Ten years of Solutreans on the ice: a consideration of technological logistics and paleogenetics for assessing the colonization of the Americas

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Abstract

In 2004, a theory positing that Western Europeans were among the first peoples to colonize North America was published within the pages of *World Archaeology*. Ten years later this theory continues to provoke academic debate (Balter 2012; Curry 2012; Runnels 2012; Anderson 2013; Bawaya 2013; Morrow 2014) and ignite public imagination (Cook 2012; Vastag 2012; Coghlan 2012) thanks to the publication of *Across Atlantic Ice* (Stanford and Bradley 2012), the most recent, comprehensive and accessible presentation of what has come to be known as the "*Solutrean Hypothesis*". In considering how debates over entry routes into North America can be taken further, we review the technological logistics of a North Atlantic crossing and Amerindian and European genetics, examining the validity of the *Solutrean Hypothesis* in 2014.

Keywords

First Americans; Solutrean Hypothesis; Arctic marine adaptation; paleogenetics.

Introduction

The core of the *Solutrean Hypothesis* has always been the similarity between Clovis and Solutrean foliate points, with the latter suggested as a technological precursor to the former, and thus indicative of a connection between America and Western Europe where these industries respectively occurred. With the publication of *Across Atlantic Ice* (Stanford and Bradley 2012), the *Solutrean Hypothesis* is no longer simply a theoretical proposition but an extensively detailed model of a Pleistocene colonization of the Americas from Europe across the North Atlantic. This format has allowed for a greatly developed description of the proposed

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colonization to be postulated. Undoubtedly, the overwhelming level of scrutiny the Solutrean Hypothesis has received (Straus 2000a; Straus, Meltzer, and Goebel 2005; Clark 2000, 2004; Buchanan and Collard 2007; Westley and Dix 2008; Meltzer 2009) was a major contributing factor in Dennis Stanford and Bruce Bradley's decision to so thoroughly lay out their model.

Through understanding how debate has shaped the development of the model we attempt to take the debate forward through the consideration of two aspects of the proposed model that we perceive to be of crucial importance: technological strategies for dealing with risk along the ice margin, and the contention of genetic affinity between Amerindian and Western European populations.

Background to the Hypothesis and subsequent debate

Although suggestions of a connection between Clovis and Solutrean industries were not new (e.g., McCown 1939; Greenman 1963), Stanford and Bradley's (2002) updated revision of the hypothesis some fifteen years ago proved an exciting alternative to conventionally supposed entry routes into the Americas, if also a polarizing one. It is perhaps fair to say that opposition to the argument from some quarters was fuelled by concern that such a hypothesis remained too outlandish to be returned to mainstream academic discussion (Straus 2000a). Although some opponents of the hypothesis have expressed dissatisfaction with the lack of a clear historical connection demonstrated between the Clovis and Solutrean (Clark 2004, 105; Meltzer 2009, 187), it is a similar dissatisfaction with the arguments for conventional entry routes that has remained at the core of Stanford and Bradley's (2012, 67–88) desire to look elsewhere for answers. As they sought to establish and develop their ideas in the face of their critics, they have also challenged the vagueness and complacency with which other theories are accepted.

In light of the fact that any sites from this crossing must now be lost to the ocean, debate has mostly focussed around comparisons of evidence. The binary style comparison of Clovis and Solutrean archaeology comprises a large and important part of the debate so far, and although disputes over the significance of observed similarities and differences doubtless may continue (e.g., Eren et al. 2013; 2014; Lohse et al. 2014), it has been largely exhausted as an avenue for investigation, and will likely remain so pending the discovery of new evidence (Stanford and Bradley 2012, 249). Writing prior to the publication of *Across Atlantic Ice*, David Meltzer (2009, 186) placed the onus firmly on the proponents of the hypothesis to prove the connection before others should concern themselves with disproving it. We feel that unfortunately, archaeological investigation cannot be practised as a conventional science. Quite simply, we doubt that the *Solutrean Hypothesis* can be demonstrably proved or disproved, at least for the foreseeable future, and this is simply a reality that is often faced when constructing large-scale archaeological narratives. How then, if at all, are we to take the debate forwards?

Bamforth interprets *Across Atlantic Ice* as seeking to make the case for serious investigation into the possibility of a Solutrean migration into North America (2013, 106). It seems to us that the development of the hypothesis dictates the direction with which the debate should continue and requires a more detailed rebuttal (Shea 2012). Through considering the limited archaeological data available, it may be possible to comment further on elements of the model that can be reviewed. At present, the *Solutrean Hypothesis* offers the most suitable candidate for such a critique, but it is our hope that in time similar reviews can be offered for alternative propositions of American migration routes, possibly even advancing a sort of test criteria, at least as far as

such criteria might be agreed upon. While many facets of the hypothesis detailed in *Across Atlantic Ice* could be further explored, we have briefly considered just two aspects below: constraints upon the toolkits carried across the Atlantic, and the evidence for a founder population from Western Europe.

The Solutrean toolkit: an arctic marine adaptation?

The question of how the proposed migration actually took place is one that has remained a largely speculative issue. *Across Atlantic Ice* (Stanford and Bradley 2012, 236–7) posits that the Solutrean crossing of the Atlantic comprised a series of expansive and contracting migrations from peoples tethered to land. The suggestion that people were traversing back and forth across the ice implies that people were highly adapted to life in these environments rather than stretched to their limits (ibid., 237). While we cannot refute this scenario, and acknowledge that the potential fecundity of ice-margin environments (see Henshaw 2003) for arctic maritime subsistence strategies is a complex issue for further investigation, we believe the sheer expanse (some 5000km across) with no access to stone and fresh vegetal materials would have posed severe pressure through risk. Severe doubts have been cast upon the productivity and consistence of the ice-edge margin ecosystems (Straus 2000a, 224; Westley and Dix 2008, 92–4). It has been argued that beyond what was carried, everything necessary for the migration could have been fashioned through seal remains (Bradley and Stanford 2004, 471), which were likely the only substantial prey available on the ice, and that this formed part of a select marine-adapted permutation of the Solutrean and a mainstay of life on the ice, even if supplemented with other dietary options (Stanford and Bradley 2012, 186; 226–9).

Evidence for Arctic coastal adaptation during the Solutrean

Evidence for deep-sea fishing and seal predation as substantial dietary contributors in the Solutrean has already been contested (Straus 2000a, 222–3), and while bone points do occur in Solutrean assemblages, they do not occur in nearly the quantity in which they are recovered from sites of Magdalenian date (Straus 1993, 89). It has been argued that the coastal locations where these maritime adapted components of the Solutrean would be most apparent are now submerged (Bradley and Stanford 2006, 705; Stanford and Bradley 2012, 208). As the cornerstone of the hypothesis, Solutrean points must have made the crossing, if not through collective memory, then presumably as part of this select adaptation. Through considering technological strategies of risk aversion (Bamforth and Bleed 1997; Bleed 1986), we consider the suitability of these pieces for life on the ice.

Bifaces in a high-risk environment

Bifacial technology is often associated with long-distance residential mobility at least in part because of potential for further flake removal (McCall and Thomas 2012, 22; Kelly and Todd 1988). While this has been documented among various early American bifacial technologies (e.g., Bamforth and Bleed 1997, 133; Kelly and Todd 1988, 237–8), we are unaware of the extent to which this was practised in the Solutrean. Multifunctional potential also increases the utility of

such toolkits on long migrations (McCall and Thomas 2012). Although some Solutrean points have been suggested as having functioned as knives (Aubry et al. 2003; Straus 1991), they are most commonly assumed to have functioned as armatures for spears. As part of a select arctic coastal adaptation, we would assume they would be geared towards seal hunting.

Experimental replication has shown copies of Solutrean points and other bifacial points to be highly prone to breakage when used as projectile tips (Geneste and Plisson 1993; Odell and Cowan 1986), a risk that would be further exacerbated by use in extreme cold or after re-sharpening to extend use-life (Elston and Brantingham 2002, 104, 107). They are also considered costly to damage or lose (Straus 2000b; 2005) because of their high expense in material procurement and production time (Aubry et al. 2008). This high risk of failure in application has been noted for other bifacial points (Bamforth and Bleed 1997, 133). Without materials within the landscape for retooling, and in pursuit of prey whose primary escape is to take to water, the risk of material loss would be prohibitively high.

Ethnographically documented examples of seal hunting toolkits are notable for their complex designs and diversity of specifically designed component tools to reduce risk of loss of prey and incurring damage (Bleed 1986, 743). Chief among these is the toggle headed harpoon that facilitates mobility for the armature to reduce stress following impact (Boas 1964, 473; Oswalt 1973, 137; 1976; Balikci 1989, 67–77; Bleed 1986). There is nothing to indicate such design features among Solutrean assemblages (Stanford and Bradley 2012, 142). Without these designs to mitigate damage through overstressing the armature head, it is difficult to envision Solutrean points functioning in this manner without high, potentially catastrophic, risk of loss.

Microliths in a high-risk environment

Microliths, specifically backed bladelets, present an alternative component of Solutrean assemblages that may have fared better on the proposed crossing. Microlithic technology is often typified as being a good strategy for risk avoidance (Bamforth and Bleed, 1997; Elston and Brantingham 2002; Torrence 2002) for what we perceive to be two main reasons.

(1) Reliability in application, maintainability in design.

It is often assumed that microliths served in hafted multi-element composite tools. The ability to function despite damage to, or the loss, of one of these elements, constitutes overdesign as insurance against failure in application (Bamforth and Bleed 1997). The replaceable nature of these elements has also led to a characterization of such tools as being maintainable in design (Torrence 2002; Straus 2005) although this is very much dependent upon the technological system of which they are a component (e.g., Pètillon et al. 2011, 1281).

(2) Flexibility in design potential

The ability to harness multiple small haft-able cutting surfaces provides potential scope for a variety of designs and purposes (Torrence 2002, 181).

It is tempting to suggest relatively cheap lithic procurement costs as a third reason. Although it seems intuitive that their small size might equate to a more economic conservation of raw

materials, comparative studies have shown at least some bifacial reduction processes to be more favourable (Elston and Brantingham 2002). In instances where microblade production is considered less costly, matters may be complicated by the use of bifacial cores (Bamforth and Bleed 1997, 131). Consequently, the assumption that microliths constitute a more cost-efficient use of raw materials is far from safe. Their costs in procurement are compensated however by their reliability in application (ibid., 133) and among Cantabrian assemblages they are indeed characterized as being low-investment and less expensive than Solutrean foliates (Straus 2005, 152; 1991, 198). Given the time envisaged spent upon the ice, even with conservatively designed technology, stone materials might have easily been exhausted without potential for replenishment.

It must be acknowledged that there are methods of seal hunting that do not rely upon harpoon technology, a topic for discussion we intend to address in future work. Our decision to consider microlithic technology rather focuses on what we perceive to be a better option for a lithic based tool-kit for survival on the ice. While there is little from ethno-historical accounts to suggest that microliths featured heavily as mainstays in seal-hunting technologies, we believe that, as an existing technological mode in the Solutrean, they might have offered a more attractive generalized toolkit for the kind of arctic coastal marine adaptation that the model anticipates. Certainly they feature commonly among Paleo-arctic assemblages where they are known as microblades (Meltzer 2009) and where it has been suggested that they may have served in toolkits precursory to toggling harpoons (Yesner and Pearson 2002, 150). Although these tools do feature in the Solutrean, generally increasing in frequency over time and perhaps even replacing Solutrean points they do not become truly prolific among many Cantabrian assemblages until the Magdalenian (Fig. 1), after the proposed timing of the crossing.

Smaller shouldered variants of Solutrean points may have also been attractive types suitable for the conservation of lithic materials either in procurement and manufacture or in use, but the currently proposed crossing took place before the popularization of this form, perhaps explaining their absence from Clovis assemblages (Stanford and Bradley 2012, 181). The implication of these and other smaller bifacial lanceolate points from both Solutrean and Clovis contexts for

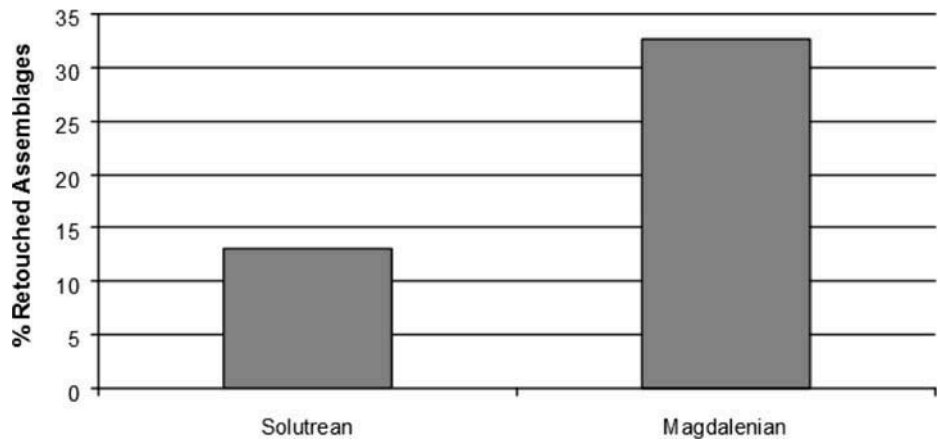

Figure 1 Comparison of backed bladelets from the Franco–Cantabrian Solutrean (26 assemblages from 9 sites) and Magdalenian (24 assemblages from 10 sites). Sites and assemblage data from Straus (1993; tables 6.1 and 6.2).

the proposed timing and nature of the ice-edge migration are issues we hope to consider more thoroughly in future investigation.

Discussions of technological fitness relating to what we know or might assume about an arctic coastal adaptation of the Solutrean remains based largely upon conjecture. We argue that microliths would be attractive here as a more reliable strategy of risk avoidance in response to the potentially catastrophic/deadly risks associated with failure on the ice-sheet (as per Elston and Brantingham 2002, 105). Alternatively, they may have been an unlikely adaptive response for strategies based upon such high mobility (Torrence 2002). Indeed Stanford and Bradley (2012, 241) themselves cite the relative ubiquity of microblade technology around the globe as an example of the problematic nature of associating technological change with adaptive responses, although the prior existence of such technology in the Solutrean means any innovation need not have been radical. Further research into seal behaviour, hunting and ethno-historic proxies for ice-sheet technology may help us better understand the conditions faced, and techniques necessary for survival.

Searching for Solutreans in Amerindian genes: present and past

If North America was first colonized by a Solutrean founder population, there should be some level of evidence for genetic commonality between Amerindians and Western Europeans. Detecting a possible genetic link may be more difficult than the above assumption implies. First, founder effect (Moreau et al. 2011) should have led to more pronounced genetic differentiation between a possible Solutrean founder population and its European parent population. Second, the recent suggestion that the Amerindian colonization of the Americas was more complex than previously assumed, spanning tens of thousands of years and involving at least three migration waves (Reich et al. 2012), implies an equally complex genetic ancestry.

There is, however, a genetic *curiosity* (Fig. 2) shared between Europeans and Amerindians that has been held up as evidence for a common link between Pleistocene Europe and North America. This link is the X mtDNA haplogroup (Brown et al. 1998; Smith et al. 1999). In fact,

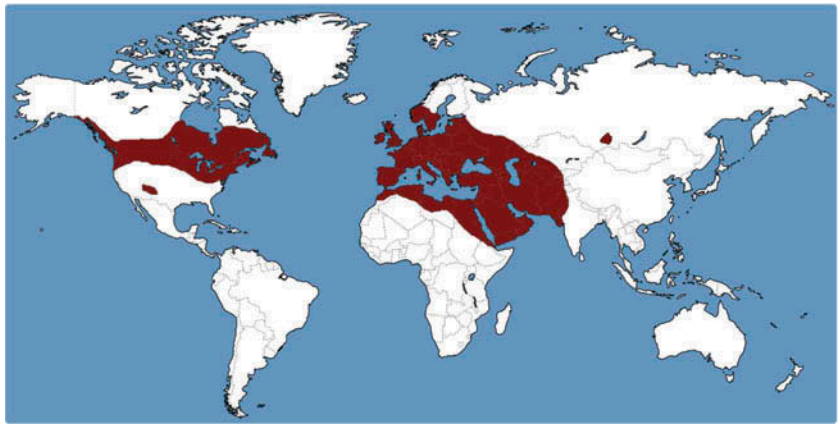

Figure 2 Global distribution of the X haplogroup. For a distribution of the X2 subhaplogroup, see Stanford and Bradley (2012, 248 fig. 11.1).

the first person to suggest such a connection was Dennis Stanford, who in the late 1990s surmised what has come to be known as the *Solutrean Hypothesis* on the now offline archived Smithsonian website "Northern clans, northern traces: journeys in the ancient circumpolar world". In the first peer-reviewed unveiling of the *Solutrean Hypothesis* it was argued that the concentration of the X haplogroup in north-eastern North America demonstrates an ancestral north-eastern Amerindian connection with Western Europe that has subsequently been diminished due to admixture with peoples migrating through the traditionally accepted beringian route (Stanford and Bradley 2002). A closer examination of the X haplogroup in North America and the old world, concerning its geographical distribution and presence in prehistoric human skeletal samples, is presented below.

The X haplogroup

The X mtDNA haplogroup is noted as being part, though at a minor frequency, of the matrilineal descent of European, Near Eastern, and North African populations. It is divided into two subhaplogroups: the X1 and X2 (Reidla et al. 2003). X1 is restricted to the Near East and North Africa with the X2 comprising the expression of the haplogroup amongst Europeans (ibid.). The X haplogroup so far has not been observed within East Asia (Maca-Meyer et al. 2001). Surprisingly, then, a variant of the X2 subhaplogroup, X2a, has been detected within some Amerindian populations.

The ethnic and geographical distribution of X2 in the Americas

The X2a subhaplogroup in the Americas shows a frequency bias towards north-eastern North America; however, the distribution of X2a is widespread. In order of greatest frequency, the ethnic groups noted thus far to be carriers of the X2 subhaplogroup are the Ojibwa with a traditional distribution from the Great Lakes to the eastern Canadian seaboard, the Sioux from the Great Plains, the Nuu-Chah-Nulth from the Canadian Pacific Northwest, the Yakima from the American Pacific Northwest, and the Na-Dene Navajo from the American Southwest (Brown et al. 1998, 1852). The geographical spread of the X haplogroup does not favour *per se* a bias that would imply an Atlantic entry and therefore explicitly European origin. That said, the Ojibwa present a significant X2a frequency of 25% (ibid., 1857). By contrast, the X2 subhaplogroup frequency in Europe is only about 4%, perhaps suggesting the kind of founder pattern one might expect if Amerindian, or at least the Ojibwa, descended from Pleistocene Europeans. Further, the geographical distribution of Ojibwa peoples near the north-eastern seaboard may suggest a North Atlantic point of diffusion of the X2a subhaplogroup.

The migration history of the Ojibwa tells a different story, however. As Malhi et al. (2002, 915) note in their analysis of the American X2 subhaplogroup, '[a]rcheological, linguistic, and genetic evidence all strongly support' a movement of ancestral Ojibwa populations out of the Great Lakes region within the past three millennia and that this population expansion favourably biased the frequency of the X haplogroup. Given the relatively recent nature of this event, the north-eastern X haplogroup bias seems to be an effect of a Middle-Late Holocene and not a Late Pleistocene migration. Therefore, the prehistoric distribution of the X2a subhaplogroup was most likely west of the Appalachian Mountains (Fig. 3). It may, in fact, have been the movement of Ojibwa peoples eastward that led to the higher frequency of the X haplogroup within

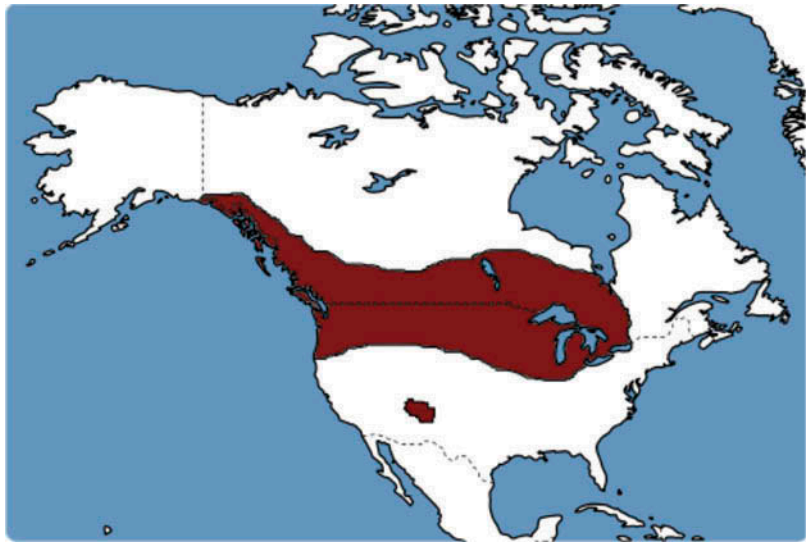

Figure 3 Proposed distribution of the X haplogroup in North America before the Ojibwa migration.

this population through a founder effect process. Genetic studies of Ojibwa populations is further complicated by post-Columbian mixing between Ojibwa and European settlers, leading to perhaps a 30% Caucasian admixture within the south-eastern Ojibwa community (Scozzari et al. 1997). So far, the only genetic samples from archaeologically excavated human remains that confirm the prehistoric presence of the X haplogroup come not from north-eastern North America, but from the western United States at a site along the Columbia River in the State of Washington (Malhi and Smith 2002, 85). Like the history of X2a subhaplogroup in North America, the old world X2 haplogroup's history is equally complex.

The X2 haplogroup in the Old World

As previously noted, the frequency of the X2 subhaplogroup in Europe is significantly less than it is among some Amerindians. In fact, the average European frequency is estimated to be as low as 1.1–5% (Fagundes et al. 2008, 589; Derenko et al. 2001, 237; Reidla et al. 2003). All five Amerindian ethnic groups noted in the study by Brown et al. (1998, 1857) as carriers of the X haplogroup, Ojibwa 25%, Sioux 15%, Nuu-Chah-Nulth 13%, Navajo (Na-Dene speakers) 7%, Yakima 5%, do so at a higher frequency than any western European population. This may, at face value, appear to undermine the potential link between the genetic history of Amerindians with Pleistocene Europe. As noted before, however, one might expect such a pattern due to founder effect, as genetic traits that occur at low frequency in a parent population can become exaggerated if part of the community becomes genetically isolated due to migration. More pertinent to the *Solutrean Hypothesis* is the genetic history of Cantabria and particularly prehistoric Cantabria.

Amongst Basque speakers, the X2 subhaplogroup is actually quite low, about 3% (Alfonso-Sánchez et al. 2008). Though this might seem to fit the assumption of the genetic characteristics of a parent population, this is actually probably not the case. This is because the process that has

Table 1 The regional frequencies of the X haplogroup according to Reidla et al. (2003), 1182, table 1. There appears to be a clear bias toward the Near East where both the X1 and X2 subhaplogroups occur. The high X haplogroup frequencies among Cypriots and Orcadians may be examples of *founder effect* discussed in this paper

X haplogroup frequencies in western Eurasia		
Region	*Mean Frequency*	*Community in Region with Highest Frequency*
Near East	2.9%	Israeli Druze combined X1 and X2 frequency = 26.7%
Mediterranean Europe	2.5%	Cypriots X2 only = 6.7%
Western Europe	1.7%	Orcadians X2 only = 7.2%
Central Europe	1.3%	Czechs X2 only 2.1%
Northeastern Europe	1.1%	Finns X2 only = 2.1%

led to the distribution frequency of the X2 subhaplogroup in Cantabria is most likely the result of diffusion into Europe after the time-range of the Solutrean. Put simply, the frequency distribution of the X2 subhaplogroup in western Eurasia points to a Near Eastern point of diffusion (Table 1). The coalescence estimates (Reidla et al. 2003) for the X haplogroup variants in western Eurasia suggest that the spread of the X2 to Iberia should have occurred after the Solutrean. In fact, the low X2 frequency within Basque communities compared to other Iberians, coupled with the increasing frequency rate of X2 toward Anatolia, the Caucasus, and the Levant, may suggest a Holocene time-range for the spread of the haplogroup into Iberia, perhaps with the spread of agricultural communities or later prehistoric population movements.

Analyses of contemporary Basque indicates that the dominant haplogroup is H, occurring in greater than 50% of the population (Alfonso-Sánchez et al. 2008, 156). Archaeological data seems to indicate that the prehistoric population of the Basque Country share a genetic affinity with extant Iberian populations. Genetic testing on a sample of human teeth (n=121) from several gravesites dating between the Neolithic and Bronze Age demonstrates that the H haplogroup was the dominant matrilineal marker for prehistoric people of the Basque Country (Izagirre and Rúa 1999). As the human remains in the sample are not of Solutrean date, the extent to which subsequent population movements may have obfuscated the genetic structure of Palaeolithic populations is unknown.

The H haplogroup, nonetheless, is argued to be a potential marker of a post-LGM population expansion out of an Iberian refugia (Achilli et al. 2004, 916). The H haplogroup is also found to be at a high frequency among non-Basque speaking Cantabrians and is only second to the V haplogroup (Alzualde et al. 2006, 399). Given their common distribution frequency and coalescence estimates, haplogroups H and V appear to be markers of the Solutrean (Achilli et al. 2004). Haplogroups H and V are most likely absent among Amerindians. In a survey of 575 Amerindian sequences across the Americas, only three showed European affinities, including the presence of the H haplogroup, which were determined to have been the result of post-Columbian admixture with Caucasians (Forster et al. 1996, 936).

Western Eurasia and North America are not the only places where the X2 subhaplogroup occurs. The X2 subhaplogroup is also present among communities of the Altai Mountains in Central Asia. Importantly, the Altaian X2 subhaplogroup along with the Amerindian X2a lacks the '225A mutation' found in the European haplogroup (Maca-Meyer et al. 2001). With the '225a' marker and later coalescence date for the Eurasian X2 subhaplogroup (Derenko et al. 2001, 237), it appears that the European X2 represents a derived form of the subhaplogroup,

further distancing the relationship between the North American and European lineages (Brown et al. 1998, 1853). Central Asia might seem like an unlikely location for an Amerindian origin point, however, linguistic, genetic, and archaeological data suggest a central Asian origin for both the X2a subhaplogroup as well as the late palaeolithic substrate of Amerindian peoples.

Linguistic, archaeological, and genetic ties between Central Asia and Native Americans

Perhaps one of the most compelling connections between central Asia and indigenous North Americans comes from linguistic analyses of the Na-Dene family of languages. To this end, the Nuu-Chah-Nulth, Yakama, and Na-Dene Navajo have been linked on close genetic and linguistic grounds (Ward 1999, 154–5). The Ojibwa themselves do not belong to the Na-Dene language group, as they are part of the Central Algonquian dialects (Bloomfield 1957). However, cladistic reconstruction of Amerindian populations (Fig. 4) suggests that Ojibwa, and other Algonquin speakers, share a common genetic ancestor with Na-Dene speakers (Reich et al. 2012). The Na-Dene language family has been linked by linguistic analysis to the central Siberian Ket people who live along the Yenisei River, forming the Dené-Yenisei language group (Ruhlin 1998). Y-DNA analyses have demonstrated that Amerindian Y haplogroups can 'be traced back to … Kets and Altaians, from the Yenisei River Basin and the Altai Mountains' (Derenko et al. 2001, 240, citing Santos et al. 1999).

To this end, a genetic analysis of extant Altai-Sayan (southern Siberian) populations has demonstrated a genetic affinity beyond the concurrence of the X haplogroup between this region and Amerindians, implying an ancestral derivation of aboriginal Americans from the Altai-Sayan (Starikovskaya et al. 2005, 67). Further, the Altai X haplogroup is has been determined to be an intermediary between the American and European haplogroups (Derenko et al. 2001).

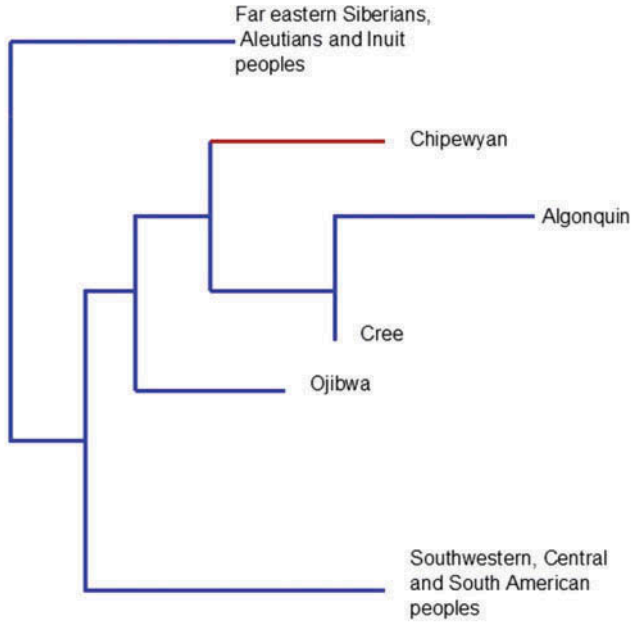

Figure 4 Cladistic reconstruction showing the close genetic affinity between the Ojibwa and Na-Dene speakers (red line). Redrawn and Reprinted by permission from © Macmillan Publishers Ltd: [Nature] (Reich et al. 2012, 371 figure 1.C) with copyright (2012).

Archaeologically, the Altai Mountains appear to form an origin point for both the expansion of anatomically modern humans as well as Upper Palaeolithic blade and microlithic technologies that spread throughout East Asia and into Alaska (Bar Yosef and Belfer-Cohen 2013, 37). Recent archaeogenetic research all but confirms this assumption.

The site of Mal'ta (Fig. 5) is located in southern Siberia on Belaya River west of Lake Baikal (Raghavan et al. 2014, 87). The site was first excavated by Gerasimov in 1928, with excavations continuing into the 1950s (Larichev, Khol'ushkin, and Laricheva 1990, 348; Goebel 1999, 216). The site itself has been of great importance in defining the Siberian Upper Palaeolithic and is one of the type-sites of the Mal'ta-Bur'et' culture or *stage* (Larichev, Khol'ushkin, and Laricheva 1990). The site is unique for Siberia in that '*Venus figurines'* were recovered during excavation, but more importantly perhaps was the recovery of a co-burial of two juveniles between the ages of two and three years old (ibid., 372), which have been dated to ~24kya (Goebel 1999, 216). The dental morphology of the juveniles has received much attention with some suggesting that the morphology implies that the Mal'ta inhabitants were derived from a western Eurasian stock (Hoffecker and Elias 2003, 38), largely because the teeth do not appear sinodontic. However, Larichev, Khol'ushkin, and Laricheva (1990, 732) note that some researchers (citing Alexeev and Gohman 1987) have claimed that the specimens do exhibit a slight shovelling. If there is a *mix* of traits presented both within the morphology of the juvenile specimens as well as the material culture, then recent genetic testing of the remains provides an explanation this pattern.

Earlier this year, Raghavan et al. (2014) published the results from their analysis of the Mal'ta juvenile remains, and while the mtDNA belongs to the U rather than the X hapologroup, the nuclear DNA suggests affinities with both extant western and eastern Eurasians as well as Amerindians. It is also important to note that the U haplogroup, for which the Mal'ta juveniles belong, is not common to the Altai region today, but has been recovered from about 80% of sampled Upper Palaeolithic and Mesolithic specimens from Europe, which may suggest that the Mal'ta remains belong to the most north-eastern range of a western Eurasian community (2014,

Figure 5 The location of the Mal'ta site and the Altai Mountains, Baikal Lake to the right. Background map data: Google, TerraMetrics 2014.

87). However, the nDNA and statistical comparison of the Mal'ta genome to extant human communities suggest that the presence of the X haplogroup within both the Altai region and Amerindian populations resulted from gene flow through Siberia during the LGM (2014, 89).

Proposition not met

Prior to the confirmation of the presence of the X haplogroup in Central Asia, the origin of the idiosyncratic X2a subhaplogroup was open to debate. Dennis Stanford and later Bruce Bradley along with Stanford were the first archaeologists to offer a hypothesis to explain the presence of the X2a subhaplogroup. To this end, the concurrence of the X haplogroup in North America as well as Western Europe seemed at first glance to suggest a shared matrilineal ancestry extending across the North Atlantic. However, research has shown that the X haplogroup does occur in Central Asia. In our review of the genetic literature pertinent to the *Solutrean Hypothesis*, we have come to the conclusion that the use of the X2a subhaplogroup as corroborative evidence of a late Pleistocene colonization of North America via the Atlantic can be rejected on the following grounds.

The north-eastern bias of the X haplogroup frequency in North America belies the actual distribution of this haplogroup, which is widespread. Further, the number of individual ethnic groups noted to carry the X haplogroup shows a western bias in contrast to the frequency bias. The frequency bias itself appears to be an effect of one ethnic group, the Ojibwa, who are noted to have undergone a relatively recent eastern migration from the Great Lakes. Palaeogenetic or archaeogenetic evidence, though limited at this point, has so far only detected a western North American confirmation for the prehistoric distribution of the X haplogroup. Further, the recent genetic testing of the Anzick human remains (Rasmussen et al. 2014) suggests a close genetic affinity with the Mal'ta juveniles and Amerindians, especially South Americans, and not Europeans. While there may be some unresolved issues concerning the association of the Anzick child and the Clovis cache, the results of the radiocarbon dating on the human remains at 10,700 ^{14}C (ibid.) fall within the chronological range of the Clovis Culture.

As far as being a marker of a Pleistocene, northern Iberian lineage, analyses of extant and prehistoric northern Iberians appear to indicate that the X haplogroup has never comprised more than a fractional amount of this region's matrilineal diversity. Instead, the H and V haplogroups appear to be better candidates for markers of a Solutrean 'ancestry'. Here, again, the evidence fails to support the *Solutrean Hypothesis* as both the H and V haplogroups are undetected in any Amerindian population.

Instead, multiple lines of evidence, linguistic, archaeological and genetic, appear to indicate a central Asian origin of the X2a subhaplogroup. The Na-Dene language family, which has an overwhelmingly north-western distribution bias, appears to demonstrate a deep cultural connection between Central Asia and some aboriginal Americans. This affinity is mirrored by the concurrence of the X haplogroup among Central Asians as well as among speakers of the Na-Dene language family. Further, all but one of the Amerindian populations that carry the X2a subhaplogroup belong to the Na-Dene language family.

All of these lines of evidence put together suggest that the first Amerindian colonizers were derived from a central Asian population prior to the genetic differentiation of Western and Eastern Eurasian populations, and therefore, from a population that must have been on the move, so to say, prior to the emergence of the Solutrean techno-complex.

Conclusion

Bladelet technology and other smaller-shouldered projectile points present arguably the best evidence that may suggest that Solutrean toolkits could be conservative in their material costs. The former are also documented in various cases as components of highly reliable toolkits for scenarios where risk is high. These smaller tool components of the Solutrean techno-complex seem to us to be ideal candidates for an extended ice voyage. The currently lacking evidence for a connection between the limited bladelet assemblages of the Clovis and those of the Solutrean does not favour our expectations of a Solutrean marine adaptation, although such theorizing is insufficient to realistically support or contradict the hypothesis in isolation.

When we first began this paper, the genetic analysis of the Anzick child had not yet been published. Now that the results of the analysis of the Clovis associated child are known (Rasmussen et al. 2014), we are more confident in asserting that there is a lack of compelling evidence to suggest a Pleistocene European contribution to the genetic makeup of Amerindians. In fact, the lines of evidence so far suggest that the first Amerindian colonizers were derived from central Asian populations prior to the divergence of western and eastern Eurasian genetic traits given the close genetic affinity of the Anzick child to the Mal'ta juveniles.

Further investigation into the technological logistics of an ice-sheet exploitation are currently being undertaken by the authors in order to assess how well Solutrean technology might have fared in such conditions, and how it compares with that of ethnographically documented ice-margin seal-hunters. This in itself is just one facet of the proposed hypothesis that we hope to explore further in our ambition to critically review established and developing theories on the prehistoric peopling of the Americas. We hope that with the continuing development of hypotheses regarding alternative colonizations, that we may expand our consideration to other models also.

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Addendum

Subsequent to the submission of our article, there have been two highly relevant publications addressing some of the issues raised in our own work. First of which is the highly informative paper by O'Brien et al. (2014) reviewing and further analysing, among other things, chronological issues with the timing of the proposed migration. The second article (Chatters et al. 2014) presents the results of genetic and morphological analyses conducted on a newly discovered human skeleton from the Yucatan Peninsula, dated to 13,000–12,000 calendar years BP. The implications of these works do not conflict with the position we take in our own article, as we do not directly address the issue of the timing of the migration, and the analyses of the Yucatan individual further suggest an East Asian point of origin of the earliest Americans.