Taiwan, Southeast Asia and the Pacific, a Genetic Perspective.

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The extraordinary spread of Austronesian languages in Southeast Asia, Oceania and Taiwan and the near-consensus among linguists that they originated in Taiwan have generated an industry among some academics devoted to demonstrating a Late Holocene physical and cultural Neolithic dispersal, emanating from Taiwan to replace pre-existing populations in Southeast Asia and elsewhere in its path. But genes and languages need not concur so closely, especially where the expanding language family meets pre-existing populations. The use of genetic tools should be objective rather than partisan. There are several general and specific implications of the composite genetic picture of Pleistocene and Holocene migrations to the Pacific. Distributions of common genetic markers in Southeast Asia and Near Oceania are regionally specific and mainly reflect Palaeolithic bio-geographic boundaries. Such a picture fits a series of progressive and cumulative colonisation events starting from Southeast Asia in the early Holocene better than a hypothetical model of a single recent Neolithic expansion from Taiwan with demic replacement of hunter-gatherers in Island Southeast Asia. Indeed there is little evidence that Taiwan is a major source of Pacific gene flow. Neither is there evidence for a massive recent gene flow across Wallace's line out of Island Southeast Asia to Melanesia, Micronesia or Polynesia. Instead, derivative Asian lineages appear to have expanded from older staging points, possibly in the Bismarcks during the early Holocene if not earlier i.e. before the Lapita horizon. In other words there may have been a pre-Lapita expansion from populations in Melanesia possessing the same Asian colonial source lineages that appear to have been associated with the later Polynesian expansion.