

Lack of correspondence between Asian-Papuan genetic admixture and Austronesian language dispersal in eastern Indonesia

Xu et al. (1) argued that a west-east cline of Asian-Papuan genetic admixture across eastern Indonesia “is in excellent agreement with inferences” (ref. 1, p. 4574) regarding the expansion of Austronesian languages from Taiwan across Island Southeast Asia (ISEA) from circa 4,000 y ago. They identify two major genetic populations within ISEA, “Asian” and “Papuan,” which allegedly reflect Austronesian language expansion and New Guinea influences, respectively. However, humans initially occupied ISEA over 50,000 y ago, yet no trace of their genetic signal seemingly survives in modern-day populations. This erasure of preexisting ISEA ancestry in their study contradicts previous findings (2) and requires inclusion of comparable genetic data from mainland Southeast Asia (mSEA) to disentangle mSEA and ISEA contributions to Asian genetic ancestry.

Furthermore, the chronologies of genetic admixture and linguistic dispersal are asynchronous. Genetic admixture begins about 5,000 y ago in the Toraja highlands, Sulawesi (ref. 1, fig. 1E). This age significantly predates the earliest appearance of Austronesian-associated and Taiwanese-derived material culture in any part of ISEA, at circa 4,000 y ago in northern Luzon (3).

Even more problematically, the directionality of west-to-east genetic admixture contradicts that of Austronesian language dispersal in eastern Indonesia. Genetic admixture is earliest in the west, becoming successively later eastward, and being most recent in the northern Moluccas (1). In contrast, Austronesian languages dispersed southward from Taiwan, first appeared in Indonesia in the vicinity of the Moluccas, and subsequently dispersed southwest across eastern Indonesia (4).

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 the results of Xu et al. (1)?

Foremost, Wallace’s Line represents a bottleneck to west-to-east gene flow. This effect, however, was more pronounced in the

past. The islands west of Wallace’s Line were mostly connected to each other and to mSEA until circa 13,000 y ago, whereas the islands of Wallacea were not connected to mSEA, to New Guinea, or primarily to each other since colonization by humans. From this deeper historical perspective, greater genetic homogenization to the west and greater heterogeneity to the east are consistent with the respective rates of genetic admixture across a formerly contiguous land mass and across a maritime barrier.

Gradients of cultural interaction between Southeast Asia and New Guinea traversed Wallacea at points throughout the Holocene. Genetic markers (e.g., the Polynesian motif) and material cultural markers (i.e., from pigs to paddle-impressed pottery) indicate eastward directionalities before Taiwanese influences (5). Eastward movements across Wallace’s Line continued after purported Austronesian language dispersal, as documented through archaeologically recovered Dong-Son bronzes (from mSEA) on New Guinea dating to 3,000 to 2,000 y ago; historically documented Indic civilizations, Islamization, and European colonialism; and ongoing state formation and transmigration programs in Indonesia.

The cumulative effects of these cultural processes, 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” (ref. 1, p. 4577) rather than with language.

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