Mitochondrial DNA Variation in the Southwest Pacific

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Abstract

Human populations in the southwest Pacific have a reputation of being particularly diverse genetically. In this preliminary survey of this region, we have identified five major clusters of mitochondrial haplotypes among 134 DNA samples from dispersed populations: From Papua New Guinea; Gende-speaking groups (Bundi) from Madang Province, groups belonging to the Torricelli language Phylum of West Sepik Province, groups near Minj in the highlands, villages near Popondetta and Garaina in Northern Province; the Baining of East New Britain Province, and Misima Island. We included, as well, samples from the Santa Cruz (see Fig. 1). Two of these clusters conform to clusters I and II identified by Lumet al. (1994). The distribution of Cluster I (a haplotype including the mtDNA Region V 9-bp deletion) is consistent with a recent introduction by Austronesians (presumably the ancestors of the Polynesians) approximately 3,000 years ago. Cluster I was detected among the Garaina, Misima Island, Popondetta, and Santa Cruz samples. We detected Cluster II in all of our mainland New Guinea populations except for Minj. We did not find any evidence of group III identified by Lumet al. but found three additional clusters (IV-VI) not found by Lumet al. (1994). Cluster IV was seen in the more easterly samples from Misima Island, Bundi, Minj, and Popondetta. Cluster V was only found in some individuals from Garaina in our study (but 2 of the 6 mutations defining haplogroup V) have been seen by others in Borneo and the Philippines (Sykes et al. 1995). Cluster VI was found widely from the Sepik and Karawari River region to Popondetta, Baining, Minj, and Misima Island. Cluster VI contains the Cambridge

reference sequence (Anderson et al. 1981) which is known to be common in Europeans, but is also widespread globally. We question whether this maternally-derived haplogroup found in widespread and remote regions of PNG and Island Melanesia is due to European admixture, as has been suggested elsewhere. Lastly, mismatch distributions of 9-bp deleted versus non-deleted PNG sequences were markedly different. The 9-bp deleted lineages appear to be quite recent in PNG (and Melanesia as a whole), The mean number of pairwise differences in 9-bp deleted lineages is 1.6, while the mean is nearly 5.8 for all the non-deleted lineages in PNG.