

Some Remarks on the DNA Study on Austronesian Origins

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In a recent DNA study entitled “Polynesian origins: Insights from the Y chromosome” is based on a sample of 551 male individuals from 36 populations living in Southeast Asia, Taiwan, Micronesia, Melanesia and Polynesia, by Bing Su et al. (2000, *PNAS* 97.15:8225-8228). Their important findings include:

(1) “nearly none of the Taiwanese Y haplotypes were found in Micronesia and Polynesia,”

(2) “a Melanesian-specific haplotype was not found among the Polynesians,” and

(3) “all of the Polynesian, Micronesian, and Taiwanese haplotypes are present in the extant Southeast Asian populations.”

The sample of their Southeast Asia populations includes not only the Austronesian language family (Malay, Batak, Javanese and Central Dusun (in Kota Kinabalu)), but also several other language families or language groups, namely, Kam-Tai (Dong, Zhuang, North Thai and Northeast Thai), Kadai (Li), Tibeto-Burman (Yi), Hmong Mien (Yao), and Austro-Asiatic (Cambodian and Orang Asli). In other words, their sample contains a great variety of gene pools from several language families, not just Austronesian. It is not unlikely that the sample contains almost all sorts of DNA markers. It is, therefore, not surprising that they find in their DNA study that “all of the Polynesian, Micronesian, and Taiwanese haplotypes are present in the extant Southeast Asian populations.”¹ A similar statement may be made about other language families in Southeast Asia, such as Kam-Tai or Kadai (Benedict 1975:xix). It is not clear at this stage how many of these language families or groups are genetically related to each other. If any two of them are proven to be genetically related, then their common ancestor belongs to a still higher super-stock language family at a greater time-depth, which would contain much more diversified populations than within a single language family today. It is most likely that the Austronesian and Austro-Asiatic language families are genetically related as two daughter language families of the Austric super-family (Reid 1994, 1999). If so, the time-depth of the Austric is greater than that of Austronesian. In fact, this DNA study confirms the hypothesis (Blust 1996) that

¹ One may wonder why Indonesia, but not the Philippines, is considered part of Southeast Asia in their study.

Southeast Asia continent (more specifically, North Burma) is the Austric homeland, rather than Austronesian.

Among nearly twenty aboriginal ethnic groups in Taiwan, their sample covers only the following five: Bunun, Atayal, Yami,² Paiwan and Amis. It does not cover four other mountain tribes: Saisiyat, Tsou, Rukai and Puyuma, or any of the plains tribes, such as Thao, Pazeh and Kavalan. One may question the validity of their claims derived from a restricted sample of a few chosen populations in Taiwan. Perhaps a more serious problem in their sample is that most of the Formosan peoples they picked seem to belong to a lower order subgroup, including Bunun, Paiwan and Amis, all believed to belong to the “Paiwanic” subgroup. It does not include Formosan populations from some other higher-order subgroups, such as Tsou and Rukai (see, e.g., Starosta 1995:691, Blust 1999:45). In short, since their sample of Formosan populations is extremely limited, it is not surprising that they found few Formosan Y haplotypes in Micronesia or Polynesia in their study.

Sometimes there are explanations for cases where linguistic evidence and DNA evidence do not match. One people may have conquered and assimilated another people of a different origin. Thus we find a “mixed race” in one and the “same” language family. Melanesia is a case in point. Melanesian islanders represent substratum speech communities of a different origin from Austronesian. This is known as the “pidginization hypothesis” by Arthur Capell (1962). Thus there is a good explanation for what they have found concerning the DNA genetic relationships between Melanesia and Polynesia, “a Melanesian-specific haplotype was not found among the Polynesians.”

In order to obtain better and more reliable results in a DNA study, geneticists should make a careful selection of populations to be included in their sample. If the main goal is to find out the Austronesian homeland, then they should pick and compare only Austronesian populations. It will help if they consult linguists familiar with the Austronesian language family.

² In fact, Yami is not a Formosan language; it is one of a Batanic languages spoken in the Philippines.

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