Reply to Denham and Donohue: Asian-Papuan genetic admixture is in excellent agreement with Austronesian dispersal in eastern Indonesia

We strongly disagree with the conclusions of Denham and Donohue (1) on our recent paper (2), in which we estimated the time of genetic admixture between “Asian” and “Papuan” genetic ancestry in eastern Indonesia and inferred that this admixture corresponded to the Austronesian expansion. The criticisms of Denham and Donohue (1) can be summarized as the following three points:

i) The time of the Asian-Papuan admixture does not correspond to the Austronesian expansion.

ii) The direction of the Asian-Papuan admixture does not correspond to the Austronesian expansion.

iii) Our admixture data therefore best fit other expansions rather than the Austronesian expansion.

Regarding the first point, given uncertainties associated with both genetic dating and determining the time of language expansions, in our view, the time for the onset of genetic admixture (4,000–6,000 y ago) does not differ from the times for the Austronesian expansion (estimated at 3,500–4,000 y ago in Indonesia). To suppose otherwise assumes that within a short time period, there was a major expansion of people that left a genetic impact but no discernible linguistic impact, followed by another expansion that left a big impact on the languages but no genetic impact.

Regarding the second point, it is true that Blust (3) inferred an east-to-west language spread across eastern Indonesia, and we already mentioned this (ref. 2, p. 4578). However, this inference is based on a model that assumes that high language diversification reflects the origin of a language spread; clearly, other factors (especially contact) can influence rate of diversification. The quantitative analyses of Gray et al. (4) [based, in part, on Blust’s data (3)] instead suggested a west-to-east spread of Austronesian, and the linguistic distances are significantly correlated with the genetic distances, in keeping with the genetic results.

Regarding the third point, we have already pointed out that although the major signal we see in the genetic data appears to coincide with the Austronesian expansion, other migration events also undoubtedly left a genetic impact (ref. 2, p. 4579). This is an area for further work, but we stand by the conclusion that the dominant signal in the genetic data corresponds to the Austronesian expansion.

Thus, we disagree with Denham and Donohue (1) on the first two points, and the third point has already been made in our paper (2).

Finally, we would emphasize that the initial peopling of Asia and subsequent population expansions could be on quite different time scales, and ancestries of well-differentiated populations that have been isolated for a long time in different geographical regions can be discerned based on modern genomic data. This is the case in our study. Therefore, our rationality and results do not contradict previous findings (5). In addition, although we estimated the time of Austronesian expansion and our analysis supported a west-to-east population movement in eastern Indonesia, we did not deduce the actual origin of Austronesian-speaking people; this point needs further examination, because we do not have sufficient information in our data to support a north-to-south movement of Austronesian languages as Denham and Donohue (1) assume.

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The authors declare no conflict of interest.

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