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Ancient Solomon Islands mtDNA: assessing Holocene settlement and the impact of European contact

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ABSTRACT

Archaeologists, linguists and geneticists generally agree that Near Oceania was subject to two major pulses of human dispersal: a Pleistocene occupation around 40,000 BP and a Late-Holocene migration at 3500 BP commonly associated with the Austronesian expansion out of Taiwan. The latter led to the development of the Lapita cultural complex in the Bismarck Archipelago which resulted in the settlement of Remote Oceania and there are a variety of competing models (express train, slow boat, entangled bank, etc.) used to explain this. Recent genetic studies have focused on this issue, but none of them have taken into consideration the bias possibly introduced by 19th-century historically reported population decline caused by European contact.

In this paper we present a case study to test the effect of 19th–20th century colonial impact on the mitochondrial DNA diversity of Solomon Islanders and to investigate the complex stratigraphy of settlement in this archipelago during and after the Lapita period. We extracted DNA from hairs and teeth belonging to 21 individuals collected by the Somerville expedition during the late 19th-century, and typed them for mitochondrial DNA (mtDNA) hypervariable region I (HVS-I) and the intergenic COII/tRNALys 9-base pair deletion (9 bp-del). Comparison of these genetic data with those available from the modern Solomon Islanders and Southeast Asian and Oceanic populations conflicts with the hypothesis of drastic changes in Solomon maternal genepool diversity, indicating that the last century putative bottleneck is not detectable through our genetic data. In addition, the ancient and modern Solomon haplogroup distribution (e.g. M27 haplogroup) suggests, in agreement with some archaeological and linguistic models, that Early Lapita populations expanding out of the Bismarck Archipelago had little or no contact with indigenous non-Austronesian populations in Bougainville and the Solomon Islands. This finding indicates smaller scale analyses reveal a more complex reality of genetic admixture in some parts of Oceania than is often assumed in current debates.

1. Introduction

Studies of mitochondrial and non-recombining Y chromosome DNA variation in the modern populations of Oceania are well established and have provided useful insights into the prehistoric colonisation of the Pacific Islands, particularly when analyzed in comparison to archaeological and linguistic data (e.g. Melton et al., 1995; Redd et al., 1995; Lum and Cann, 1998; Cox and Lahr, 2006; Friedlaender et al., 2002, 2005, 2007; Kayser et al., 2006, 2008; Ricaut et al., 2008). In general the genetic ancestry of populations in Melanesia and Polynesia can be traced to the initial Pleistocene era settlement of Papua New Guinea and offshore islands some 40,000 years ago (BP), and subsequent admixture with Southeast Asians in the mid-Holocene. The latter process is thought to be associated with the rapid eastward spread of the Austronesian (AN) language family and a Neolithic economy, culminating in human expansion into Remote Oceania after 3200 BP (Bellwood, 2005).

Within this context a key focus of genetics research has been to define the extent of admixture between the indigenous populations and the AN speaking newcomers, with research favouring either little or no mixing (the 'fast train' scenario) or significant

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mixing (the 'slow boat' scenario). Increasingly, archaeological and genetic data lend support to models that posit the integration of Asian (AN speaking) peoples into indigenous Melanesian (non-AN speaking) communities in the vicinity of the Bismarck Archipelago circa 3450–3350 BP, leading to the development of new cultural forms (the 'Lapita cultural complex'), new languages (the Oceanic subgroup of AN) and populations of mixed ancestry, which ultimately went on to colonize Remote Oceania and Polynesia a few hundred years later (Kayser et al., 2008; Green, 1991; Kirch, 1997).

The genetic evidence for this mixing is seen most clearly when comparing the mtDNA and NRY phylogeographies of descendant populations. Polynesian mtDNA types are mostly (94%) of East Asian origin (Kayser et al., 2006), with a particular mtDNA HV1 motif (the 'Polynesian motif') able to be traced back through Island Melanesia to Eastern Indonesia, and arguably towards Taiwan (but see discussions in Friedlaender et al., 2007; Hill et al., 2007; Soares et al., 2008), the linguistic homeland of Austronesian (Redd et al., 1995; Trejaut et al., 2005).

The Polynesian motif is characterised by a set of mtDNA polymorphisms in the non-coding part of the mtDNA (nucleotide positions 16189, 16217, 16247 and 16261) that defines subgroup B4a1a1 within haplogroup B, which in turn is defined by the 9 bp-del (Redd et al., 1995). The Polynesian motif is found at highest frequency in Polynesia, with varying frequencies among coastal populations in Island Melanesia. However, the motif has not been found in the New Guinea Highlands, and is relatively rare in Island Southeast Asia although it does occur sporadically in both central and eastern Indonesia (Melton et al., 1995; Redd et al., 1995; Richards et al., 1998; Pierson et al., 2006; Friedlaender et al., 2002, 2005, 2007; Hill et al., 2007; Kayser et al., 2006, 2008; Ricaut et al., 2008). The presence of the Polynesian motif has also been confirmed in Madagascar – the western edge of the Austronesian expansion (Soodyall et al., 1995, 1996; Hurles et al., 2005). It has been argued that this motif developed in eastern Island Southeast Asia or Near Oceania (Trejaut et al., 2005; Friedlaender et al., 2007) during the mid/late-Holocene, between 10 kya and 4 kya (Pierson et al., 2006). Its immediate precursor has been identified through whole mtDNA sequencing in Taiwanese aboriginal groups (Trejaut et al., 2005), seemingly corroborating the Holocene Austronesian expansion out of Taiwan which led to the development of the Lapita cultural complex in the Bismarck Archipelago and the subsequent settlement of Polynesia and Micronesia.

Polynesian Y chromosomes on the other hand, are of predominantly (66%) Melanesian origin (Kayser et al., 2006). This disparity suggests sex-biased admixture influenced by matrilocal residence and matrilineal kinship reckoning amongst immigrant AN communities that resided in Melanesia for sometime before expansion to Remote Oceania (Hage and Marck, 2003; Cann and Lum, 2004; Kayser et al., 2008). Amongst indigenous non-Austronesian communities in coastal New Guinea and Island Melanesia we also see evidence of this mixing, but here mtDNA suggests a larger contribution of AN women, in keeping with patrilocal non-AN (Papuan) social conventions (Ricaut et al., 2008: 363; Kayser et al., 2008).

Consequently, the regional-scale pattern of Holocene population history is generally depicted as involving a single eastward expansion of southeast Asian populations, which either slowed down (Kayser et al., 2008) or paused (Green, 1991; Anderson, 2001; Specht, 2007) in the Bismarck Archipelago, incorporating local peoples before continuing towards Polynesia in one movement. At the sub-regional scale however, there is archaeological and linguistic evidence for a more complex situation.

The archaeological distribution of Lapita sites is generally discontinuous, occurring on some offshore islands and coastal locations in the Bismarck Archipelago but not others, and being absent along the north coast of New Guinea (Lilley, 2008). The present-day distribution of Austronesian languages there, happened much later in the post-Lapita period, with islands such as Karkar having a complex linguistic and genetic stratigraphy (Ross, 1988; Ricaut et al., 2008). The earliest Lapita settlements outside the Bismarcks are in the Reefs-Santa Cruz islands at 3200 BP (Green, 2003), perhaps suggesting that the initial Lapita expansion bypassed the entire main Solomons chain where there are no Early Lapita sites (i.e. 3400–2800 BP) (Sheppard and Walter, 2006). Recent linguistic analyses of the Reefs-Santa Cruz languages indicate that they derive from an early branch of the Oceanic subgroup whose proximal homeland is the Bismarck Archipelago, in agreement with the archaeological evidence of a 'leapfrog' colonisation (Ross and Næss, 2007; Næss and Boerger, 2008). The Austronesian languages of the main Solomons belong to a later branch of the Oceanic subgroup (Ross, 1989), perhaps having arrived 2800–2600 BP when we first begin to see Late Lapita sites in the archaeological records of Buka, the Western Solomons, and Santa Ana (Sheppard and Walter, 2006). Prior to this period it is likely that the Solomon Islands were occupied solely by non-Austronesian speaking populations as evidenced by the patchy distribution of non-AN languages there today, and the presence of pre-Neolithic archaeological sites, such as Kilu cave on Buka, dating to 29,000 BP (Wickler, 2001), and Vatuluma Posovi on Guadalcanal, dating to 6400 BP (Roe, 1993). Similar complexities are considered in recent debates about the grammatically anomalous AN languages of southern Vanuatu, which have been argued by some to indicate non-AN speakers were among the earliest inhabitants of the islands (approx. 3100 BP). In this scenario an early non-AN Lapita population first colonised the island, quickly followed by an AN Lapita population (Blust, 2008; Donohue and Denham, 2008), although this is highly contentious (Pawley, 2006).

It seems evident at this point that Holocene population movements associated with the spread of AN languages and Neolithic economies did not follow a strict 'wave of advance' model during expansion through Melanesia to Polynesia (Spriggs, 1997). Thus, more attention to localised sub-regional genetic patterns is warranted. However, whilst population genetics studies have been quite successful at elucidating the broad patterns of settlement in the Pacific, smaller scale analyses are fewer and problematic, with unexpected inversions in language and DNA ancestry remaining difficult to explain (Cox and Lahr, 2006; Ricaut et al., 2008; Friedlaender et al., 2007). Studies using modern DNA to infer demographic processes in the distant past are highly susceptible to the confounding effects of recent population movements. As Hunley et al. (2008) have recently argued localised genetic and linguistic exchanges tend to obscure microevolutionary patterns, yet leaving broader patterns still detectable.

The issue of post-settlement interaction and exchange in Melanesia is often completely ignored in genetic reconstructions. This is surprising since Melanesia is renowned for its numerous exchange networks, fluid social organisation, and mobile populations. Furthermore, it is archaeologically well established that populations went through extreme processes of post-Lapita diversification and regionalisation, involving the breakdown of region-wide exchange networks into smaller circuits of increasing specialisation and complexity (Spriggs, 1997; Kirch, 2000). Compounding this is the fact that Island Melanesian populations were subject to various important disruptions after European contact – introduced diseases caused population bottlenecks (with losses of up to 97% on some islands), pacification removed social boundaries once maintained by warfare, engagement in wage labour on plantations caused new movements and intermarriage, and the rapidity and ease of travel was facilitated by new modes of transportation.