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Peopling time, spatial occupation and demography of Late Pleistocene–Holocene human population from Patagonia

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ABSTRACT

The settlement of Patagonia has been the subject of extensive research, although key questions about the timing of arrival of the first humans and the subsequent patterns of dispersal and demographic changes within the region remain largely unresolved. In this study we evaluated the most probable date for the initial peopling of Patagonia and explored the temporal and spatial changes in population size along Late Pleistocene–Holocene by using robust statistical methods for the analysis of radiocarbon dates and molecular data. We suggest that the first humans probably arrived to Patagonia around 17,000–14,000 years BP, a few thousands of years earlier than generally stated. Within the region, the populations experienced a sustained and slow growth until the transition Pleistocene–Holocene, when the population size started to increase, with a remarkable acceleration after 7000–5000 years BP and reaching its maximum at 1000 years BP. The spatial occupation was not homogeneous across the region though, changing from a more intense continental occupation to a coastal occupation in the Late Holocene. This pattern of peopling and population expansion, obtained here on the basis of a rigorous and comprehensive quantitative approach, will allow the future evaluation of formal models about the ecological and cultural processes that drove the evolution of the human populations from Patagonia.

1. Introduction

Patagonia was the last continental region of the world to be colonized by modern humans. The archaeological evidence most widely accepted suggests that they spread into the region from the Northwest of South America by around 14,000 years ago, probably following the Pacific coast and reaching southern Patagonia ca. 13,000 years ago (Miotti and Salemme, 2003; Steele and Politis, 2009; Prates et al., 2013). There is increasing genetic data, from modern and ancient mtDNA and Y chromosome, supporting that the early populations that inhabited the region descended from Asian groups. This evidence also points out that early populations probably gave rise to Late Holocene and historic populations, suggesting a local biological evolution of Patagonian groups (Moraga et al., 2000; Garcıa-Bour et al., 2004; Goebel et al., 2008; Perego et al., 2010; Bodner et al., 2012; de Saint Pierre et al., 2012a). The spatial pattern of early human occupations in Patagonia seemed to have occurred almost simultaneously along the Atlantic and Pacific coasts, while the Andean foothills were colonized much later (Borrero, 1994–1995; Miotti and Salemme, 2003; Prates et al., 2013). Previous studies also postulate that human populations were small and stable along Late Pleistocene and Early Holocene, and that an increase in the occupation density only occurred during the Late Holocene, particularly during the last 1000 to 500 years BP (Martínez et al., 2013; Barberena et al., 2015; Zubimendi et al., 2015). It has also been postulated that in some areas of Patagonia population density decreased during the Middle Holocene

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(Barrientos and Perez, 2005; Neme and Gil, 2008; Salemme and Miotti, 2008). In spite of these apparent agreements, the timing and process of peopling as well as demographic changes in Patagonia have been the focus of intense debate for the last decades (Kelly, 2003; Goebel et al., 2008; Salemme and Miotti, 2008; Dillehay, 2009; Steele and Politis, 2009; Méndez et al., 2015).

In order to address these issues, significant effort has been devoted to obtain extensive databases of radiocarbon dates, while the conceptual and methodological approaches to analyze them have received less attention. In this sense, the pattern of dates is usually taken as a direct evidence of the initial peopling and demographic dynamic of the Patagonian populations. However, these assumptions are at least arguable. First, it has long been accepted that the archaeological record is incomplete and longtime gaps may exist between the oldest known archaeological evidence and the initial peopling (Marshall, 1990; Saltré et al., 2015; Villavicencio et al., 2015). Therefore, the earliest dated site cannot be assumed as the evidence of the first peopling in a given region. Additionally, it is widely recognized that the taphonomic processes, sample size and sampling strategies of radiocarbon dates can generate biases in the estimations of the spatial occupation and demographic dynamics of hunter-gatherer groups (Williams, 2012; Timpson et al., 2015; Torfing, 2015). Given that these conceptual and methodological problems have not been taken into account in previous studies, the temporal and spatial processes of Patagonian peopling are far from being well described and understood.

In this study, we estimate the most probable time for the earliest peopling of Patagonia and explore the temporal changes in population size along Late Pleistocene–Holocene by using robust statistical methods for the analysis of radiocarbon dates. We also investigate the temporal changes in the spatial occupation and population density of the region. In addition, we obtained independent estimations of the earliest peopling and posterior demographic changes using molecular data. Here we study the peopling time, spatial occupation (or geographic distribution) and demography together because they are part of the same process of colonization and posterior population dynamic in a region (Drummond et al., 2005; Avise, 2009; Lemey et al., 2009). To investigate the time and temporal dynamic of peopling we assembled a comprehensive dataset of radiocarbon dates of archaeological sites from the southern cone of South America and analyzed them by means of time series and stratigraphic statistics (Marshall, 1990; Surovell and Brantingham, 2007; Williams, 2012; Shennan et al., 2013; Saltré et al., 2015). The spatial occupation of the region was explored using the distribution of the frequency of radiocarbon dates employing spatial statistical analyses (Legendre and Legendre, 1998). The molecular-based estimations of the earliest time of Patagonian peopling and the posterior demographic changes were performed using modern and ancient mtDNA data and Bayesian methods (Drummond et al., 2005; Ho and Shapiro, 2011; Perez et al., 2016).

2. Material and methods

2.1. Radiocarbon and molecular data

We assembled a dataset of 1785 radiocarbon dates from different bioarchaeological and archaeological sites from South Buenos Aires and Mendoza to Tierra del Fuego (between 36 and 55 degree of South Latitude; Fig. 1; Table A.1; Borrero and Franco, 2000; Gil, 2006; Salemme and Miotti, 2008; Tessone and Belardi, 2010; Boschín and Andrade, 2011; Morello et al., 2012; Fernández et al., 2013; Martínez et al., 2013; Prates et al., 2013; San Román, 2013; Gil et al., 2014; Pallo and Ozan, 2014; Barberena et al., 2015; Berón, 2015; Campbell and Quiroz, 2015; García Guraieb et al., 2015; Martínez et al., 2015; Zubimendi et al., 2015; Perez et al., 2016). Sites from neighbor areas such as Southern Cuyo and South Pampa were also included because they have been previously discussed together with Patagonian sites in studies that address the peopling of this region. The final dataset was generated after eliminating dates of the same site that overlapped in the informed standard deviation, including in the dataset the dates with the narrower standard deviation. In this way, we avoid possible biases related to the intensity of excavation in the same archaeological site or the quantity of economic resources invested for investigating specific periods of greatest interest (e.g. the early peopling of the region). All dates were calibrated using the Calib 7.0 software and the *SHCal13* Southern Hemisphere Calibration Curve (Stuiver et al., 2014).

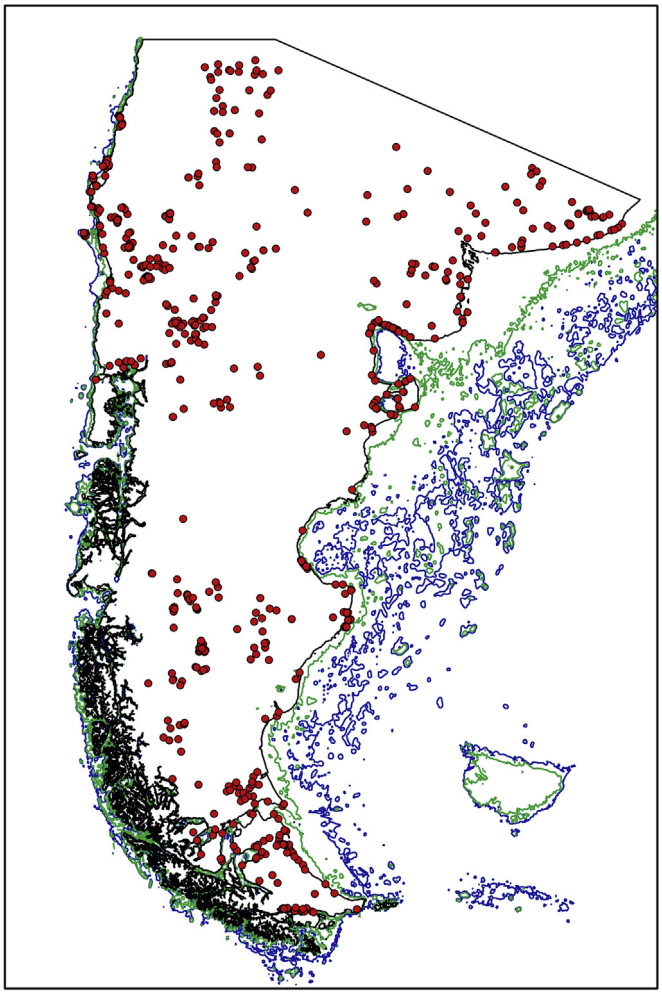

Fig. 1. Distribution of studied archaeological sites (red points), current coastline (black line) and the estimated coastlines at 11,500 Cal BP (green line) and 17,000 Cal BP (blue line). The coastlines are drawn following Prates and collaborators (2013). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

Modern and ancient human mitochondrial DNA (mtDNA) sequences were downloaded of the GenBank database and of previous publications (Table A.2; Ginther et al., 1993; Moraga et al., 2000; Garcıa-Bour et al., 2004; Perego et al., 2009; Bobillo et al., 2010; Moraga et al., 2010; Catelli et al., 2011; Bodner et al., 2012; de Saint Pierre et al., 2012a, 2012b; de la Fuente et al., 2015). We analyzed sequences from descendants of aboriginal populations carrying mtDNA variants (haplotypes) with high frequencies and/or mainly restricted to populations from the extreme south of South

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