A Different Paradigm for the Initial Colonisation of Sahul:

Archaeological, genetic, demographic and geographic perspectives

Jim Allen

School of Archaeology and History, La Trobe University

James F. O'Connell

Department of Anthropology, University of Utah

20 Aug 2019

Corresponding author: J. Allen jjallen8@bigpond.net.au

Abstract

The questions of when and how humans reached Sahul, the Pleistocene continent of Australia and New Guinea, has remained a central issue of Australian archaeology since its development as an academic discipline in the mid-twentieth century. Additionally, this has been a dominant theme linking Australian and world archaeology. Modelling this event has persistently appealed to minimal assumptions – the simplest watercraft, the shortest routes, the smallest viable colonising groups. This paper argues that Australian archaeology can no longer ignore the way our understanding of this initial colonisation is being reshaped by current genomic research. It reviews this evidence and concludes that a colonising wave of hundreds or perhaps low thousands of people were involved. If correct, it suggests that we need to rethink our models, modify or discard the minimalist assumptions that have so far driven them and consider how this different paradigm affects our understanding of early settlement in Sahul.

Key Words: Sahul, Wallacea, colonisation, isolation, genomics, mitochondrial DNA

We must not be obsessed with the route to Australia involving the shortest water crossings.

Rhys Jones (1968:190)

Together and independently over the last four decades we argued questions of initial Sahul colonisation with our friend John Beaton, even after his career moved away from archaeology. He had more than a passing interest in this wide subject (e.g. Beaton 1985, 1991, 1995). Beaton loved the notion of thinking outside the square and we offer here some different ideas on Sahul colonisation as a mark of respect to our late colleague.

In inferring human behaviour from archaeological data it is prudent to create minimalist models of that behaviour because such models usually demand the fewest assumptions to infill the gaps in the material evidence, such as those reflecting human motives, objectives, co-operation, information-sharing, and so on. There is a general if uneven correlation between the minimalism of such scenarios and the time depth involved. This partly reflects greater evidence gaps for the deep past, but also an earlier, sometimes lingering view that early anatomically modern humans (AMH) were restricted in their ability to solve new problems. Some still choose to view long-term history in social evolutionary stages, from savagery to civilisation, if you will, where the associated capabilities of Pleistocene hunter-gatherers were implicitly inferior to ours.

Minimalist modelling is no more apparent in Sahul archaeology than in discussions of Sahul's initial colonisation. Ever since Grafton Elliot Smith argued in 1914 that the proposed antiquity of the Talgai cranium showed that Sahul's first colonists were also the world's earliest sailors, periodic examinations and reconstructions of this seaborne colonisation have mostly appealed to the simplest explanations, particularly in respect of the sea as a barrier.

Historical background

The rise in professional archaeology in Australia from the 1960s onwards led to speculation on various aspects of the initial human arrival in Sahul. Despite Jones' insightful 1968 admonition, the dominant early theme was that accidental crossings at times of lower sea levels that provided potentially shorter inter-island distances were to be favoured (Mulvaney 1975:144; Hallam 1977:130; Jones 1979:449, 1989:753-6; White and O'Connell 1982:46). Calaby's (1976:23-4) whimsical proposition of a pregnant woman on a log being the Aboriginal Eve touched on two further themes subsequently much developed, those of minimal sea transport and the minimum number and age/sex composition of a viable colonising population. An early contributor here, demographer Norma McArthur (1976; McArthur et al. 1976) glimpsed the future when she and colleagues reported computer simulations of demographic viability suggesting that while Australia might statistically have been populated by one man and two women of reproductive age, the overwhelming probability was high failure rates for small colonising groups. Another emergent theme, that rising sea levels reduced the availability of land and forced eastwards movement (Thiel 1987) had already been countered a decade earlier by Dunn and Dunn (1977) who showed that Sunda, when the sea was at 100 m below present levels, possessed less than 50% of the present length of coastline. One consequence of this idea, developed firstly by Chappell and Thom (1977) and elaborated by Chappell (1993) and Terrell (2004) was the idea that higher sea stands promote the development of productive littoral zones, including reefs, lagoons, estuaries and swamps. This suggested that movement might best have been undertaken during these higher stands and offered a counter to the minimalist lower sea levels argument.

A third minimalist theme concerned routes. Birdsell (1977) became and continues to be a perennial reference for this, although his paper was concerned with other things as well, watercraft capabilities and a preference for lower sea levels among them. Irwin's (1991, 1992) perceptive elaboration of Birdsell's ideas, especially questions of intervisibility, allowed us (e.g. Allen and O'Connell 2008:37-8, 43) to advocate the probable primacy of Birdsell's northern route into the Bird's Head of New Guinea, even though many Australian researchers then and now favour the southern route through Timor, freeing them from considering the New Guinea evidence. Throughout, models and interpretations of the data on routes, including ours, remained minimal.

This summarises some salient points elaborated elsewhere both by us (Allen and O'Connell 2008; O'Connell et al. 2010; O'Connell and Allen 2012) and others (e.g. Anderson 2000; O'Connor 2010; O'Connor and Veth 2000). What these and other summary papers (e.g. Davidson and Noble 1992) also tried to address were what factors might have led to this diaspora and how it might have been achieved. Working from the available archaeological evidence in Wallacea and using aspects of optimal foraging theory (OFT) (see also Anderson 1981, 2009 and refs) we proposed a model for this colonisation that might be tested in the expanding archaeological record. This involved the primacy of reef/littoral resources, especially shellfish, as both a major subsistence target for expanding AMH groups moving through Wallacea and also an impetus for movement into pristine coastal environments as the most attractive resources diminished in occupied areas. The model grew from the ethnographies of tropical coastal hunter-gatherers (Meehan 1982; Bird and Bliege Bird 1997) and available archaeological evidence (Gosden and Robertson 1991; Leavesley and Allen 1998; see also Codding et al. 2014) and the knowledge that people moving east through Wallacea increasingly encountered islands with diminishing land faunas before reaching Sahul. We recognised the simplicity of this model, given the variability of the Wallacean islands in terms of sizes and concomitant availability and sustainability of food sources, but saw that it offered an alternative to untestable explanations like human curiosity. While the littoral model has drawn some criticism (e.g. Anderson 2018) it has been largely adopted by others (e.g. Kealy et al. 2016; O'Connor et al. 2017; Norman et al. 2018).

Inevitably discussions of colonisation became linked to questions of the chronology of first arrival. Our earliest summary (O'Connell and Allen 1998) promoted our view of a short chronology linked to purposeful colonisation. Colleagues favouring the longer 60 ka chronology (O’Connor and Veth 2000:103-5; Chappell 2000) pointed to the disparity between this age for Australian sites and then current dates, up to 30 ky younger, for Island South East Asia and Melanesia. They took this to indicate a more random colonisation of Sahul, an argument also seen to favour the Timor route (O’Connor 2007). While the chronology of Sahul colonisation remains important we see no arguable cause-and-effect nexus between when Sahul colonisation first occurred and AMH ability to achieve it (cf. Davidson and Noble 1992). If we exclude the extreme age claimed for Madjedbebe (Clarkson et al. 2017) the increasing consensus of available evidence currently puts this event in the range 47 ka to 51 ka. Despite some suggestions (e.g. Cooper and Stringer 2013; Jacobs et al. 2019) there is so far no serious challenge to the proposition that the colonisation of Sahul was only achieved by *H. sapiens* and never by archaic humans. However a radical extension of this time frame, perhaps to 80+ ka on the published Madjedbebe evidence would call this view into question (see criticism of this in O’Connell et al. 2018).

Where are we now?

A survey of recent literature mostly indicates a continuation of the same or similar themes using better maps and marine charts and more powerful computing and modelling programs.

Anderson (2018) elaborates a theme he has previously developed (e.g. Anderson 2000, 2010) where the availability of warm seas and large diameter bamboos and many island targets in Wallacea made marine mobility easy. We do not see how the coalition of these factors might necessarily force early maritime migration in the region, although they certainly facilitated it. Our argument that serial depletion of high-ranked resources propelled AMH through Wallacea is not challenged or replaced by Anderson’s proposition, which lacks a necessary explanation of motive(s). Nonetheless Anderson offers compelling evidence for the primacy of bamboo rafts as watercraft, which required limited tools and technical skill to construct. Such vessels might keep 50-100 individuals seaborne almost indefinitely. If the technical complexity of such craft were, in Anderson’s words, ‘below the AMH paygrade’, he remains mischievous by continuing to promote minimalist drift voyages on rafts with no means of steerage, where simple paddles or even paddling by 100 hands might offer some directional control - ‘inventions’ also below the AMH paygrade. The obvious question here is what might motivate 100 modern humans to build and board a raft without any control over an eventual landfall? Somewhat contrarily Anderson (2018:225) questions our serial depletion model by arguing for high skill in marine and terrestrial food acquisition by the earliest colonisers, suggesting that for such people local shellfish depletion would not force migration. Certainly the wide range of terrestrial foods referenced at Niah Cave (Piper and Rabett 2017) indicates that AMH had such terrestrial skills prior to leaving Sunda. Even east of Wallace’s Line, where the variety of terrestrial prey diminished, tropical Pleistocene hunter-gatherers certainly targeted terrestrial foods such as the fruit bat on New Ireland (Leavesley 2004). However, in a recent summary O’Connor et al. (2017) have reviewed Pleistocene dietary remains in sites from Sunda to Sahul and noted an unusual distinction between archaic human and AMH deposits across

Wallacea, where archaic human sites reflect no dependence on littoral/marine resources and AMH sites show the opposite:

> All records indicate that *H. sapiens* that moved through the islands east of Huxley's Line were able to do so as a result of ecological flexibility and innovation, which allowed them to successfully subsist on the most depauperate of islands through the exploitation of almost purely marine resources (O'Connor et al. 2017:S578).

Shellfish, and especially species from fringing reefs, form the most consistent aspect of these assemblages although none of the sites reviewed apparently relate to the initial colonisation. Optimal foraging theory suggests that in these circumstances larger species of shellfish, such as *Tridacna spp*. (Bird and Bliege Bird 1997; O'Connell et al. 2010; Codding et al. 2014) would have been frequently exploited high-ranked resources because of low search time and easy processing. When such resources are depleted, OFT suggests that the predator either adds lower-ranked prey to its diet or moves to a new location where the higher-ranked resources are more common. Moving to pristine shell beds was likely an obvious strategy, particularly in the eastern islands of Wallacea where terrestrial resources may have consisted only of reptiles, rats and bats.

Despite the argument that higher sea stands support the most food-productive littoral zones, the idea that lower sea levels may have facilitated onward movement between islands has had a recent resurgence for various reasons, none of which should be accepted uncritically. For example, Norman et al. (2018) begin with the premise that AMH had reached Sahul c. 60-70 ka, at which time low sea levels enlarged islands and reduced distances between them. Here the argument is predicated on the Madjedbebe dates; the lower sea levels of this period require an accommodation to fit the dates rather than offering an explanation for human transit. These authors apply an intervisibility analysis ('bi-directional macro-viewshed analyses') and test the results against various simulations involving, for example, push-pull factors and ocean currents. They conclude that their model predicts that entries into Sahul via both of Birdsell's northern and southern routes were 'almost certain'. Although the discussion is obscure these authors flag 'the potential for temporally phased migrations into Sahul through the northwest shelf and the Bird's Head' which we take to mean that they favour an earlier entry into north Australia from Timor. This is *post hoc* justification.

Bird et al. (2018) are concerned mainly with routes and develop an argument that the southern route would have provided the best corridor for first colonists with 'savannah-adapted skills' as a basis for supporting initial arrival into north Australia from Timor. They work within a wider time framework for this event, between 70 ka and 47 ka, to cover the long and short chronologies. They note that sea levels, the major determinant of the relevant palaeogeography and palaeoenvironments, fluctuated c. 10 m during this time, with the greatest dry land exposure and shortest island crossings coinciding with the claimed date of 65±5 ka for Madjedbebe. Accepting a conservative drop of sea level to -75 m and using intervisibility and drift modelling, Bird et al. propose that the Sahul Banks, between north-western Australia and Roti-Timor were both visible and feasible AMH habitats in terms of available food and water and thus add support to the viability of Birdsell's southern route. At the same time these authors do not deny the probability of the northern route being used, nor the possibility that it provided AMH access to Sahul equally as early as the Timor route. Much depends on the claimed viability of the Sahul Banks for human sustenance, argued by Bird et al. on modern analogies with an island in the Pacific, another in the Indian Ocean and nearby Ashmore Reef. The reliability of these comparisons is worth further examination.

De Deckker et al. (2019) suggest on evidence from a new deep-sea core that the climate cooling of MIS 4 between 71 and 59 ka was more extreme than currently believed and was a major glacial period in the Southern Hemisphere. They argue that glacial conditions peaked at 65 ka at which time sea levels were lowered by c. 100 m and sea surface temperature dropped c. 5^0 C. Leaving aside the diminishing of Anderson's warmer seas and other environmental effects - perhaps including a more limited distribution of bamboo at this time - these authors uncritically accept the coincidence of the central age of this stadial interval and the nominated age for Madjedbebe, without acknowledging the uncertainties of this comparison or noting previous criticisms made of the Madjedbebe evidence (O'Connell et al. 2018).

Three further papers by Kealy et al. (2016, 2017, 2018) remain more centrally concerned with routes that are determined by island intervisibility. The 2016 paper is part review but also draws attention to c. 100 submerged Wallacean islands that may have been exposed depending on Pleistocene sea levels, arguing that lowest sea level points are less important than understanding the total seascape during the relevant colonisation period. The 2017 paper develops this theme by offering five palaeogeographic constructions of sea levels and uplift rates at 5000-year intervals between 65 ka and 45 ka. These data are then used to construct intervisibility models that indicate a visual pathway from Timor to northwest Australia before 62 ka and after 47 ka but not between. Instead, as Irwin showed in 1992, Kealy et al. (2017:69) conclude that on the basis of intervisibility Birdsell's northern route was 'the more likely route for initial colonisation.' The 2018 paper elaborates these themes further, taking 70 ka as a proxy for the highest sea level and 65 ka as a proxy for the lowest sea level during an assumed colonisation period of 70 ka to 40 ka. Using least-cost pathway models (see Kealy et al. 2018:63 for explanation) these authors conclude, contra Norman et al. (2018) and Bird et al. (2018) that their models result in 'overwhelming support' for initial entry via the northern route, whether one considers the highest or lowest sea-stands in the relevant period. Of minor importance here, some details of these papers will need adjustment if the sea levels during the MIS 4 glacial period argued by De Deckker et al. (2019) are correct.

In reviewing these papers, we cannot escape the conclusion that current research on this subject is discovering more and more about less and less. Birdsell had arrived at many of the current conclusions in 1977 using only the data available to him at that time, as did Irwin in 1992. More elaborate data bases and computing might provide more 'robust' evidence for the same conclusions, but if they only reinforce what we already know, is this a worthwhile advance? When arguments revolve around whether intervisibility is to be measured from a reconstructed sea level, or 10 m above that sea level or from the highest available mountain, has research become pedantry?

At the same time, many of these papers now touch the edges of important new conclusions. Evidence from Wallacea and Sahul has slowly accumulated to judge the cognitive, technological and artistic skills of late Pleistocene AMH (see Bird et al. 2018:437 for a summary and references). The idea that both of Birdsell's routes were viable at roughly contemporaneous times seems an inevitable conclusion from the multiple papers dealing with this aspect. Kealy et al. (2016:170) elaborate this idea by proposing that AMH movements in Wallacea are better seen as 'a radiation of island colonisation' than direct west-to-east movement. Various lines of evidence, especially genetics, indicate higher numbers of first colonists than earlier minimalist models required. For most archaeologists accidental colonisation of Wallacea and Sahul by AMH is no longer seriously considered (but cf. Bird et al. 2019).

Genomic data demand the attention of archaeologists

Molecular anthropology has had an increasing impact on archaeological practice worldwide since the publication of the highly influential paper on mitochondrial DNA and human evolution by Cann et al. (1987). Analyses of progressively larger samples of DNA have enhanced understanding of genetic diversity in living populations, including those of New Guinea and Australia. Improvements in protocols for the treatment of ancient DNA have helped alleviate contamination problems and now provide more precise estimates of mutation rates in the Late Pleistocene, fundamental to estimating the antiquity of indigenous Sahul genetic lineages. Opportunities for more comprehensive integration with archaeological findings are steadily increasing. Nevertheless, similar to the acceptance of radiometric dating techniques that are not completely understood by archaeologists, so far Australianists have been content to cherry-pick interpretations of genomic analyses that coincide with their arguments. Broader consideration of the results of genetic analyses is essential to appreciate their implications for understanding the process of Sahul colonisation. The necessary comprehensive review is beyond the scope of this discussion but reference to recent work on mitochondrial DNA (mtDNA), currently the best understood and reported segment of the genome, indicates some of the more important insights to be gained from this research. While here we are mostly concerned with mtDNA, note that Y-chromosome data show parallel patterns, with deeply rooted Sahul-specific haplogroups C and K diverging from the most closely related non-Sahul lineages c. 54 ka and dividing into Australia- and New Guinea-specific lineages c. 48-53 ka (Bergström et al. 2016).

Geneticists have known for more than a decade that the first AMH populations colonising Sahul included representatives of all three Eurasian mtDNA macrohaplogroups, now called M, N, and R (Huoponen et al. 2001; Ingman and Gyllensten 2003; van Holst Pellekaan et al. 2006). Estimates of the minimum *effective* founder population sizes (the numbers of reproductive-age women) required to insure the post-arrival persistence of each of these groups have led to further estimates of the minimum total (a.k.a. census) populations of which they were a part. Initially the census estimates were in the scores of individuals for each macrohaplogroup (O'Connell et al. 2010) and in the hundreds for all three combined (O'Connell and Allen 2012). Developing more accurate figures has required identifying a more complete inventory of indigenous Australia-New Guinea mtDNA lineages, determining their respective ages relative to the date of initial Sahul colonisation, and inferring whether they are likely to have evolved either offshore before colonisation or after their ancestors arrived on the continent. Evidence of their presence outside Australia-New Guinea may point to an exotic origin, since indications of back-flow from Sahul remain limited. Nonetheless, this possibility complicates the inference, as do the further possibilities that evidence of their presence in Sunda or Wallacea prior to Sahul colonisation may have disappeared over time, or that some colonising mtDNA haplogroups have since disappeared within Sahul.

In two recent studies of whole genome and control region mitochondrial diversity in samples obtained from hundreds of living Aborigines in many parts of Australia, Nagle et al. (2017a, b) identified at least three common haplogroups - M42, S^N and P^R – together with M15, M16, O^N and N13. All are highly diversified, implying long-term presence on the continent. Tobler et al. (2017) reporting on a different but still relatively large whole genome dataset developed from hair samples collected in the last century from living Aborigines, most of Arnhem Land and South Australian origin, found at least five well-defined haplogroups - M16, M42, S^N, O^N and P^R, again mostly highly diversified. Over a decade ago, Friedlaender et al. (2005, 2007) and Merriwether et al. (2005) published on more than a thousand whole mitogenome and control region sequences, mainly from Island Melanesia, most assigned to haplogroups Q^M and P^R but with a notable few placed in M27-29. Haplogroups Q^M and P^R were again highly diversified, with most of those in P^R (P1-2, 3b, 4) representing haplotypes not found in Australia (see also Tommaseo-Ponsetta et al. 2013).

Precise estimates of the ages of these various haplogroups (i.e. their respective 'times to most recent common ancestors,' or TMRCAs) vary depending on the sources and numbers of individual haplotypes included in analyses and on the estimated inclusion (mutation) rate for characteristic genetic markers (Table 1). Two rates cited in recent literature are important here: one based on phylogenetic comparisons (Soares et al. 2009); the other on analyses of ten ^{14}C-dated Late Pleistocene *H. sapiens* skeletons distributed across Eurasia (Fu et al. 2013). The rates are similar but both Nagle et al. and Tobler et al. consider the Fu et al. rate to be more accurate. Relying on that rate, Tobler et al. estimate median TMRCAs for five haplogroups in the range 43-48 ka, though with 20-30 ky error bars (95% CI) associated with each (Table 1). Given those estimates, inspection of the basal splits shown in their overall phylogeny (Tobler et al. 2017: Figure 1) leads them to suggest that those between three older sets of Sahul haplogroups representing each of the main Eurasian lineages (M16 and M42 within M; O, S and N13 in N; P within R) took place c. 50 ka. Assuming that the median dates listed in Table 1 are relatively precise, that estimated ages for the older splits are accurate, and that initial colonisation took place somewhere in the range 47-51 ka (Allen and O'Connell 2014; Veth et al. 2017], then as many as six pre-Sahul mitochondrial haplogroups may have been represented among the founders (Tobler et al. 2017).

Tobler et al. 2017		Nagle et al. 2017a			Nagle et al. 2017b	
Calibration	Fu et al. 2013		Fu et al. 2013	Soares et al. 2009		Soares et al. 2009
		M42a'c	53 (42-66)	50 (39-62)		
M42	45.7 (35.4-56.6)	M42a	36 (27-46)	39 (31-47)	M42a	55.2±16.7
		Q	44 (34-55)	53 (37-68)	Q	53.1±12.9
S	47.2 (36.9-58.6)	S	51 (40-64)	49 (39-59)	S*	49.5±10.2
O	42.5 (31.6-61.3)	O	37 (25-50)	43 (28-59)	O	39.5±13.4
		P	60 (50-73)	62 (54-70)	P*	57.4±11.7
P4b	45.7 (36.1-56.1)	P11	50 (39-62)	39 (29-48)	P4b	48.4±15.5
P5	43.8 (33.6-55.9)	P5	31 (23-41)	28 (18-39)		

Table 1. Estimated time to most recent common ancestor (TMRCA) (median, 95% CI calibrated in ka) for selected mtDNA haplogroups. Labelled groups are similarly but not identically defined across all published sources. TMRCA estimates are based on different haplotype samples; hence differences in those estimates are not unexpected. M42a'c includes M42a and M42c; P5 is derived from P; P11 is a relabelled version of P4b.

Nagle et al. (2017a, b) offer a more comprehensive set of TMRCA estimates based on both the Fu et al. and Soares et al. replacement rates, including at least one estimate >50 ka for six lineages but again with wide error bars (Table 1). Early estimates listed here for basal P along with the presence of P9-10 haplotypes in the Philippines are seen by some (e.g. Larruga et al. 2017) to indicate an offshore origin for earliest Sahul representatives of this haplogroup. Others prefer an intra-Sahul emergence based on similar estimated time depths for P9-10 versus Australian P subtypes (Nagle et al. 2017 a, b; John Mitchell pers. comm. 2019), though this begs the question of its presence in the Philippines. Comparably-grounded calculations are unavailable for Melanesian haplogroups P1-2, 3b and 4, Q and M27-29 reported by Merriwether et al. (2005) and Friedlaender et al. (2007) but their published mutation counts and phylogenies suggest that TMRCAs for some of these may also be >50 ka. Our reading of Cooper (section on 'Genetics' in O'Connell et al. 2018) leads us to suggest that as many as 9-10 haplogroups may have been present among the Australian founders. Based on the Friedlaender et al. and Merriwether et al. findings, we would add perhaps 2-3 among the earliest arrivals in New Guinea.

Despite the obvious and important uncertainties in all of this and the possibility that some founding lineages disappeared after arriving in Sahul, the number of mtDNA haplogroups represented among the colonisers must have been at least four (M, N, R and P), five if we include Q whose status is less clear, and possibly as many as a dozen or more overall. Assuming, as above, that each haplogroup was represented by an effective population numbering in the tens and a census population numbering in the scores, the colonising meta-wave might have been in the low thousands. Relying on essentially the same genetic data, Bird et al. (2018:437) make this point explicitly. It is repeated by Kealy et al. (2018:63). Notions of significant transport capacity – watercraft capable of holding scores of passengers and of maintaining technically-aided headway in contrary currents – are reinforced.

The crucial question at this point is whether the descendent haplogroups of M, N and R had diversified before arrival in Sahul or after. Bergström et al. (2016) advocate a single founder group settling what is now Australia and New Guinea, but one that separated soon after arrival. As just proposed, we consider that the data can equally be read to imply haplogroup diversification prior to arrival in Sahul. Both the projected time constraints between an initial arrival date of c. 50ka and the estimated TMRCAs for the haplogroups listed in Table 1, and their geographic distributions, about to be reviewed, lead us to this view.

Further inferences from genomics

Although at this stage problematic, the distribution of indigenous mtDNA haplogroups across modern Australia-New Guinea offers hints about landing points on Sahul. Three contiguous locations suggest themselves. The New Guinea Bird's Head would allow colonisers to move either east along the north coast of Sahul or south onto the eustatically exposed Arafura Plain. Colonisers might also have landed on the Arafura Plain itself, then moved eastwards to the east coast and south into the woodlands underlain by the Great Artesian Basin, connecting with the Murray-Darling Basins and the south coast of Australia. Landing on the Arafura Plain or further south in the Kimberley region would also allow access south along the west coast and deep to the interior via rivers such as the Ashburton, Fortescue and Gascoyne.

Although both Australian Aborigines and New Guineans share the founding mtDNA macrohaplogroups M, N, and R, distinct north-south differences are apparent. For example, from R, the deep subclade P is found in Australia and New Guinea as haplogroups P3a and P11 in the south and P3b and P4 in the north. Similarly, within M, a characteristic variant nucleotide position, 13500, is widespread in New Guinea and island Melanesia but has only a single cited presence in Australia (Hudjashov et al. 2007) that may be a product of recent history (Nagle et al. 2017a,b). The Y-chromosome data indicate similar deep time splits. On a more regional basis the prevalence of mtDNA haplogroups Q^M, M27 and New Guinea-specific subsets of P^R in the Highlands and further east in island Melanesia as well as their absence to the continental south point to the arrival of these groups on the Bird's Head. Relatively high numbers of haplogroup O^N along the west Australian coast suggest a landing in the Kimberley, possibly via Timor. The prevalence of haplogroups M42, S^N and Australia-specific P^R across most of Australia but not northern New Guinea fits best with arrival on the Arafura Plain. No single line of advance across Wallacea nor any single landing point on the Sahul shore is indicated. Instead a spatially complex wave, internally structured along mitochondrial and other genetic lines, is strongly implied. At the moment such patterns offer a possible line of enquiry that might one day find resonance in the archaeological record or in other aspects of the genetics. It is intriguing that the cultural divisions between Australian Aborigines and New Guineans may have had their origin in the earliest Pleistocene settlement patterns rather than the formation of the Torres Strait. Certainly, the central New Guinea cordillera and the wet forests of southern New Guinea would have provided a formidable barrier between people moving along the northern New Guinea coast and those who moved south. That division appears to be reflected in these haplogroup data.

This raises the question of the arrival period(s) for founding haplogroups. Did they land in Sahul close in time or spaced out over millennia? Current research is silent on this issue, partly because at this stage the archaeological record cannot resolve it. Without human skeletal remains, haplogroup identities are not reflected in that record, though if they were, increasing precision in radiocarbon results might provide intriguing insights. Moore (2001) showed that smaller populations were at risk of extinction within a millennium, especially if they were isolated from other groups. Larger founding census populations located close enough to exchange mates would enhance the prospects for small group survival. On this basis, nearly simultaneous, geographically proximate arrivals at different points along the Sahul shore are implied. If further apart in time and space, such landings were less likely to result in individual group survival.

This reasoning has further implications for conditions in Sunda source-zones. A push eastward across Wallacea implies significant population increase and associated resource depletion in those areas. Though data pertinent to the latter point are extremely limited, the use of high-cost plant foods such as *Pangium* and *Alocasia* (Barton and Paz 2007) at 40-48 ka at Niah Cave is consistent with such depletion. On population increase, Atkinson et al. (2008) appealed to mtDNA variation and used coalescent theory – loosely like considering evolution in reverse - to estimate past growth phases in populations across Eurasia, Australia and into the Americas following AMH exit from Africa. They found that southern Asia shows ‘the earliest and most pronounced population expansion outside Africa, with a 5-fold increase in population size estimated by c. 52 kya’ (2008:470). Though the date and scale of this particular increase is now subject to adjustment in light of more recent estimates of mtDNA mutation rates, if substantiated it would indicate a powerful push factor for movement into Sunda and across Wallacea.

Was Sahul isolated from the rest of the world during the LGM?

Genetic research in the first decade of this century supported a two-stage model of AMH population movement across the Sunda/Sahul arc, the first involving the initial dispersal of AMH, the second the Holocene spread of Austronesian speakers eastward across the region and out into the Pacific. On the basis of recent surveys of Y-chromosome and mtDNA haplogroups in Wallacea scholars now propose a four-stage spread, the first involving the pioneering AMH dispersal and a second Pleistocene dispersal (sometimes called the ‘early train’ model), this latter roughly placed in the range 40 ka - 10 ka. Some authors (e.g. Karafet et al. 2010) suggest that this dispersal may have occurred after the LGM, timing that would be consistent with inferences above about post-LGM increases in littoral resource availability. Stage one is marked by the derivatives of mtDNA and Y-chromosome haplogroups reviewed above, while the second is marked by mitochondrial haplogroups B4, B5, D and E and Y-chromosome haplogroups O-M119*, O-M95*, O-P203 and O-M122 that swamped lineages associated with initial AMH dispersal across the region (Karafet et al. 2010; Jinam et al. 2012; Tumonggor et al. 2013; Gomes et al. 2015; Hudjashov et al. 2017).

The second stage population spread resulted in a strong division in the genetic make-up of east and west Wallacea with the east genetically reflecting the original founding stage unaltered by the second stage influx. It is unclear whether this means the second stage did not penetrate the eastern Wallacean islands or whether this could reflect back flow from Sahul. The boundary between the two genetic zones coincides with A. R. Wallace's phenotypic division of 'Malayans' and 'Papuans', a line running south between Sulawesi and Maluku and then west of Flores (Fig. 1) (Wallace 1869 vol. 2 chap. 40). This should not be confused with Wallace's biogeographical divide known as the Wallace Line, or other Wallacean divisions such as Weber's Line or Lydekker's Line. Cox (2017:111) underlines the genetic importance of this divide, suggesting people on opposite sides of Wallacea exhibit amongst the largest differences in genetic diversity anywhere: 'Differences of this magnitude have only been observed elsewhere when imposed by major geographic barriers such as the Himalayas or the Sahara Desert. ….. [C]urrent interpretations favour restricted mobility of hunter-gatherer populations during the Pleistocene'.

Why might AMH mobility be apparently unrestricted at c. 50 ka, but restricted by the terminal Pleistocene? One plausible hypothesis is that falling sea levels inhibited previous levels of AMH mobility. Terrell (2004) suggested that during periods of low sea level the north coast of New Guinea may have become uninhabitable as reefs, lagoons, floodplains and swamps were replaced by dry land, rocky coasts and entrenched rivers, and that New Guinea may have therefore been isolated during the terminal Pleistocene. We believe this argument should be extended to Sahul and considered for the Wallacean islands.

In general terms and following the sea level curve proposed by Lambeck and Chappell (2001), sea levels at 50 ka were between -40 m and -50 m relative to present levels. Subsequently sea levels fluctuated gradually downwards to c. -80 m between 35 ka and 31 ka, after which they descended rapidly towards a low stand of c. 120 m. Lambeck et al. (2014) using data from several different world locations suggest a rapid fall of c. 40 m in <2000 years, between 31 ka and 29 ka. Recent fossil reef drilling data from two locations on the shelf edge of the Great Barrier Reef (GBR) indicate a second plunge towards the full extent of the LGM that occurred at c. 22 ka (Yokoyama et al. 2018; Webster et al. 2018). The oldest reef in this part of the GBR (Reef 1) died from subaerial exposure, an event constrained by dates of 35.6±0.3 ka and 34.3±0.3 ka. Reef 2 began to grow after the 40 m plunge at c. 27 ka, but died when subaerially exposed between 22.11±0.23 ka and 21.87±0.24 ka, the point at which the sea fell a further c. 20 m in a second 1-2 millennia period.

From c. 21 ka to c. 17 ka modelling of global sea levels suggests that they dropped further to between -125 m and -130 m and slowly rose to -120 m at c. 17 ka, after which sea levels rose rapidly with deglaciation. Given that these large episodic sea level falls occurred during such relatively limited time periods, change may have been noticeable within human lifetimes; even if not, the overall environmental effects must have been dramatic.

Accepting the subsistence dependence on coastlines and reefs argued earlier, it is especially pertinent to ask what occurred with fringing reefs during the sea level descent towards the

LGM. There is a vast literature on the evolution of tropical coral reefs and especially the GBR, but much of it relates to periods when post-glacial rising seas provided appropriate conditions for fringing reef systems to grow and expand. Coming to terms with the opposite proposition, that fringing reefs shrank in size or disappeared in periods of sharp sea level decline, confronts not only a much smaller research literature but also the wider problem that factors affecting reef evolution may be highly island- or area-specific. Apart from changes to reef accommodation space during changing sea levels, reef growth is affected by sea surface temperature, tectonic subsistence or uplift, the steepness of marine slopes, water turbidity/light and the production levels of $CaCO_3$ among other factors (Montaggioni 2005). Various researchers point to the inhibiting factors for reef development during periods of declining sea level (e.g. Webster et al. 1998, 2018; Camoin et al. 2001:339; Abbey et al. 2011:75; Gischler et al. 2013:1463). The GBR research referred to above showed that Reef 2 began to grow as low sea levels stabilised in the LGM between 27.35±0.14 ka and 27.34±0.07 ka. 'At this time the GBR formed a very narrow and ephemeral reef system' (Webster et al. 2018:428). As a generality, whether fringing reefs grew during periods of descending sea levels appears to depend on both the speed of sea level descent and the steepness of underwater slopes. Since inter-island distances in Wallacea were not significantly increased when sea levels descended to -120 m (Irwin 1992:22) this implies that the submarine topography of many Wallacean islands involves steep slopes not conducive to reef growth in times of falling sea levels. In addition, fringing reefs will preferentially accrete vertically (Kennedy and Woodroffe 2002) and die when exposed subaerially as sea levels drop. Depending on their morphologies, a common predicted palaeo-shoreline would be raised coralline cliffs, not unlike present-day *makatea* islands found in the Pacific (although there created by uplift) that would offer both difficult landings and poor foraging locations.

Testing the hypothesis of drastically reduced mobility coinciding with sea level decline remains difficult. A simplistic proposition might be that if true, Wallacean island sites should reflect depopulation especially during the LGM. The archaeological record indicates that some sequences indicate abandonment but in others occupation occurs immediately at and around the LGM. To take a few examples reviewed by O'Connor et al. (2017), Liang Sarru in the Talaud Islands was occupied at 35-30 ka, then at 21-17 ka and not again until the Holocene (Ono et al. 2009). A large suite of dates from Golo Cave and Wetef Shelter on Gebe Island in the Maluku Islands suggest initial occupation of both sites c. 36 ka, continuing to c. 26 ka and then abandonment until the terminal Pleistocene/Holocene (Bellwood et al. 1998, in press Table 1.1). Daeo 2 on Morotai in Halmahera was first occupied between 16.8 ka and 15.9 ka (Bellwood in press, Table 1.1) during the rapid post-LGM sea rise. O'Connor (2007: Fig.3) reports a calibrated date of c. 42 ka for basal deposits for Jerimalai shelter on Timor, 50 cm below a date of c. 14 ka. It is unclear whether the shallow deposits between these dates represent continuous occupation, but with an average accretion rate of <2 cm/1000 yr, possibly not. Also on Timor, Lene Hara cave is now shown to be of the same antiquity as Jerimalai (O'Connor et al. 2010) but appears to be abandoned from c. 30 ka until the last several thousand years (O'Connor et al. 2002). Similar but slightly younger ages have been proposed for cave art in the Maros karsts of Sulawesi (Aubert et al. 2014). Tron Bon Lei shelter on Alor Island in the Lesser Sunda Islands was occupied from c. 21 ka to 18 ka then not again until the early Holocene (Samper Carro et al. 2016). Three sites on Roti

Island have yielded 13 ^{14}C dates of which one from Lua Meko cave was c. 24 ka while the remainder were Holocene (Mahirta 2009). An OSL date from basal sand 10 cm below the Pleistocene date for Lua Meko provided a 'tentative' age of c. 29 ka. The author notes reduced deposition during or after the LGM during which time human occupation was much more infrequent or absent.

Although it needs remembering that available data sit above current high sea levels, implying much must now be submerged, few other islands in Wallacea have yet revealed any evidence of Pleistocene occupation by AMH. Even allowing for the sample to be unrepresentative it is interesting that no site ages have yet been reported that overlap the range of 47 ka to 51 ka demonstrated for Sahul. Any extension of the colonising date for Sahul to 65 ka or older increases this dichotomy. Here we note but pass by the tantalising possibility that the re-excavation of Leang Burung 2 on Sulawesi (Brumm et al. 2018) and the on-going excavation at the less-disturbed and nearby Leang Bulu Bettue (Brumm et al. 2017) might provide such evidence, given that deep-trench excavations at neither of these sites have reached bedrock below cultural deposits spanning c. 50 to 40 ka; also the continuing work at Liang Bua on Flores (Sutikna et al. 2016, 2018; Morley et al. 2017). Presently, and beyond the Timor sites, most Pleistocene sites in Wallacea only become archaeologically visible at a time when sea levels descended towards -60 m and beyond. It is tempting to link occupation after c. 35 ka and especially those sites dating around the LGM with the observation by O'Connor et al. (2017) that lowered sea levels connected small island archipelagos into larger land masses that provided more subsistence viability for human occupation. If this correlation holds it might imply that terminal Pleistocene humans remaining in Wallacea were adapting the strandlooper strategy of the earliest colonists to one where falling sea levels reduced both reef area and high-ranked reef resources, requiring these people to extend the food quest to include a wider range of lower ranked resources. For example, it may be telling that Golo Cave contains mostly small shell species (Peter Bellwood pers. comm. 2019). Are all Wallacean sites younger than c. 35 ka the same?

Under this hypothesis it appears possible that the marine 'highway' that facilitated AMH entry into Sahul became less productive and less accessible by c. 35 ka and increasingly difficult into the LGM. Might Sahul have been effectively isolated by this changed ecology for unknown millennia until rising sea levels again linked it to Wallacea? Might the Wallacean archaeology from these periods be reflecting remnant populations adapting to this massive environmental shift? These ideas are in step with the proposition that high sea levels facilitated both AMH occupation in, and transit through Wallacea towards Sahul (Chappell and Thom 1977; Chappell 1993; Terrell 2004). They pose questions to others like Clarkson et al. (2017), Norman et al. (2018) and De Deckker et al. (2019) who favour low sea level transit at c. 65 ka. Such ecologically-driven isolation would also explain the Wallacean/Sahul genetic disjunction.

Conclusion

Advances in genetics, and in our case advances in Sahul-specific mtDNA in particular, lead us to conclude that the colonisation of Sahul involved at least hundreds and possibly more people who arrived within a time frame sufficiently limited to permit and promote the continuing growth of founder populations that quickly spread through the continent. This model builds on previous discussions of various factors affecting successful colonisation (e.g. Allen and O’Connell 2008; O’Connell et al. 2010; O’Connell and Allen 2012, 2015).

While this paper was in preparation, Bradshaw et al. (2019) reported a similar conclusion to us. Based on an entirely different modelling procedure these authors proposed a census founding population of 1300 to 1550 people arriving at a single point in time or within a period of about 700 to 900 years. A similar founding population of 1000 to 2000 people was previously proposed by Williams (2013).

If these models prove accurate the demographic scale of this colonisation was such that the process must have been far more complex than has so far been acknowledged. However, researchers coming from an archaeological base have been content to refine old paradigms that do not confront the complexities implied by such founding numbers. Minimalist constructions that were once appropriate need revisions that accommodate these new models. Beyond this, we need to avoid creating scenarios made to support secondary arguments, such as privileging low sea levels to support the long settlement chronology. We are reminded that several decades ago, claimed dates of c. 46 ka for the disappearance of the megafauna caused colleagues to switch from favouring the long colonisation chronology for the short one, in order to preserve the concept of blitzkrieg.

We have offered here further data and argument about why we are sceptical of the low sea level argument. In the same way that our discipline has assessed accidental colonisation to be so unlikely that most no longer consider it, we should also move on from the sea level debate and abandon the argument about routes. There is now consensus in the literature that all routes were possible and choosing the primacy of one over another seems only to depend on which variable is stressed. Given our proposed demographic model, we think that Birdsell’s west-to-east migration routes, that have served us so well until now, might better be replaced by considering a general eastwards-moving human progression that occupied most or all of the useful islands of Wallacea in turn (see also Kealy et al. 2016), eventually to access Sahul at various locations.

The discipline should now be integrating palaeoenvironmental, archaeological and genetic data that lead to the recognition and formulation of the next-generation set of problems. As a start, we would include among them 1) determining more accurately how many first-wave colonising groups arrived in Sahul; 2) the time period over which these mitochondrial populations arrived; 3) the distribution of their respective landfalls and patterns of dispersal across the continent; 4) the size, internal complexity and subsistence economies of their respective SE Asian source populations, being factors that framed the ‘push’ for movement into and across Wallacea; 5) Wallacean Pleistocene histories against the backdrop of significant sea level change; and 6) the effects of potential isolation for Sahul populations through the LGM.

In the Arcadian days of Australian archaeology, another Rhys Jones adage was that if someone published an idea that was not disproved in five years it was probably not worth publishing in the first place. Mis-placed or not, such idealism has long been absent from our discipline in Australia. Interpretations are clung to at any cost, the works of others are cited uncritically when supportive and increasingly ignored when not. At this point we lose sight of the fundamental purpose of archaeology - to understand the evolution of modern humans and our behaviours, where we came from and how we got here. One long-term basic issue in Australia has been to understand how Sahul was first inhabited, but despite an increasing and changing data base we have all, ourselves included, too often relied on the same unchanging models to understand the problem. Here we have advanced some alternate ideas for our colleagues to disprove.

Acknowledgements

For information and comments on earlier drafts we thank Peter Bellwood, Michael Bird, Adam Brumm, Brian Codding, Murray Cox, Iain Davidson, Kristen Hawkes, Lisa Matisoo-Smith, John Mitchell, Nano Nagle, Steven Simms, Ray Tobler, Jody Webster, Peter White and Alan Williams. Shannon Arnold-Boomgarden drew the map.

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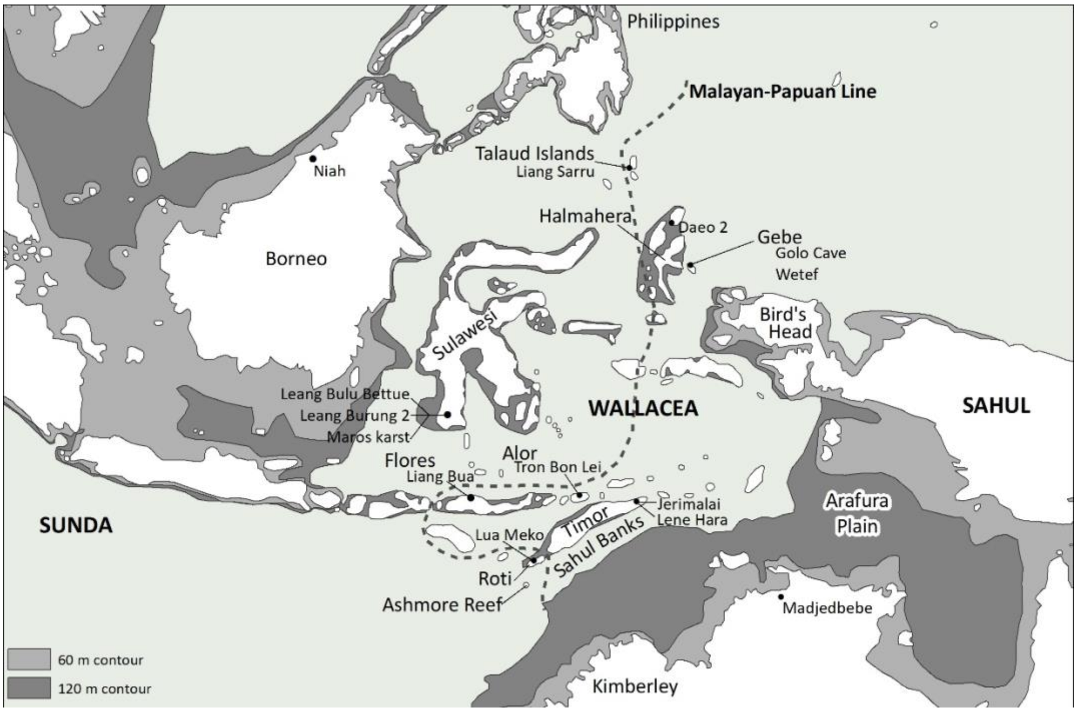
Figure 1 and Figure 1 caption

Figure 1. Wallacea and adjacent parts of Sunda and Sahul, showing locations mentioned in text and land exposed by -60m and -120 sea level falls relative to modern.


Philippines
Malayan-Papuan Line
Talaud Islands
Liang Sarru
Niah
Halmahera
Daeo 2
Gebe
Golo Cave
Wetef
Borneo
Sulawesi
Bird's Head
WALLACEA
SAHUL
Leang Bulu Bettue
Leang Burung 2
Maros karst
Flores
Alor
Liang Bua
Tron Bon Lei
Jerimalai
Lene Hara
Arafura Plain
SUNDA
Lua Meko
Timor
Sahul Banks
Roti
Ashmore Reef
Madjedbebe
Kimberley
60 m contour
120 m contour