

# **THE END OF THE TRAIL: THE GENETIC BASIS FOR DERIVING THE POLYNESIAN PEOPLES FROM AUSTRONESIAN SPEAKING PALAEOPOPULATIONS OF MELANESIAN NEAR OCEANIA**

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If any single question can be said to dominate the discourse on Pacific prehistory, it must certainly be the vexing issue of the origins of the Polynesians. Roger Green has contributed extensively and significantly to this quest. In numerous articles, he has put the process of interpreting Pacific prehistory in perspective by asking whether inferred solutions conform to situations 'on the ground' (e.g., Green 1967, 1985, 1989, 1991, 1992). In his works, Green has applied a systematic anthropological approach to Pacific prehistory which conscientiously integrates, as appropriate, linguistics, geomorphology, and human biology as well as archaeology (e.g., Green 1976, 1978, 1979, 1989, 1991, 1992, Kirch and Green 1987, Pawley and Green 1973, 1984).

Systematic attempts to study human biology in the Pacific can be traced to the years following World War II. One study has been to determine whether the Polynesians could, in any substantive way, be related to the populations of Melanesia. For many years, the answer to this question was simply 'no' (e.g., Howells 1943, 1979), not necessarily because Polynesians bear no affinity to any of the populations situated to the west, but rather, because a premise upon which these comparisons were made (i.e., a single Melanesian population) was seriously flawed (cf. Green 1967, 1989, Brace and Hinton 1981). Genetic studies conducted within Melanesia beginning in the late 1940s had resulted in the discovery and description of such extraordinary genetic heterogeneity among the numerous small isolated populations that inferences about the region's prehistory often seemed untenable (Simmons 1973, Terrell and Fagan 1975). However, since the 1960s, a body of genetic data has emerged which independently links the peoples of Polynesia with populations in Melanesia and in Asia (Hill *et al.* 1985, 1987, 1989, Hertzberg *et al.* 1988, 1989, Serjeantson and Hill 1989, Stoneking *et al.* 1990, Clark and Kelly 1993).

In this paper, I will briefly examine an alternative to a genetic model of rapid expansion of pre-Polynesians out of Asia. The standards for judging this alternative will be the application of principles generally applied to population genetic data, rather than a discussion of how these data are consistent with a particular model of Pacific colonisation. I will recount how, from the vantage provided by the insights of Green and others, the evidence points to the Polynesians having been derived from Austronesian speaking palaeopopulations of Melanesian Near Oceania. The terms 'Near Oceania' and 'Remote Oceania', as defined by Green (1991) will be used throughout this discussion. Ancient Near Oceania consists of the islands of Southeast Asia and the islands of Western Melanesia through the main Solomons. These two geographic sub-areas will be referred to as Asian Near Oceania and Melanesian Near Oceania, respectively, following Clark and Kelly (1993). In the initial formulation of Pawley and Green (1973), the term Near Oceania was restricted to Melanesian Near Oceania. Remote Oceania refers to all other islands of Oceania. This terminology is useful because, as argued by Green, it provides a more appropriate division for dealing with prehistory in the Indo-Pacific region, and because it ultimately impacts on how one thinks about the prehistory of the region (e.g., arguments about internal development versus external contacts).

## **POLYNESIAN ORIGINS AND THE LAPITA 'PEOPLES'**

The importance of Lapita distribution is derived from several features, not the least of which is the fact that the people occupying Lapita sites in the Fiji-West Polynesia region demonstrably constitute the ancestral Polynesian population (Kirch and Green 1987, Green 1992). In large part due to this association, the term Lapita, although technically a ceramic style, may be applied to the people who made those pots as well as to their culture.

The peoples of Polynesia, in common with numerous populations of island and coastal Melanesia as well as populations of Southeast and East Asia, speak one of the Austronesian languages. For some Pacific prehistorians, the Lapita peoples equate with Austronesian speakers (e.g., Shutler and Marck 1975, Bellwood 1979, 1991, Kirch 1988, Bellwood and Koon 1989, Spriggs 1989). While this view is not universally

accepted, Clark and Kelly (1993) have provided a basis for equating the makers of Lapita ceramics with the Austronesian speaking colonisers of Melanesia. Drawing upon evidence that Austronesian speaking populations possess a genetic advantage over Non-Austronesian speakers with regard to malaria (Kelly 1988, 1990, 1992), and noting that archaeological sites with Lapita ceramics are consistently located in coastal lowlands (which in many parts of Oceania would have been malarious), Clark and Kelly (1993) have argued that the inhabitants of those Lapita sites spoke one or more of the Austronesian languages.

In recent years two contrasting schools of thought have developed on the question of Lapita origins. Scholars in the first argue that the origin of Lapita lies in Asian Near Oceania, with a migration into Melanesian Near Oceania (Bellwood 1979, 1984-85, 1989, Kirch 1988, Spriggs 1989). The second school advocates 'internal' development (i.e., within Melanesian Near Oceania), specifically in the western islands of this region (Green 1979, Terrell 1986, White *et al.* 1988). However, the people who made Lapita ceramics were not the first inhabitants of the Pacific. In Melanesian Near Oceania, one finds indigenous peoples who speak languages unrelated to Austronesian (i.e., Non-Austronesian speakers) (Bellwood 1989). It is widely accepted that the spread of humans through the Indo-Pacific took place after 40,000-50,000 years ago with the move from Sundaland across Wallacea and into Sahul (Clark 1991). New Guinea was occupied by 40,000 B.P. (Groube *et al.* 1986). New Ireland, in the Bismarck Archipelago, was colonised by 35,000 B.P. (Allen and Gosden, this volume), and by about 28,000 B.P. humans were on Buka in the Northern Solomon Islands (Wickler and Spriggs 1988). Whether one subscribes to the notion that the essential cultural elements of Lapita were imported into Melanesian Near Oceania or believes that, while pottery and some other elements may have been introduced into Melanesian Near Oceania from Asian Near Oceania, 'the basic developments that lay behind the Lapita cultures occurred within the Bismarck Archipelago' (White *et al.* 1988:416), the makers of Lapita pottery and the descendants of the people who arrived before them have some shared history in Melanesian Near Oceania.

## THE GENETIC TRAIL

In recent years, the external model has been adopted by a group of investigators as a framework for interpreting population genetic data (e.g., Serjeantson *et al.* 1982, Serjeantson 1984, 1985, 1989, Hill *et al.* 1985, Trent *et al.* 1988, Hertzberg *et al.* 1989, Serjeantson and Hill 1989, O'Shaughnessy *et al.* 1990, Gao and Serjeantson 1991, Chen *et al.* 1992, Gao *et al.* 1992a, Hagelberg and Clegg 1993). The various lines of this 'external' genetic model have been fostered by Serjeantson, who first suggested that the genetic data might be used to address whether the Lapita potters 'were derived from the earliest Austronesian speakers in Eastern Melanesia or represent a second wave of Austronesians from Eastern Indonesia (Serjeantson *et al.* 1982:906, Serjeantson 1985: 134).

In a subsequent summary of genetic studies of Pacific populations (Hill and Serjeantson 1989), Serjeantson and Hill (1989), echoing the sentiments of Howells (1979) from a decade earlier, advanced a view of Oceanic prehistory in which the extant Polynesians are derived from people of Asian origin who settled in and then quickly dispersed from the Bismarck Archipelago into Polynesia. During their diaspora, these 'Polynesians acquired [certain] island Melanesian markers while leaving relatively little evidence of their own Polynesian markers in island Melanesia' (Serjeantson and Hill 1989:288). Bolstered by the Serjeantson and Hill (1989) conclusions, Bellwood and Koon (1989:614) observed that

the linguistic and genetic records leave little doubt that the Polynesians, a major group of direct descendants of the Lapita colonizers, are basically of Island Southeast Asian origin. A similar origin applies linguistically, but less so genetically to the Austronesian-speaking Island Melanesian, who would appear to have a more complex ancestry combined of both indigenous Melanesian and *intrusive* Austronesian elements.

Consequently, in a recent and extreme rendition of the external genetic model, Gao *et al.* (1992a:35) have asserted that

AN-speaking Melanesians apparently arrived in New Caledonia and Fiji after the early Polynesians [citing Bellwood 1989], possibly having acquired sea-going skills and Austronesian languages from the pre-Polynesians, so some remnant Polynesian genetic elements may be expected in these populations also.

The events suggested by Gao *et al.* (1992a) differ from the earlier genetic versions of Pacific colonisation in one very crucial element. They imply that only one Austronesian colonisation occurred. According to this

scenario, the presence of Austronesian speaking peoples in Melanesian Near Oceania post-dates the development of incipient Polynesian culture. Austronesian speaking populations exist in Melanesia because at some point back in time, endemic Non-Austronesian speaking populations adopted Austronesian languages and acquired Asian genes from the advancing Polynesian colonisers.

While scholars undoubtedly will continue to debate whether its homeland lies in the area of South China to Taiwan (Foley 1980, Bellwood 1984-85, Blust 1984-85, Tryon 1984-85), Taiwan to the Philippines (Pawley and Green 1984) or insular Southeast Asia (Meacham 1984-85, Solheim 1984-85), the weight of the linguistic evidence suggests Asian Near Oceania or mainland Asia is the *ultimate* origin of Austronesian languages. If all Austronesian speaking peoples were descended from common ancestral stock, the genetic data would not discern whether the Lapita people were the first or among the subsequent Austronesian speakers to arrive in New Guinea (see Serjeantson and Hill 1989, see also Serjeantson 1984:161). Nevertheless, various lines of evidence independently attest that the Austronesian speaking Polynesians are descended from the Lapita potters (Kirch and Green 1987, Green 1992). However, if one simply applies the external model to the interpretation of Polynesian origins, extant Polynesians simply become the embodiment of the Lapita colonisers. Having 'validated' modern Polynesians as the representatives of the ancestral population (Serjeantson 1984, 1985, 1989), one can then make estimates of admixture with Lapita peoples for populations in the path of the Lapita advance from Melanesia into Polynesia (e.g., Serjeantson 1984, 1989, Serjeantson and Hill 1989).

Unfortunately, it is the origin and subsequent migrations of Lapita peoples that the genetic evidence has been assembled to address. Accepting the assumption does not prove the model. If one assumes that the Polynesians are the sole descendants of a single Austronesian migration, then the linguistic and genetic traits that extant Melanesian populations share with populations in Asia and Polynesia are intrusive by definition, not by discovery. On the other hand, if one assumes that the Austronesian speaking populations of Melanesia and Polynesia are derived from that same migration, the linguistic and genetic traits that extant Melanesian populations share with populations in Asia and Polynesia are signs of that shared ancestry by definition, not by discovery. Consequently, because the Lapita peoples moved into Polynesia from Melanesia, the Austronesian speaking populations of Melanesia are, by definition, the direct descendants of the forbears of the Polynesians.

Given the genetic traits and linguistic features which link certain Austronesian speaking populations of Melanesian Near Oceania with Austronesian speaking peoples of Polynesia to the east as well as to populations in Asia, what is the need for and basis of the external genetic model? As summarised by Serjeantson and Hill (1989:287):

the lack of particular coastal New Guinea markers in Polynesians, such as the high-frequency  $-\alpha^{4.2}$  thalassemia deletion, the albumin NG variant, the HLA-B13.Cw4 haplotype, and the B allele of the ABO blood group, all argue that the pre-Polynesians moved rapidly through this part of Melanesia.

However, on examination each aspect of the argument either fails or is irrelevant:

- 1) The absence of the  $-\alpha^{4.2}$  thalassemia deletion:  $-\alpha^{4.2}$  thalassemia is a north coast deletion (Hill *et al.* 1989) rather than an Island Melanesian deletion. On the other hand,  $-\alpha^{3.7}$ III, common among populations in Island Melanesia, is also found among Polynesians. Consistent with archaeological evidence placing the Lapita heartland (*nee* homeland) in the islands and not on the coast, Serjeantson and Hill (1989:287-88) note, that the 'presence of the  $-\alpha^{3.7}$ III but not the  $-\alpha^{4.2}$   $\alpha$  thalassemia deletion indicates that ... contact' [or was it their origin] 'was probably mainly in northern island Melanesia rather than in New Guinea.'
- 2) The absence of the albumin NG variant among Polynesians: This is, without a doubt, the most specious piece of evidence cited by Serjeantson and Hill (1989). In the lone discussion of albumin NG preceding the Serjeantson and Hill (1989) summary chapter, Kirk (1989:74) cites three sources pertaining to the frequencies or distributions of albumin variants. Kirk provides Weitkamp *et al.* (1973) as the source of summary information. Weitkamp *et al.* (1969) are identified as having 'first reported two different albumin variants in New Guinea,' and McDermid and Vos (1971) are cited to support that albumin NG 'is most widespread in coastal [New Guinea] areas.' Kirk (1989) notes that the other New Guinea variant, 'albumin Uinba, appears to be restricted' to a single village in Western Highland Provinces and that '[n]o albumin variants have been detected in Australian Aborigines'. Polynesian populations are not mentioned in Kirk's discussion of albumin variants. Neither are Polynesian populations identified by Weitkamp *et al.* in 1973 or in more recent

discussions of albumin variants such as Arai *et al.* (1990). Therefore, at least at this juncture, the absence of the albumin NG variant among Polynesians is due to the fact that no one has looked.

- 3) The absence of the HLA-B13.Cw4 haplotype: Crane *et al.* (1985) is cited by Serjeantson (1989) as having demonstrated the HLA-B13.Cw4 haplotype as a marker of coastal Melanesians. Crane *et al.* (1985:248) collected data on 'forty-two unrelated Coastal New Guineans, who were temporary residents in Sydney.' Indeed, the haplotype was found among this group of coastal New Guineans at a frequency of 0.125. However, these coastal New Guineans 'came from a variety of birthplaces, but predominantly from the North Coast of mainland New Guinea' (Crane *et al.* 1985:248). Thus, as in the example of the  $-\alpha^{A2}$  thalassaemia deletion, the data reflects conditions on the north coast of New Guinea rather than among populations on the islands to the east.
- 4) The absence of the B allele of the ABO system in Polynesia: While the significance of the albumin NG distribution cannot be assessed, the interpretation of B allele data is simply wrong. While it is true that the B allele is 'effectively absent' among 'Polynesian populations in the central Pacific' (Kirk 1989:62), it is present in Tonga and Samoa (7-10%), and therefore is present in Polynesia at frequencies comparable to many Austronesian speaking Melanesian populations (e.g., Fiji: 5-10%, Vanuatu: 7%, New Caledonia: 4-10%) (see Kirk 1989:62).

Thus, upon inspection, the Serjeantson and Hill (1989) claim of the absence of certain 'coastal Melanesian' polymorphisms among Polynesians provides no basis for suggesting that the forbears of the Polynesians bypassed (only in the genetic sense) the Austronesian speaking populations in Melanesian Near Oceania and therefore, provides no evidence for the rapid dispersal of the Lapita peoples.

#### DERIVING THE POLYNESIANS FROM AUSTRONESIAN SPEAKING PALAEOPOPULATIONS OF MELANESIAN NEAR OCEANIA

The most likely source of a genetic test of the external model comes from the recent discovery of a nine base-pair deletion in mitochondrial DNA [mtDNA]. This polymorphism probably arose once in human evolution and marks populations of East Asian origin. The fact that this marker is found in Asia, Indonesia, the Philippines, coastal New Guinea (specific populations and language affiliation unspecified), and Polynesia but is absent in Highland New Guinea (a Non-Austronesian region) points to Austronesian speaking populations having originated in Asia rather than having been derived from within Melanesia (Hertzberg *et al.* 1989, Stoneking *et al.* 1990). This 'Asian-specific deletion' is fixed in many of the Polynesian populations examined (93% overall) and occurs in 82% of Fijians (Hertzberg *et al.* 1989). However, the deletion occurs among coastal and Island Melanesians at frequencies (8-14%) which are remarkably similar to the frequencies observed among populations in Asia (16-18%) (Hertzberg *et al.* 1989).

Hagelberg and Clegg (1993:168) recently have reported that the 'Asian-specific marker was found in DNA extracted from relatively recent prehistoric Polynesian bone but was absent in specimens from Melanesia and the central Pacific associated with Lapita archaeological sites.' Nevertheless, Hagelberg and Clegg (1993:168) note that the 'present-day distribution of the 9 [base-pair] deletion in Oceania supports the view of a recent Southeast Asian ancestry for Polynesians' and remarkably suggest that the central Pacific had been populated by an earlier 'Melanesian' occupation.

Hagelberg and Clegg (1993) conclude, and I agree, that the mtDNA results imply that 'Lapita culture' was carried from Melanesia. However, I believe it is incorrect to infer that modern Polynesians cannot be derived from these early colonisers. Hagelberg and Clegg's speculation about the homeland of the earliest inhabitants of the central Pacific is based on the fact that the 9 base-pair deletion was not detected in any of the five bone specimens from early Lapita sites in Fiji, Tonga, and Samoa. The authors add caution to their conclusions, noting the small samples sizes and the fact that their interpretations are built on negative evidence. Therefore, it behoves us to ask: what is our expectation of finding the deletion among the skeletal remains of an ancestral Polynesian population? We can address this question by referring to standard statistical tables used to obtain the confidence intervals for binomial distributions (Conover 1980: 433-44, Table A3). For example, given that the expected population frequency of the deletion is 0.90 (i.e., comparable to, but less than the frequency observed among modern Polynesians), it is very unlikely that *none* of the five specimens would exhibit the deletion ( $p = 0.0000$ ). On the other hand, the probability of not finding the deletion in any of the five specimens, given that this central Pacific group is representative of East Asians (20%), is 0.3277. If these bone specimens are representative of 'Melanesian' frequencies of the deletion

(10%), the probability is 0.5905. Thus, the population represented by bone specimens from central Pacific Lapita sites fall with the range of extant East Asians and extant Melanesians and outside the range of extant Polynesians. In other words, the mtDNA data cannot be used to exclude either an Asian or a Melanesian origin for these early inhabitants of the central Pacific.

While the deletion occurs at higher frequencies among extant East Asians than among extant Melanesians, the differences are marginal (16-18% in Asia as opposed to 8-14% in Melanesia). However, it is important to remember that while the deletion is observed at high frequencies among modern Polynesians (93% overall), it only occurs in less than one out of five East Asians. Presumably, if the deletion had been discovered in 20% (one out of five) of the central Pacific specimens, the frequency observed among populations from which numerous authorities cited above deem it necessary to derive modern Polynesians, Hagelberg and Clegg would not have suggested that the central Pacific had been occupied by an earlier 'Melanesian' occupation. However, if the absence of the deletion in a sample of five specimens demonstrates that these early Lapita people have little connection with the extant Polynesians, then using that same criterion, we must also exclude any connection between extant Polynesians and extant populations in Asia or in Melanesia.

The Polynesians *did* come from somewhere. However, if we are unwilling to accept the continuity between these early Lapita sites and modern occupants (Kirch and Green 1987, Green 1992), then we must invoke an additional migration, a necessary event also in the Hagelberg and Clegg interpretation. But a migration from where? Based on the mtDNA criterion, we must exclude populations in Asia and Melanesia, that is, unless these differences arose from a population bottleneck.

Hagelberg and Clegg (1993:168) explain the high frequency of the deletion among extant Polynesians 'by population bottlenecks during [their] migrations into the central Pacific and eastern Polynesian islands.' Earlier, Hertzberg *et al.* (1989:508) had concluded the high frequencies of this deletion suggest that the forbears of the extant Polynesians were 'a relatively small and independent colonizing in the Pacific who derived from an east Asian precursor population.' When and where that bottleneck occurred has not been clear. However, in the absence of alternative mechanisms, one is compelled to agree that the high frequencies of the deletion seen among modern Polynesian are the result of a population bottleneck. This bottleneck is presumed to have occurred because the deletion occurs at lower frequencies among the descendants of the candidate ancestral populations (16-18% in Asia). However, if we are willing to consider populations with lower frequencies of the deletion, such as populations in Southeast Asia, we must consider the populations in Melanesia as well as the population represented by the skeletal remains associated with the Lapita sites in the central Pacific. At the present time, the mtDNA data provides no justification for excluding the population represented by the bone specimens in the central Pacific Lapita sites from the Polynesian lineage. Moreover, the populations represented by the bone specimens from the central Pacific Lapita sites occur at the time and place where one would expect to find the forbears of the Polynesians. In fact, directly to the point of this thesis, the absence of the deletion among this small sample places, as Hagelberg and Clegg (1993) have concluded, the proximate origin of these peoples and their associated culture in Melanesia.

## FIJI, THE FIRST POLYNESIAN BOTTLENECK?

In various venues (e.g., Serjeantson 1984, 1985, 1989, Serjeantson *et al.* 1982, Serjeantson and Hill 1989), Serjeantson has asserted that 'the HLA data cannot support the theory of Polynesian evolution within eastern Melanesia' (1984:171). Serjeantson suggests that the

early Polynesians had haplotypes HLA-A9.Bw22 [HLA-A24.Bw22 in Serjeantson 1989] and HLA-A2.B40 ... found in contemporary Mongoloid populations. (Serjeantson 1984:171)

HLA-A2 has a low gene frequency in coastal and inland Melanesia, ranging from 4-8%, but increases appreciably in Polynesia to 18-30% In all of these groups, HLA-A2 is in significant linkage disequilibrium with HLA-B40, indicating a common source of the origin of the A2 allele. (Serjeantson 1984:167)

HLA-A11 and -B40 are significantly associated with each other in Australia, in Melanesia and in Nauru. In contrast, these antigens have a different source of origin in Polynesian populations, where they are not significantly linked. HLA-A9 [A24] and Bw22 are tightly linked in Polynesia and also Fiji, clearly indicating that Fiji is a mixture of both Melanesian and Polynesian genetic influences. (Serjeantson 1984:167)

HLA-A9 [HLA-A24] and HLA-Bw22 are also found among contemporary Austronesian speaking populations in Melanesian Near Oceania. However, these antigens do not exhibit significant linkage disequilibrium in those groups, hence the finding that HLA-A9.Bw22 [HLA-A24.Bw22] is not present (Serjeantson *et al.* 1982, Serjeantson 1984, 1989).

The Polynesians could not have evolved within 'Eastern Melanesia' (according to the HLA data) because the populations of Polynesia and Fiji exhibit a subset of the HLA antigens and HLA linkage relations observed among the Austronesian speaking populations of Melanesian Near Oceania (see Serjeantson 1984, 1989). However, after recognising that 'there are clearly differences between western and eastern Polynesia' (Serjeantson 1989:142), Serjeantson (1989:166-67) reasoned that

eastern Polynesia was probably colonized by only a small number of settlers, since some antigens, such as HLA-B13 and B27, were not represented in the migrating groups. Gene frequency distributions, as well as linkage relationships, clearly place the Maoris of New Zealand in the eastern Polynesian branch, together with Hawaiians and Easter Islanders.

Some scholars have taken archaeological evidence to suggest two major points of dispersal, Samoa and later the Northern Marquesas, during the colonisation of Polynesia (e.g., Brockway 1983). The genetic data suggest that events in Melanesian Near Oceania also significantly shaped the composition of the subsequent Polynesian gene pool. In fact, in their discussion of genetic affinities of Eastern Polynesians, Hill *et al.* (1987:460) concluded that

data on several markers in the globin gene complex provide clear evidence of founder effects during colonization and provide substantial genetic affinity with island Melanesia — and also, to a lesser extent, with Southeast Asia.

Similarly, Gao *et al.* (1992b:153) recently have reported that the 'Polynesian HLA class II genetic repertoire is not readily derived from the island Southeast Asian gene pool.' If genetic drift can be invoked to explain the clear differences between Eastern and Western Polynesians, why not put the first population bottleneck in Fiji to explain genetic affinities of the first Fijians and the later Polynesians?

In their account of the genetic affinities of the first Fijians, Serjeantson and Hill (1989) have suggested that 'the proportion of Lapita women amongst early Fijians was about 80 per cent, even though Lapita people as a whole comprised only 20 per cent of the population'.<sup>1</sup> Serjeantson and Hill (1989) appear to be attempting to explain what they perceive as an incongruity between the populational affinities suggested by mitochondrial DNA [mtDNA], a maternally inherited chromosome, and populational affinities suggested by HLA antigens. The 80% figure for Lapita women comes from analysis of mtDNA among extant Fijians (Hertzberg *et al.* 1988). The 20% figure for the total population comes from estimates of 'triracial admixture' derived from HLA data (Serjeantson 1984, 1985, 1989). While the Serjeantson and Hill (1989) discussion illustrates one of the many problems with interpreting estimates of admixture, it also suggests that a population bottleneck occurred in Fiji. Such an explanation provides a more parsimonious explanation of the Fijian data than does the population mix of mainly Lapita women (i.e., Polynesians) and, evidently, predominately 'Melanesian' men invoked by Serjeantson and Hill (1989).

The barrier to Remote Oceania, initially Vanuatu, then New Caledonia and Fiji, and eventually all of Polynesia, does not appear to have been crossed until just a few thousand years ago (Wickler and Spriggs 1988, Green 1991). Green (1979) has suggested that the Polynesians evolved from populations moving out of the Bismarcks to Santa Cruz and Vanuatu. According to this scenario, Fiji as well as New Caledonia were then colonised from Vanuatu. Elsewhere (Kelly 1988, 1990), I have suggested that Fiji represents a transitional area where the absence of malaria resulted in the relaxation of selective pressure on the maintenance of high frequencies of the immunoglobulin haplotype<sup>2</sup>, IGHG1\*A,F G3\*B0,B1,B3,B4,U, which characterises the Austronesian speaking populations in Island Melanesia, to variable frequencies of IGHG1\*A,F G3\*B0,B1,B3,B4,U, IGHG1\*A,Z G3\*G1,U and IGHG1\*A,X,Z G3\*G1,U, typical of Austronesian speaking Polynesians. Fiji's position as an area of cultural, linguistic, archaeological, and genetic transitions from things Melanesian to things Polynesian seems secure. Perhaps the genetic as well as the cultural transitions observed among populations as one moves from Near into Remote Oceania are best understood as a series of population bottle-necks beginning with a small group of Lapita potters who made their way to Fiji from Vanuatu (cf. Green 1979).

## THE END OF THE TRAIL

Two features account for the current attraction and, for what I believe will be, the ultimate decline of the external genetic model. The first is the very evident reliance on typological thinking to account for genetic composition of populations along the trail. The second is the fallacy of seeing the Polynesian as the main line of evolution in the Pacific. Clearly, if one simply subscribes to the notion that the Polynesian forbears moved rapidly out of Asia and into the central Pacific, evolutionary events (biological as well as cultural) which may have occurred in Melanesia are of little importance to Polynesian prehistory. Accordingly, proponents of the external genetic scenario have continually seen similarities between extant Austronesian speaking populations in Melanesian Near Oceania and populations in Southeast Asia as signs of the pre-Polynesian advance, rather than interpreting these features as simple evidence that Austronesian speaking peoples of Melanesia and of Polynesia share a common genetic and linguistic origin. When the evidence has suggested that events in Melanesia are relevant to the origins of the Polynesians, another migration of Austronesian speaking Southeast Asians often is invoked to provide a mechanism whereby the Melanesian elements of the endemic population can be superseded and thus, maintain the integrity of the model.

Clearly, the most parsimonious interpretation of the genetic data is that the Polynesians were derived from Austronesian speaking palaeopopulations of Melanesian Near Oceania. Unfortunately, the genetic data has little bearing on whether major components of 'Lapita culture' developed in the Bismarcks or in Asia, for that is truly an archaeological question. Nevertheless, the distributions of numerous genetic polymorphisms attest that events associated with developments within and movements from Melanesian Near Oceania have shaped the genetic and cultural profiles of the peoples of the central and eastern Pacific.

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## NOTES

1. In defence of these estimates, Serjeantson and Hill (1989:289) cite Wurm (1967), noting that 'Lapita peoples settled in Fiji, followed quite closely by Melanesians'. In fact, what Wurm (1967, 1983) suggested, on linguistic grounds, was that Austronesian speakers first settled in Vanuatu (New Hebrides), New Caledonia and Fiji, and were later overlaid by a Papuan (Non-Austronesian) migration.

2. The Gm nomenclature used here follows the recommendations of Shows *et al.* (1987). Initial reports of these findings (i.e., Kelly 1988, 1990) followed earlier conventions. In addition, the complete series of recognised "B" allotypes is identified rather than the abbreviated format as used by Kelly (1988, 1990).

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