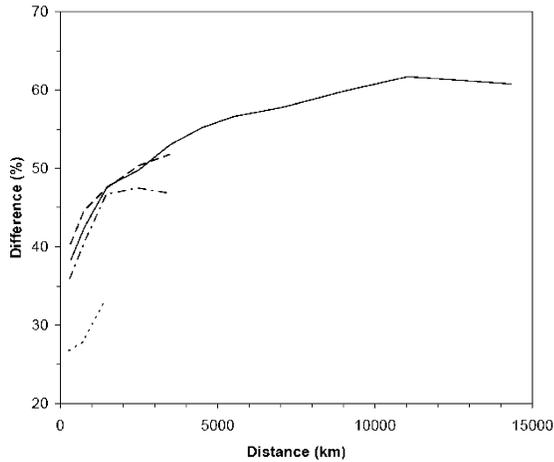
## 6. Distance-decay Effects

Peter Gould considered ‘distance decay’ to probably be the most significant geographical concept (Peter Gould, pers. comm., 1999–2001; Gould, 1999). In simple terms, distance decay represents the diminution or attenuation of interaction or influence between two points as the distance between them increases. Distance decay effects do not necessarily represent Euclidean space, namely straight line distance. For biogeographical processes, distance decay effects will vary depending upon contiguity of land and water bodies; altitudinally and latitudinally determined climatic tolerances; obstacles to dispersal such as deserts, mountain ranges and rivers; prevailing winds and sea currents; and so on. For social processes, distance decay requires consideration of the ease or difficulty of interaction across social space, that is, the space people inhabit, using different technologies. To exemplify, distance decay effects will vary between land and sea, and will vary between populations with open-ocean voyaging canoes (traditionally) or aircraft (modern) and those without these technologies. However, in all cases, the general principle holds: the mutual influence between locale A and locale B will usually decrease as the distance between the two locales increases.

Based on this principle alone, general clines would be anticipated to exist across ISEA that represent decreasing ‘Asian’ influences and increasing New Guinean influences from west-to-east (such as those observed by Xu et al., 2012). These clines represent distance decay effects from source region. There is nothing unusual or particularly noteworthy in such distributions. In addition to the appearance of such clines in the genetics literature, we note that distance is the major factor that accounts for linguistic difference as well. We have already cited the substantial literature on the role of distance in the determination of lexical similarity. Work by Holman et al. (submitted) shows similar trends operate in the realms of linguistic typology (Fig. 2) and ethnographic traits (Fig. 3) (results replicated in Baayen, 2009; Donohue, 2009; Donohue et al., 2011). Both these figures show the calculated mean difference between sample points for the relevant dataset as a function of the distance between those two points. The different kinds of lines reflect different linguistic relationships, from those points that represent dialects of the same language (dotted line, at bottom of figures) to points representing languages which are members of the same ultimate family (dashed line), and all languages in the dataset (solid line, at top of Fig. 2). While it is clear (and unsurprising) that membership in the same language family (and even more, same subgroup) plays a role in determining whether two languages are similar to each other or not, all kinds of relationships between languages show strong distance decay effects (with some confounding influences between the more closely related pairs of languages, most likely reflecting the sociolinguistic role of linguistic differences in identity formation).



**Figure 2.** The percentage differences between languages plotted against the spatial distance between them. Legend: solid line = languages in different families; dashed = languages in the same family but different genera; dot-dashed = languages in same genus but different dialect clusters; dotted = languages in the same dialect cluster (Holman et al., submitted, Fig. 1).



**Figure 3.** The percentage differences between societies plotted against the spatial distance between them. Legend: solid line = societies in different language families; dashed = societies in the same language family but different genera; dot-dashed = societies in same language genus but different dialect clusters; dotted = societies in the same dialect cluster (Holman et al., submitted, Fig. 2).

For ethnographic traits it is clear that linguistic association is not as significant as would at first be considered (Fig. 3). If two societies share the same language, they will be more similar than two societies that do not share a common language; but beyond this close dialectal level we cannot identify a role for linguistic classification in the description of cultures. Regardless of language affiliation, we can see unambiguously that distance is essential to understanding ethnographic differences.

### **7. ISEA Was Not a ‘No-[hu]man’s Land’**

The indigenous ISEA component has most often been completely underestimated in terms of genetic, linguistic and agricultural contributions. In one paper already discussed, Xu et al. (2012: 4574) assert that, prior to Austronesian dispersal, ISEA consisted of ‘Mesolithic hunter-gatherer communities,’ implying that these communities did not have a significant impact on the societies that subsequently emerged. There is ample evidence from substratal signals in the Austronesian languages of ISEA that contact with the pre-Austronesian populations of the region was highly significant in shaping the modern languages (e.g., Reid, 1994; Donohue, 2004, 2005, 2007a, 2007b; Donohue and Schapper, 2008; Donohue and Whiting, 2011; Klamer et al., 2008, and many others). This suggests that, rather than being overlooked without consequence, the indigenous ISEA populations were socially prominent enough in post-Austronesian ISEA to continue, over a long period, to affect the lexicon, phonology, morphology and syntax of the new Austronesian languages. These indigenous linguistic components survived into historical times in regions that were largely ‘Austronesianized’ linguistically.

From an archaeological perspective, Victor Paz (2010: 244) has emphasized the need to consider the interactive nature of pre-Austronesian ISEA cultures, suggesting ‘the possibility of a pan-ISEA existence of much more complex societies that, at least, were maritime, had a developed suite of shell material culture, perhaps had non-cereal-based agriculture.’ He notes (Paz, 2010: 244) that ‘Austronesian-speaking cultures did not simply encounter small bands of hunter-gatherers as they moved through the landscape.’ While evidence for the nature of these pre-Austronesian societies is not highly visible, it can be inferred; for example, as discussed above, the dispersal of plants before Austronesian language influence is suggestive of forms of vegetative cultivation in some parts of ISEA (Denham, 2010, 2011).

### **8. Reconnecting from the Bottom Up**

Far from believing that interdisciplinary perspectives on the history of ISEA offer irreconcilable lines of evidence, we firmly assert that, without interdisci-

plinary perspectives, we would miss much of what is exciting in the study of human societies in the region. We believe, however, that the approach to interdisciplinary studies has often been organized in an unhealthy manner and needs to be rethought, along the lines presented by Oppenheimer (2004). The data from different disciplines should be considered independently, without a prior assumption that there will be congruence, and these data should construct local histories first. A history built from the bottom up, and not reliant on top-down assumptions, is not simply a question of scale, but one of approach: a bottom-up history is firmly grounded in the data, while a top-down one is built on the assumption of congruence. We propose some simple principles that will go a long way towards establishing more empirical and less entrenched views of regional social histories:

- Build from bottom up, not reliant on top-down assumptions (not a question of scale, but a question of approach)—the former built on data, the latter built on assumption.
- Avoid retrofitting data to a historical template. Although not proven, it seems that there is a tendency to collapse differences and flatten time into an ‘Austronesian template’ that now appears to be unfounded.
- Need to reorient our thinking about social histories with ISEA and to restart with a series of basic questions, rather than assumptions:
  - What evidence is there for agricultural dispersal from Taiwan in ISEA? This is fundamental to the whole farming-language dispersal hypothesis. If there is no reliable archaeological evidence for farming dispersal, then the whole metanarrative collapses. To date, there is no robust archaeological evidence for the early (c. 4500–4000 cal BP) spread of farming practices, plants or animals beyond northern Luzon (Hung et al., 2012). Consequently, the idea of farming-language spread falls down, and an alternative framework for historical interpretation of the distributions of genes, languages, material culture and domesticates in ISEA is needed.
  - What evidence is there that Austronesian language dispersal was accompanied by the dispersal of material-cultural items? Recent reviews of the archaeological evidence conclude that there was no agricultural or archaeological package of material-cultural elements that spread through ISEA with Austronesian languages (Bulbeck, 2008; Donohue and Denham, 2010). There is some historical linguistic evidence—but most items appear to have been incorporated into the Austronesian lexicon within ISEA (namely at level of Proto-Malayo-Polynesian) (Pawley, 2007).
  - Why assume what we see today has much bearing on how things were 4500–3000 years ago? Reliance on recent or modern ethnographic, linguistic and genetic records cannot be taken to be indicative of

distributions in the long-term past. Such a view ignores the cumulative effects of social processes operating geographically through time. The relationships between present and past have to be investigated and reconstructed, not just directly inferred.

- Why assume that there was just one major event in ISEA history, namely Austronesian language dispersal, that left an indelible record on the distribution of languages, peoples and things in ISEA? Such an interpretation collapses history and ignores the flow of historical events before/ after this ‘event horizon.’

The main thrust of this paper has been to reassert the primacy of geography and history in order to understand cultural, genetic and linguistic changes in ISEA during the mid-to late Holocene. Rather than historical rhetoric and the desire to pursue simple models, we emphasize the need to consider each line of evidence as valid and informative, even if sometimes awkward and difficult to place in a single metanarrative of the past, whether at the scale of one island or across a whole region.

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