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Abstract

The genetic composition of Amerindian descendants from Patagonia has long been a focus of interest, although the information available is still scarce for many geographic areas. Here, we report the first analysis of the variation in the mtDNA control region for an area of northwestern Patagonia, the North of Neuquén, with the aim of studying the processes and historical events that modeled the evolutionary history of these human groups. We analyzed 113 individuals from two localities of northern Neuquén, along with 6 from southern Neuquén and 223 mtDNA sequences previously published from neighboring areas from Argentina and Chile. We estimated the haplotypic variation and spatial structure of molecular variability. Amerindian subhaplogroups predominate in the two samples from northern Neuquén (N= 70), being D1g and C1b13 the most represented, although in different proportion. These samples exhibit Amerindian mtDNA haplotypes similar to the variants from neighboring areas. Most of haplotype variability is observed within group, while variation among groups is relatively low and scarcely associated to geographical space. The most frequent subhaplogroups in northern Neuquén are characteristic of native populations from Patagonia and Chilean Araucania, and probably originated in the region during the Late Pleistocene or Early Holocene. However, the spatial variation of mtDNA haplotypes departs from a latitudinal pattern and suggests differential levels of gene flow among areas during the Late Holocene; with moderate levels across the North of Neuquén as well as between this area and neighbouring populations from Chile and the South of Neuquén and Río Negro.

The genetic variation of Amerindian populations from the southern cone of South America has been shaped by microevolutionary processes and events that generated the patterns found at large spatial scales –resulting from the initial peopling of the region around 17,000 and 12,000 years ago–, as well as patterns observed at more local scales that were established after the settlement of the first groups (Bodner et al., 2012; de Saint Pierre et al., 2012a; Perez et al., 2016a). At a continental scale, the low levels of genetic variation and the strong latitudinal arrangement in the frequency of the founding mitochondrial haplogroups, characterized by an increase of C1 and D1 and a reduction of A2 and B2 from North to South, is thought to be the result of a serial founder effect during the rapid expansion in a north to south direction across this region (e.g., Merriwether et al., 1995; Moraga et al., 2000). Recent studies, based on the sequencing of the control region and complete mitochondrial genomes, described new subhaplogroups and haplotypes that differ between the northern and southern populations (Perego et al., 2010; Bodner et al., 2012; de Saint Pierre et al., 2012a; Moreno-Mayar et al., 2018). However, the patterns of genetic variation at smaller spatial scales are still unknown for a large number of geographic areas, which limits the discussion of locally occurring evolutionary processes and events, as well as their contribution to maintain or modify the patterns of mtDNA variation at a wider spatial scale originated during the early peopling.

One of the geographical areas for which studies of molecular markers are still lacking is the Northwest of Argentinian Patagonia, specifically the area known today as province of Neuquén. This province comprises the territory limited to the north and southeast by the Colorado and Limay rivers and to the west by the Andean mountain range (Fig. 1). The elevation of the Andes increases from South to North while humidity increases in the opposite direction, resulting in a heterogeneous environment, characterized by an arid to semi-arid climate (around 200 mm of annual precipitation) with predominance of shrub

steppes to the North and by a humid climate (ranging from 1000 to 2000 mm of annual precipitation) with forests to the South (Fig. 1; Cabrera 1976; Oyabal et al., 2018). The northern area of Neuquén is also crossed by a high mountain range called Cordillera del Viento, that runs parallel to the Andes, and represents an important barrier for human mobility (Zöllner & Amos, 1973; Fig. 1).

Moreover, the archaeological evidence suggests different population histories across Neuquén. From the initial peopling to historic times, the North of the province was inhabited by small groups of mobile hunter-gatherers that mostly relied on the hunting of guanaco (*Lama guanicoe*) and ñandú (*Rhea pennata*) (Barberena et al., 2015; Perez et al., 2016b; Rindel, 2017; Gordón et al., 2018, 2019). These groups have been characterized by a relative isolation and low levels of interaction on the basis of differences in rock art styles at both sides of the Cordillera del Viento (Fernández, 1979), although the presence of pottery fragments decorated with styles typical from Centeral Chile suggests some level of contact with neighbouring groups after 1500 years BP (Cuneo, 2010; Hajduk et al., 2011). In contrast, the South of Neuquén was characterized by an increase in population size by the Late Holocene, along with changes in subsistence such as the use of pottery for food storage and processing and the incorporation of domesticated plants (e.g., corn and squash) (Hajduk et al., 2011; Pérez & Erra, 2011; Gordón et al., 2019). A sustained contact between populations from Southern Neuquén and the Chilean Araucania for at least the last 2000 years is supported by the presence of the same techniques of pottery manufacture and decoration, the same cultigens and similar burial contexts, together with evidence of networks of exchange that include obsidian artifacts and turquoise ornaments at both sides of the Andean mountain (Hajduk et al., 2011; Pérez & Erra, 2011; Campbell et al., 2017, 2018). The incorporation of horses and the exchange of livestock after 500 years BP increased the range

of mobility of aboriginal groups from Patagonia and Chile, which might have favored the contact with more distant groups (Mandrini & Ortelli, 2002).

On the basis of geographical and environmental characteristics, along with the archaeological evidence, we can derive some expectations about the genetic variation in the area. The high elevation of the Andean mountains in the North and the presence of the Cordillera del Viento could have restricted the genetic flow with populations settled to the West side producing conditions of relative biological and cultural isolation (Fernández, 1979; Cuneo, 2010). Conversely, the southern part of the mountains, characterized by low passages, might have favored the contact with populations from the Chilean Araucania, resulting in higher levels of gene flow with populations from neighbouring regions (Fernández, 2006; Pérez & Erra, 2011; Cobos et al., 2012; Cobos & Bernal, 2017; Perez et al., 2017; Bernal et al., 2018; Gordón et al., 2018, 2019).

Here, we analyze the molecular variation in the mtDNA –Hypervariable regions I and II (HVR I and II)– of individuals with American ancestry of two localities from northern Neuquén located at both sides of Cordillera del Viento, and compare them with samples from southern Neuquén-western Río Negro, southern Mendoza and Central Chile (Bodner et al., 2012; de Saint Pierre et al., 2012a; Motti, 2012). We explicitly assess to which extent the mtDNA variants carried by individuals from these areas mainly reflect the early settlement and local evolution of the populations in the region. Under this hypothesis we expect a high frequency of mtDNA variants characteristic of northwestern Patagonia and a similar composition in samples from neighboring areas at similar latitude. Alternatively, if more recent processes, such as differential gene flow with neighboring groups and long distance migratory events, altered the early pattern of variation, we would expect significant differences between the two localities from northern Neuquén and neighbouring groups while groups from southern Neuquén will be closer to those from Centeral Chile. To test these

hypotheses, we first characterized the composition and diversity of mtDNA in northern Neuquén; then, compared it with the diversity from neighboring areas; and finally, analyzed the evolutionary relationships and spatial structure in Northwest Patagonia and Central Chile.

Materials and Methods

Samples

We collected 113 saliva and cheek swab samples of individuals from two localities of northern Neuquén, Las Ovejas, Minas Department (Lov, n=28) and Rincón de los Sauces, Pehuenches Department (RdlS, n=85) (Fig. 1). Given that the aim of this study was to characterize the Amerindian component, the sampling was done according to the following criteria: prioritize local-born individuals, exclude first-degree relatives, and whenever possible the older member of the maternal lineage was sampled. Local informants recruited individuals and a researcher collected the saliva and cheek swab samples at the housing units and the community center in Las Ovejas. All individuals decided to participate voluntarily in this study and informed consent was obtained prior to saliva and cheek swab sampling. The geographical location of the individuals and the place of birth of the participants, their mother or their maternal grandmother was the only information revealed, the rest was kept confidential. Taking into account this information we generated seven geographical groups: North Region (Bolivia, North of Argentina and Paraguay), Northwest Neuquén (NW-Nqn), Central-South Neuquén (CS-Nqn), Northeast Patagonia (NE Patagonia; Río Negro, Buenos Aires and La Pampa), South of Cuyo (Mendoza and San Luis), Eurasia (España and Rusia), Chile (mainly Central Chile) (S2 Table). With this grouping of the birthplace, together with the mitochondrial lineage of each individual, we constructed bar charts representing the diversity of origins of each of the two locations under study.

Ethical approval was obtained from the Hospital Italiano de Buenos Aires Ethics Committee (reference number 1356; 3/12/09) and Maimonides University Ethics Committee (07/04/15).

For comparative purposes we collected Amerindian mitochondrial sequences from neighboring areas available on GenBank and published studies (Bodner et al., 2012; de Saint Pierre et al., 2012a; Motti, 2012). The database obtained includes 229 sequences –including 223 previously published plus 6 sequences from this study– that were grouped by their geographical proximity. The groups conformed following this criterion are: Mendoza (MZ, n=54) and southern Neuquén-western Río Negro (sNQN-wRN, n=57) from Argentina; Bío-Bío region (BB, n=42) and Araucanía-Los Lagos-Los Ríos regions (A-LL-LR, n=76) from Chile (Fig. 1; S1 Table). Additionally, we compared the pattern of mtDNA variation in Northwest Patagonia with the variation found in the Southern Cone of South America, employing 1288 sequences of HVRI and HVRII retrieved from previous studies (Cabana et al., 2006; Marrero et al., 2007; Bobillo et al., 2010; Gayá-Vidal et al., 2011; de Saint Pierre et al., 2012; Sandoval et al., 2013; Cardoso et al., 2013; Batai et al 2014). We determined the subhaplogroup of each individual and estimated their frequency in each of the following geographic groups: Chubut (Chu), Islands from Southern Chile (sChile), Buenos Aires (BsAs), Southern Brazil (sBr), Chaco and Formosa (Ch-F), Northwest Argentina (NwA), Northern Chile (nChile) and Centralu-South Andes (c-sAndes) (Fig. 1; S3 Table).

Molecular Analysis

We extracted all DNA using a volume of lysis buffer (Tris 50 mM pH8, EDTA 50 mM, sucrose 50 mM, NaCl 11 mM and SDS 1%). After the addition of 150 microliters (ul) of SDS 10% and 30 ul of Proteinase K (Qiagen®), we incubated the samples overnight at 53ºC. The following step was the incorporation of 400 ul of NaCl 5M in an ice bath for 10 minutes

(min). The samples were centrifuged for 10 min at 13000 rpm. Supernatant was separated and 500 ul of absolute alcohol was added. The final step was the DNA extraction with QIAamp DNA mini kit (Qiagen®) which allows a greater purity. HVR I and II amplification was carried out in a unique segment of 1027 bp (base pairs; positions 15978 to 436 bp) using the specifications for the MINT master mix (Inbio Highway®), in 30 cycles of PCR with 54°C as melting temperature for the primers FL 5'CACCATTAGCACCCAAAGC3' (similar to the one used in Bravi, 2004) and RH 5'GGGGTGACTGTTAAAAGTGCAT3' (designed for this study). This protocol was designed by Dr. Laura Morelli (Leloir Institute, IIBBA-CONICET) and modified following her recommendations to guarantee the extraction of high quality mtDNA from saliva samples.

For HVR I and II amplified fragment purification we used Bioneer PCR purification Kit (BIONEER, Inc.). Sequencing of this DNA fragment was performed by Macrogen (South Korea). With MEGA 7.0.26 (Kumar, Stecher, & Tamura, 2016) we edited and aligned the sequences with algorithm FFT-NS-2 implemented by MAFFT v7.012b (Katoh & Standley, 2013). We obtained polymorphisms of each sequence using Sequencher 4.9 vDemo and comparing with the revised Cambridge Reference Sequence (rCRS, Andrews et al., 1999). After that, we characterized the HVR I and II sequences using the HaploGrep 2 platform (Weissensteiner et al., 2016) and recent studies of populations from southern South America (Bodner et al., 2012; de Saint Pierre et al., 2012a).

Furthermore, a Restriction Fragment Length Polymorphism (RFLP) analysis was performed to determine the presence of Amerindian haplogroups in individuals from which no control region sequence could be obtained. For haplogroups A, C and D the DNA samples were processed with restriction enzymes following the protocols used by Postillone et al. (2017). For the detection of the 9bp deletion characteristic of haplogroup B, amplification was directly visualized in a 3% agarose gel (Postillone et al., 2017).

Statistical Analysis

Descriptive statistics. We analyzed the number of segregating sites (S), haplotypes (h), haplotype diversity (Hd), nucleotide diversity (π) and mean number of pairwise differences (K) for the five groups, using the software DnaSP v6 (Rozas et al., 2017). For obtaining a more detailed description of the molecular variation in the two localities from North of Neuquén, we reconstructed hierarchical networks by hand for the two most frequent haplogroups, C1 and D1, according to previous studies (de Saint Pierre et al., 2012a). To build the topology of the hierarchical networks we considered the mutations shared by all the haplotypes and those unique for each individual, using previous works as reference (Achilli et al., 2008; Perego et al., 2010; Bodner et al., 2012). The unique mutations for each individual are those considered by Weissensteiner et al. (2016) as local private mutations, which have not been observed within the subhaplogroup of interest although they were described for other haplogroups.

Additionally, we constructed phylogenetic networks for subhaplogroup C1b13 and various subhaplogroups of D1 with the purpose of estimating the possible relationships that exist between the obtained haplotypes and others from neighbouring areas. This analysis was performed using the Network 5.0.0.3 software (Fluxus Technology Ltd, 2004-2018), with median joining and maximum parsimony as post-processing options. Each polymorphic site was weighed following the estimates of Soares and colleagues (2009).

Analysis of population structure. To explore the variance among the groups from North of Neuquén (Lov and RdlS) and neighbouring areas (MZ, sNQN-wRN, BB, A-LL-LR) we performed a molecular variance analysis (AMOVA) and calculated the fixation index (FST) to estimate the molecular differentiation between groups using Arlequin v. 3.5.2.2 (Excoffier

& Lischer, 2010). The significance of differences was tested using 1000 permutations. To assess the pattern of differences among groups we calculated Principal Components (PC) on the frequencies of subhaplogroups, estimated with HaploGrep 2 (Weissensteiner et al., 2016). Then, we estimated a neighbor-joining tree (NJ) using FST distances and plotted the NJ on the first two PCs. Both analyses, PCs and NJ, were obtained in PAST 3.15 (Hammer et al., 2001). A second PC analysis was performed on the 14 groups from the Southern Cone of South America.

Finally, in order to explicitly explore genetic and geographic structure in the region of interest, we applied a spatial analysis of molecular variance (SAMOVA; Excoffier et al., 1992; Dupanloup et al., 2002) using the groups from North of Neuquén and neighbouring areas. Unlike the AMOVA analysis, where a hierarchical profile of genetic diversity can be obtained in a determined set of populations, SAMOVA is the most appropriate analysis when there is no obvious criterion that defines different groups of populations (K). This method allows estimating a possible structure in the space between populations, defining K groups of populations. To define the number of K groups the SAMOVA considers a different fixation index to the FST (distance between populations) called FCT, which accounts for the difference between groups by maximizing the proportion of genetic variation (Excoffier et al., 1992; Dupanloup et al., 2002).

Results

Mitochondrial DNA haplogroups were determined for 26 individuals from Las Ovejas and 69 from Rincón de los Sauces. In both localities the proportion of Amerindian haplogroups was greater than that of Europeans. In Lov we observed 21 (81%) individuals carrying Amerindian haplogroups and five (19%) carrying European haplogroups, while in RdlS the proportion was 49 (71%) and 20 (29%) for Amerindian and European haplogroups,

respectively (Fig. 2). The haplogroups of ten individuals from RdlS were defined by RFLP (four D, four C and two B). No African haplogroups were detected in any of the individuals from North of Neuquén. Regarding haplogroups of European origin, in Lov we identified two individuals with haplogroups H2, two with K1 and one with K2. In RdlS the European ancestry was more diverse with 11 individuals carrying H2a2, four T2, three H3, one J1 and one K2 (Fig. 2; S2 Table). The geographic origin of the mother or maternal grandmother of the individuals from the two localities of North of Neuquén mainly corresponds to immigrants from neighboring areas, especially other towns from northern Neuquén, Chile and the Pampean region; although migrants from other regions of Argentina and Chile were also found in RdlS (Fig. 2; S2 Table). The subsequent analyses were performed using only the Amerindian haplogroups (60 individuals) recovered by sequencing, which comprises a total of 21 sequences from Lov and 39 from RdlS.

The frequency of Amerindian subhaplogroups was different between the two localities from North of Neuquén (Fig. 2; Table 1). Lov displayed a greater proportion of subhaplogroup D1g (52%), followed by the nodal haplogroup D1 (14%), while RdlS had a greater representation of subhaplogroup C1b13 (38%) followed by D1g (28%). Haplogroups C1 and D1 also have a high frequency in the other four groups analyzed (MZ, sNQN-wRN, BB and A-LL-LR), although they also exhibit a striking proportion of A2 and B2, mainly B2i (Table 1), compared to the two localities from North of Neuquén. Moreover, measures of variability showed differences between Lov and RdlS in the values of diversity of Amerindian haplotypes (h) and in the number of segregating sites (S; Table 2). The values of h and S are higher in RdlS (S= 75, h= 34) than in Lov (S=38, h=15), suggesting a more ancient population history or a higher level of gene flow in the first locality.

Because haplogroups C1 and D1 were the most frequent in the two localities from North of Neuquén, their internal variability will be described in more detail. Subhaplogroup D1g

showed great internal variability in Lov and RdlS (Fig. 3A). There was a large representation of D1g1b characterized by the C16245T polymorphism and its derived haplotypes in both samples of North of Neuquén. Four individuals of RdlS and one of Lov were detached from D1g1b because they possess the additional mutations 291d, 325d, T16086C and T16088C (Fig. 3A). Three individuals of Lov and one of RdlS also had the mutation T16189C and in four other individuals had mutations that further differentiated them as particular haplotypes. On the other hand, Lov presented a high frequency of D1g2 subhaplogroup defined by the mutations G143A and T16189C, with an additional T16092C in three individuals and an insertion 16186.1C in another individual. In Lov we also found individuals with the C16142T polymorphism that characterizes D1f plus the extra mutation A16497G. In the same locality, an individual presented T152C, A16051G, A16241G and T16342C polymorphisms that determine a haplotype derived from subhaplogroup D4h3. The only D1 subhaplogroup found in RdlS, different to D1g, was D1j given by mutations T152C, C16242T and T16311C (Fig. 3A). The network analysis shows that the subhaplogroup D1g1b is also present in high frequency in A-LL-LR, while the D1g2 has a high frequency in BB (Figs. 4A and 5).

The highest variability of C1 haplotypes was observed in RdlS with a high proportion of haplotypes derived from C1b13 characterized by the C258T polymorphism (Fig. 3B). Eleven individuals of RdlS and two of Lov presented this subhaplogroup but differing from the nodal by one to four mutations. However, the result of our analysis is not totally concordant with the current subhaplogroup classification, probably due to the weighting given to some polymorphisms (Soares et al., 2009) that defined the C1b13 subhaplogroup. This puts the current classification of subhaplogroup C1b13 into question, needing further study in order to clarify its status. Besides, RdlS presented other haplotypes within C1a characterized by mutations T195C, G207A, 325d, C16192T and T16356C, C1d defined mainly by C194T and A16051G and other C1 derivatives with additional local mutations (Fig. 3B). The haplotype

of one individual of Lov (Lov 20) differed from C1b13 by T16311C mutation (Fig. 4B). In the same sense, most of the variants of C1b13 from RdlS are not present in Lov (Fig. 4B), although related haplotypes are observed in the other groups (Fig. 5).

Regarding molecular variation, the results of AMOVA for the six groups suggested that the greatest variability was within groups (94.05%), while variation among them was relatively low (5.95%). However, this variation among groups was significant (p-value < 0.00001) (Table 3), which would indicate that at least one of them differs considerably from the rest. Principal Component analysis obtained from the subhaplogroup frequencies helps to better understand this result of AMOVA, showing that RdlS and MZ were the groups that differ the most from the rest along PC 1 (Fig. 6). However, both groups are separated along PC 2. Groups A-LL-LR, sNQN-wRN and BB formed a cluster with similar frequencies of subhaplogroups and non-significant FST distances between them but significant with the rest of the groups. Lov was closer to this cluster, although it had a significant FST distance (Fig. 6). RdlS also displays significant differences with the other groups (Fig. 6).

SAMOVA results showed that all FCT estimates were similar. Estimated FCT were significant only when the groups form four clusters, with a percentage of variation among clusters of 5.58% (FCT: 0.05580; p-value: 0.04008). Table 4 shows that considering these four clusters, RdlS, Lov and MZ are separated from each other and from the cluster composed by BB, A-LL-LR and sNQN-wRN, in agreement with the PC results (Fig. 6).

The Principal Component analysis of the frequencies of Amerindian subhaplogroups in the Southern Cone of South America (S3 Table) displays a strong geographical clustering of the groups, showing differences between northern and southern groups along PC1, with the former also differing between east and west in the PC2 (Fig. 7). The groups from the northern part of the region show a high frequency of B2 in the west and A2 in the east, while towards

the south the most frequent subhaplogroups are derived variants of D1 and C1 (mainly D1g1 and C1b13; Fig. 7).

Discussion

Results of this work indicate that the localities from North of Neuquén have a high proportion of Amerindian mitochondrial haplogroups, which are present in 81% of the individuals from Lov and 71% from RdlS. These values are similar to those reported for Northeast and Center of Patagonia and Mendoza where the proportion of maternal Amerindian haplogroups is between 70-80%, contrasting with the lower percentage (ca. 50%) found in populations from South of Pampa, the region immediately north to Patagonia (Avena et al., 2007; Avena et al., 2010; Bobillo et al., 2010; Motti, 2012). The high percentage of maternal Amerindian haplogroups compared to those of other origins, can be explained by the fact that Patagonia was one of the last territories to be incorporated into the Argentine National State, as a consequence, the indigenous communities kept their autonomy for a longer time (Avena et al., 2010). These results are better understood considering the post-contact unequal contribution of maternal and paternal lineages to the ancestry of Patagonian populations found in previous studies (Avena et al., 2010; Corach et al., 2010). Since the arrival of Europeans, the scenario prevailing in Argentina has been the crossing of native women with men of another origin (Avena et al., 2006), leading to an imbalance in the genetic contributions of both sexes to the gene pool of these populations. It is thus expected that the Amerindian contribution is greater when analyzing mitochondrial haplogroups.

In this sense, the two localities from North of Neuquén exhibited a higher frequency of mtDNA Amerindian variants corresponding to D1g and C1b13 subhaplogroups. These two variants, together with B2i and D4h3, have only been detected in high proportions in native populations from Patagonia and Chilean Araucania, and probably originated in the region

during the Late Pleistocene or Early Holocene (Moraga et al., 2010; de Saint Pierre et al., 2012a,b; de la Fuente et al., 2015; Motti et al., 2017). In agreement with previous studies, D1g presented the highest degree of variation (Bodner et al., 2012; de Saint Pierre et al., 2012a). Given the estimated age of about 15,000 years for D1g, it has been suggested that the haplotypes derived from this subhaplogroup arose locally soon after the initial settlement of the area, which for the North of Patagonia is estimated between 17,000-14,000 years BP (Bodner et al., 2012; Barberena et al., 2015; Perez et al 2016a,b). The substitution rate proposed by Endicott and Ho (2008) for the mtDNA control region analyzed in this paper is 0.302 substitutions per nucleotide site every one million years, resulting in a new mutation every 3.224 years, which adjusts to the average number of polymorphisms among D1g haplotypes (Fig. 4A). A different scenario was proposed for the haplotype network of C1b13, characterized by a central node with reticulations of the derived haplotypes that differ by a smaller number of polymorphisms (de Saint Pierre et al., 2012a). On the basis of Bayesian analyses of modern mtDNA it was suggested that this subhaplogroup differentiated around 12,000 years BP, in a population with rapid growth due to favorable environmental conditions (de Saint Pierre et al., 2012a). These results suggest that a large proportion of the modern mtDNA variation in northern Neuquén was generated during the early settlement of the region.

The analysis of ancient DNA from skeletal samples dated in the final Late Holocene supports the presence of D1g and C1 in North Patagonia before the European contact, although the lack of older human remains limits the use of ancient DNA to assess the genetic variants carried by the first settlers (Postillone, 2016; Crespo et al., 2017a, 2017b). Particularly, a high frequency of D1g has been found in individuals from northeastern Patagonia dated between 2500 and 500 years BP (Postillone, 2016; Crespo et al., 2017a, 2017b). The presence of C1, but with lower frequency, was also confirmed (Postillone, 2016;

Crespo et al., 2017a, 2017b). Whether or not it corresponds to the C1b13 subhaplogroup has been difficult to determine because most of the studies in ancient DNA only have results for HVR I and the polymorphism that characterizes that subhaplogroup is found in HVR II.

Independently of the time of the origin of C1b13 and D1g, the two localities from northern Neuquén differ with respect to which subhaplogroup is most represented. While 52% of the individuals from Lov carry the subhaplogroup D1g, most of the individuals from RdlS are carriers of C1b13, followed by D1g. Moreover, RdlS displays a greater diversity of mitochondrial Amerindian haplotypes within haplogroups D1 and C1, in relation to Lov. In addition, the spatial pattern of variation among groups from North of Neuquén and neighbouring areas does not show a clear geographic clustering. The samples from Chile, the South of Neuquén and West of Río Negro are similar, while the two localities from northern Neuquén differ from them, especially RdlS, which is more similar to Mendoza. This suggests that patterns of genetic variation at local scales differ from those found at a macro-regional scale, in which the main trends seemed to be generated during the early peopling (Fig. 7; Merriwether et al., 1995; Moraga et al., 2000). Recent processes such as gene flow between neighboring groups, migratory events before and after European contact or differential degree of isolation could account for such differences.

Particularly, the spatial pattern found here suggests that while the North of Neuquén had a moderate gene flow with neighboring areas –with more elevated values between Lov and Chilean populations–, the South of the province and Río Negro had a relatively higher gene exchange with the Chilean Araucania (Fig. 5). In this sense, the singularity of RdlS, compared to the rest of the samples, can be partially explained by its location at the East side of Cordillera del Viento mountain range. In prehispanic times, this mountain range seemed to be acted as a more important barrier than the Andes mountains for gene flow with populations at its West side (Cobos & Bernal, 2017), favoring the effect of genetic drift on

the frequencies of mtDNA subhaplogroups. On the other hand, our results are consistent with the existence of a common social system and/or unique population in the regions of Chile, the South of Neuquén and West of Río Negro during the Late Holocene, as is suggested by archaeological evidence that indicates high levels of exchange among these areas (Pérez & Erra, 2011; Hajduk et al., 2011). Moreover, although the Amerindian variants found here could be ancient in the region and some are restricted to the North of Neuquén, a high percentage of derived variants —53.3% of Lov and 46% of RdlS— are shared with neighbouring areas (Fig. 5), indicating sustained levels of gene flow during the Holocene. We can highlight that the D1j variant found in Neuquén is also present in Mendoza, as well as in the Center of Argentina (Garcia et al., 2012), while a high frequency of the D1g1b subhaplogroup was also described in Central Chile, and that the D4h3 subhaplogroup is very frequent in southern Patagonian populations (de Saint Pierre et al., 2012a).

Although the main pattern of diversity in mtDNA sequences can be related to pre-contact processes (Hajduk et al., 2011; Campbell et al., 2018), differences in the composition of Amerindian mtDNA and internal diversity between the two localities from North of Neuquén may have been further accentuated by more recent processes related to their distinct post-contact histories. While Las Ovejas town was founded by the end of the 19th century as a small agricultural and pastoral colony, that maintained a low population size until today, Rincón de los Sauces did not have a stable population until 1970 but underwent a significant increased population size in the last 15 years with migrants from neighbouring areas (Censo Nacional de Población, Familias y Viviendas, 1970; Censo Nacional de Población, Hogares y Viviendas, 2010). This particular history of each locality can explain not only the higher diversity of Ameridian mtDNA sequences in Rincón de los Sauces, but also the higher frequency of European haplogroups and the larger percentage of individuals from other regions in this locality compared to Las Ovejas (Fig. 2). Our results suggest that European

migration has a variable role in the recent population history across this area, and thus, further studies might benefit from using ancient genetic data along with modern DNA.

Overall, the pattern of variation of Amerindian mtDNA suggests a relatively old settlement for the region and a local and sustained permanence of the same populations in the Northwest of Patagonia Argentina and the Chilean Araucanía. de Saint Pierre and colleagues (2012a) propose that the existence of specific regional subhaplogroups in the Northwest of Argentinean Patagonia and the Chilean Araucanía can be related to the early and rapid settlement of the region, followed by a relative isolation and genetic drift processes at regional level, as it has been postulated in other studies based on the distribution of haplogroups in the southern cone of South America (Merriwether et al., 1995; Moraga et al., 2000). Results obtained for the localities of North of Neuquén are generally in line with this scenario. However, the similarities of haplotypes among different areas on both sides of the Cordillera support the existence of a trans-cordilleran gene flow sustained at different times during the Holocene, as suggested by archaeological and ethnohistorical evidence (Goñi, 1986-1987; Mandrini & Ortelli, 1992; Silveira, 1996; Hajduk & Cuneo, 1997-1998; Perez, 2006; Hajduk et al., 2011; Campbell et al., 2018). Future studies that incorporate more samples of different antiquity and other molecular markers, will allow modeling the evolutionary history of populations from Northwest Patagonia along the Holocene in greater detail, by clarifying the specific contribution of processes related to the initial peopling and the posterior differential gene flow and genetic drift, potentially occurring in small and relatively isolated groups.

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Table 1. Frequencies of Subhaplogroups for Each Group

Abrev.: Mendoza (MZ), southern Neuquén-western Río Negro (sNQN-wRN), Bío-Bío (BB), Araucanía-Los Lagos-Los Ríos (A-LL-LR), Las Ovejas (Lov) and Rincón de los Sauces (RdlS)

Subhaplogroup	BB	sNQN-oRN	MZ	A-LL-LR	Lov	RdlS
A2	7.14	14.04	24.07	7.89	4.76	0.00
B2	0.00	1.75	16.67	1.32	0.00	5.13
B2i	26.19	38.60	0.00	26.32	14.29	2.56
C1	0.00	0.00	0.00	0.00	0.00	15.38
C1b	0.00	10.53	12.96	5.26	0.00	0.00
C1b13	28.57	7.02	5.56	19.74	9.52	38.46
C1c	0.00	0.00	3.70	0.00	0.00	0.00
C1d	0.00	1.75	5.56	0.00	0.00	5.13
D1	0.00	3.51	3.70	2.63	14.29	2.56
D1g	0.00	8.77	16.67	0.00	19.05	10.26
D1g1	38.10	12.28	0.00	32.89	33.33	17.95
D1j	0.00	1.75	11.11	0.00	0.00	2.56
D4h3	0.00	0.00	0.00	3.95	4.76	0.00
total	100.00	100.00	100.00	100.00	100.00	100.00

Table 2. Diversity Indexes for Each Group

S: number of segregating sites; h: number of different haplotypes; Hd: Haplotypic diversity; π: nucleotide diversity; K: average of nucleotide differences between sequences. All values for each index are standardized to vary between 0 and 1.

	S	h	Hd	π	K	N
Bío-Bío southern	39	18	0.927	0.00917	8.97	42
Neuquén-western Río Negro	70	40	0.980	0.01048	10.23	57
Mendoza	65	45	0.992	0.00995	9.70	54
Araucanía-Los Lagos-Los Ríos	71	43	0.975	0.00890	8.68	76
Las Ovejas	38	15	0.968	0.00874	8.56	21
Rincón de los Sauces	75	34	0.993	0.00963	9.29	39

Table 3. AMOVA Results for the Two Localities from Northern Neuquén and Neighboring Groups

AMOVA

Source of variation	d.f.	Sum of Squares	Variance Components	Percentage of variation
Among Groups	5	127.034	0.40308	5.95
Within Groups	285	1815.678	6.37080	94.05
Total	290	1942.711	6.77388	100
FST: 0.5951			p<0.00001	

Table 4. SAMOVA Results for the Different Agrupations of the Two Localities from Northern Neuquén and Neighboring Groups

Abrev: Mendoza (MZ), southern Neuquén-western Río Negro (sNQN-wRN), Bío-Bío (BB), Araucanía-Los Lagos-Los Ríos (A-LL-LR), Las Ovejas (Lov) and Rincón de los Sauces (RdlS).

				Percentage of variation		
K	Groups for each cluster	FCT	P-values	among clusters	among groups - within clusters	within groups
2	1: RdlS 2: BB, sNQN-oRN, MZ, A-LL-LR, Lov	0.05516	0.17204	5.52	3.72	90.76
3	1: Rdls 2:Lov 3:BB, sNQN-oRN, MZ, A-LL-LR	0.06269	0.05963	6.27	2.68	91.05
4	1:RdlS 2:Lov 3:MZ 4:BB, sNQN-oRN, A-LL-LR	0.0558	0.04008	5.58	1.5	92.92
5	1:RdlS 2:Lov 3:MZ	0.05316	0.06549	5.32	0.86	93.82

4:BB

5:sNQN-oRN, A-LL-

LR

Supplementary Table S1. HVR I and II Polymorphisms of All the Sequences Used Grouped by Geographical Proximity

Sample	Individual	Lineage	Control Region Polimorphisms	References
A-LL-LR	H93	A2	16111 16156 16223 16263 16290 16319 16362 16438 64 73 146 153 235 263 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H112	A2	16111 16156 16223 16263 16290 16319 16362 16438 64 73 146 153 235 263 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H109	A2	16111 16156 16223 16263 16290 16319 16362 16438 64 73 146 153 235 263 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H113	A2	16111 16156 16223 16263 16290 16319 16362 16438 64 73 146 153 235 263 523d 524d 573A	de Saint Pierre et al., 2012a
A-LL-LR	H49	A2	16111 16156 16223 16263 16290 16319 16362 16438 64 73 146 153 235 263 523d 524d 573A	de Saint Pierre et al., 2012a
A-LL-LR	H24	A2	16111 16223 16290 16319 16357 16362 64 71 73 146 153 235 263 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA19	B2i	16142 16183C 16189 16217 73 263 499	de Saint Pierre et al., 2012a
A-LL-LR	MA20	B2	16142 16183C 16189 16217 73 263 499	de Saint Pierre et al., 2012a
A-LL-LR	MA23	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	MA27	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H70	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H10	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H116	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H122	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H114	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H05	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H78	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H85	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H101	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H119	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA13	B2i	16136 16183C 16189 16217 16249 73 153 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H53	B2i	16183C 16189 16217 16249 73 153 195 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H75	B2i	16182C 16183C 16189 16217 16249 73 146 153 207 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H17	B2i	16183C 16189 16207 16217 73 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	MA07	B2i	16183C 16189 16207 16217 16291 73 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H72	B2i	16182C 16183 16189 16207 16217 16291 73 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	H97	B2i	16182C 16183 16189 16207 16217 16291 73 263 470 499	de Saint Pierre et al., 2012a
A-LL-LR	MA26	C1b	16223 16297 16298 16325 16327 73 249d 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a

A-LL-LR	H56	C1b	16223 16298 16325 16327 73 152 300 3249d 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA11	C1b	16126 16147 16223 16298 16325 16327 73 249d 263 290d 291d 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA15	C1b	16185 16223 16240 16298 16325 16327 73 203 249d 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H52	C1b13	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493	de Saint Pierre et al., 2012a
A-LL-LR	MA08	C1b13	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA10	C1b13	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H26	C1b13	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H106	C1b13	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H03	C1b13	16223 16298 16325 16327 73 243 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H38	C1b13	16223 16298 16325 16327 73 243 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA22	C1b13	16221 16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H08	C1b13	16223 16298 16311 16325 16327 73 150 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H125	C1b13	16223 16298 16311 16325 16327 73 198 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H33	C1b13	16223 16298 16311 16325 16327 73 198 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H19	C1b13	16223 16298 16311 16325 16327 73 249d 258 263 279 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA09	C1b13	16075 16223 16234 16298 16325 16327 72 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	MA25	C1b13	16223 16266 16294 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
A-LL-LR	H95	C1b13	16223 16298 16311 16325 16327 16368 16390 73 151 152 249d 263 290d 291d 379 489	de Saint Pierre et al., 2012a
A-LL-LR	H80	D1	16093 16223 16325 16362 73 195 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H34	D1	16093 16223 16325 16362 73 195 263 489	de Saint Pierre et al., 2012a
A-LL-LR	MA18	D1g1	16187 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H92	D1g1	16187 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H41	D1g1	16187 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H123	D1g1	16187 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H86	D1g1	16187 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H02	D1g1	16187 16223 16325 16362 73 263 489 573.1C 573.2C 573.3C 573.4C 573.5C	de Saint Pierre et al., 2012a
A-LL-LR	H115	D1g1	16187 16223 16325 16362 73 207 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H105	D1g1	16187 16223 16325 16362 73 150 195 207 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H01	D1g1	16187 16223 16325 16362 73 150 195 207 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H09	D1g1f	16178 16187 16223 16325 16362 73 150 199 263 374 489	de Saint Pierre et al., 2012a
A-LL-LR	H13	D1g1f	16178 16187 16223 16325 16362 73 150 199 263 374 489	de Saint Pierre et al., 2012a
A-LL-LR	MA24	D1g1c	16187 16223 16304 16325 16362 16399 73 263 489	de Saint Pierre et al., 2012a

A-LL-LR	MA29	D1g1	16187 16189 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H04	D1g1	16187 16189 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H27	D1g1	16187 16189 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H07	D1g1	16187 16189 16223 16234 16325 16362 16445 73 185 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H54	D1g1	16187 16189 16223 16311 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H32	D1g1	16187 16189 16223 16311 16325 16362 73 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H68	D1g1a	16187 16223 16325 16362 16390 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H98	D1g1a2	16187 16223 16245 16325 16362 16390 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H11	D1g1a2	16187 16223 16245 16325 16362 16390 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H15	D1g1a2	16187 16223 16245 16325 16362 16390 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H61	D1g1a2	16187 16223 16245 16325 16362 16390 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H73	D1g1a2	16187 16223 16245 16270 16325 16362 16390 63 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H37	D1g1a	16187 16223 16325 16352 16362 16390 16399 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H28	D4h3a	16223 16241 16301 16342 16362 73 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	MA14	D4h3a	16223 16241 16301 16342 16362 73 146 152 263 489	de Saint Pierre et al., 2012a
A-LL-LR	H108	D4h3a5	16051 16223 16241 16342 16362 73 152 263 489	de Saint Pierre et al., 2012a
BB	T40	A2	16111 16129 16223 16290 16319 16362 64 73 146 153 195 235 263 523d 524d	de Saint Pierre et al., 2012a
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BB	T21	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
BB	T46	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
BB	T28	B2i	16182C 16183C 16189 16213 16217 16249 73 263 470 499	de Saint Pierre et al., 2012a
BB	T97	B2i	16182C 16183C 16189 16213 16217 16249 73 263 470 499	de Saint Pierre et al., 2012a
BB	T110	B2i	16182C 16183C 16189 16213 16217 16249 73 263470 499	de Saint Pierre et al., 2012a
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BB	T67	C1b13	16223 16298 16325 16327 73 195 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
BB	T22	C1b13	16067 16223 16298 16311 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
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BB	T72	D1g1e	16187 16189 16209 16223 16325 16362 55 56 64 73 195 263 489	de Saint Pierre et al., 2012a
Lov	Lov27	A2	16084d 16111 16189 16194 16290 16319 16362 16413 64 73 146 153 235 263	This study
Lov	Lov17	B2i	16183C 16189 16217 16270 16296 16380 16467 64 73 129 198 207 253 263 393d	This study
Lov	Lov18	B2i	16183C 16189 16355 16380 16439 16444 16451 16478 16488 16508 16511 73 114 132 151 194 198 207 261 263 470 499	This study
Lov	Lov3	B2i	16031.1A 16182C 16189 16194 470 499	This study
Lov	Lov20	C1b13	16223 16298 16311 16325 16327 73 258 263 286d 287d	This study
Lov	Lov2	C1b13	16223 16298 16325 16327 16355 73 249d 258 263 290d 291d 489 493	This study
Lov	Lov26	D	16038 16041 16078 16092 16186.1C 16189 16223 16362 73 143 263 489C	This study
Lov	Lov13	D1	16142 16223 16295 16325 16362 16497 73 263 334.1T	This study

Lov	Lov24	D1	16142 16179 16223 16295 16325 16362 16497 73 263 489	This study
Lov	Lov1	D1g	16187 16223 16245 16325 16362 16390 73 146 152 263 419 489	This study
Lov	Lov21	D1g	16092 16187 16189 16223 16362 73 143 263 489	This study
Lov	Lov5	D1g	16031.1A 16092 16187 16189 16223 16362 73 143 263 352d 371d 385d 432d 489	This study
Lov	Lov7	D1g	16092 16187 16189 16223 16362 73 143 263 489	This study
Lov	Lov11	D1g1b	16187 16223 16245 16325 16362 16390 73 146 152 196.1T 235.1C 249.1A 263 284.1A 323.1G	This study
Lov	Lov12	D1g1b	16187 16189 16223 16245 16325 16362 16390 73 146 152 489	This study
Lov	Lov16	D1g1b	16187 16189 16223 16245 16325 16362 16390 73 125 146 152 263 267.1T	This study
Lov	Lov19	D1g1b	16187 16189 16223 16245 16325 16362 16390 73 146 152 263	This study
Lov	Lov22	D1g1b	16027 16301 16187 16223 16245 16325 16362 16390 73 146 152 189.1A 208 225.1G 249.1A 260.1G 263 285.1A	This study
Lov	Lov8	D1g1b	16187 16223 16245 16325 16362 16390 73 146 152 263 489	This study
Lov	Lov9	D1g1b	16187 16223 16245 16325 16362 16390 73 146 152 263 489	This study
Lov	Lov25	Dah3a5	16051 16223 16241 16342 16362 73 152 263	This study
MZ	MZSal03	A2	16111 16223 16290 16319 16362 64 73 146 150 153 263 523d 524d	Motti, 2012
MZ	MZ008	A2	15972 16111 16189 16223 16290 16319 16362 64 73 146 152 153 235 263 523d 524d	Motti, 2012
MZ	MZ007	A2	15972 16111 16189 16193.1C 16193.2C 16223 16290 16319 16362 64 73 146 153 235 263 523d 524d	Motti, 2012
MZ	MZ091	A2	16111 16192 16209 16223 16290 16319 16362 64 73 146 153 235 263 523d 524d	Motti, 2012
MZ	MZ035	A2	16111 16156 16223 16263 16290 16319 16362 16438 64 73 146 153 235 263 523d 524 d 573A	Motti, 2012
MZ	MZ027	A2	16111 16223 16290 16319 16362 73 146 153 235 263 523d 524d	Motti, 2012
MZ	MZ051	A2	16111 16223 16290 16319 16362 73 146 153 235 263 523d 524d	Motti, 2012
MZ	MZ088	A2	16111 16223 16290 16319 16362 73 146 153 235 263 523d 524d	Motti, 2012
MZ	MZ126	A2	16111 16223 16290 16319 16362 16512 16547 16551 16551.1G 73 146 153 263	Motti, 2012
MZ	MZ033	A2	16111 16223 16290 16319 16362 64 73 146 150 153 235 263 523d 524d	Motti, 2012
MZ	MZ119	A2	16111 16223 16290 16297 16319 64 73 143 146 150 153 235 263 523d 524 d 574	Motti, 2012
MZ	MZ141	A2	16111 16223 16290 16311 16319 16362 64 73 146 153 185 189 235 263 523d 524d	Motti, 2012
MZ	MZ101	A2	16111 16223 16290 16319 16362 64 73 146 152 153 235 263	Motti, 2012
MZ	MZ109	B2	16182C 16183C 16189 16217 73 143 146 263 499	Motti, 2012
MZ	MZ055	B2	16183C 16185 16189 16193d 16217 73 263 499 573.1C 573.2C 573.3C	Motti, 2012
MZ	MZ010	B2	16183C 16189 16193.1C 16217 63 64 73 146 215 263 455.1T 499	Motti, 2012
MZ	MZ050	B2	16183C 16189 16193.1C 16207 16217 16291 73 263 470 499	Motti, 2012
MZ	MZ018	B2	16183C 16188 16189 16217 263 499	Motti, 2012
MZ	MZ034	B2	16183C 16189 16193.1C 16217 16381 73 263 499	Motti, 2012
MZ	MZ37	B2	16142 16183C 16189 16193.1C 16217 16261 73 263 499	Motti, 2012
MZ	MZ142	B2	16142 16183C 16189 16193.1C 16217 73 263 499	Motti, 2012

MZ	MZ015	B2	16183C 16189 16193.1C 16217 16266 73 186 263 499	Motti, 2012
MZ	MZ146	C1b	16223 16298 16325 16327 73 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ39	C1b	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 52 d 524d	Motti, 2012
MZ	MZ64	C1b	16051 16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ111	C1b	16223 16298 16311 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ57	C1b	16092 16223 16298 16325 16327 73 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ144	C1b	16223 16298 16325 16327 73 194 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ068	C1b	16223 16298 16325 16327 73 146 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ087	C1b	16223 16298 16325 16327 73 146 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ017	C1b	16136 16223 16298 16325 16327 73 146 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ140	C1b	16093 16129 16223 16298 16300 16325 16327 16362 73 242 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ040	C1b	15904 16223 16297 16298 16325 16327 16362 73 228t 249d 263 290d 291d 489 493 523d 524d	Motti, 2012
MZ	MZ019	C1c	16051 16223 16298 16325 16327 73 194 195 249d 263 290d 291d 489 523d 524d	Motti, 2012
MZ	MZ116	C1d	16051 16223 16298 16325 16327 73 194 195 249d 263 290d 291d 489 523d 524d	Motti, 2012
MZ	MZ106	C1d	16223 16293 16325 16362 73 97 106d 107d 108d 109d 110d 111d 195 263 489 523d 524d	Motti, 2012
MZ	MZ114	C1c	15930 16129 16223 16261 16298 16325 16327 73 152 249d 263 290d 291d 489	Motti, 2012
MZ	MZSal02	C1c	15930 16223 16298 16325 16327 73 249d 263 290d 291d 485 523d 524d	Motti, 2012
MZ	MZ125	D1	16187 16189 16209 16223 16325 16362 55 56 73 185 263 489 499	Motti, 2012
MZ	MZSal15	D1	16223 16242 16311 16325 16362 73 152 263 489	Motti, 2012
MZ	MZ022	D1	16223 16242 16311 16325 16362 73 150 152 263 489	Motti, 2012
MZ	MZ131	D1	15924 16189 16223 16325 16362 73 146 263 489	Motti, 2012
MZ	MZ012	D1	15930 16187 16189 16223 16362 73 143 263 489	Motti, 2012
MZ	MZ143	D1	15930 16092 16187 16189 16223 16362 73 143 263 489	Motti, 2012
MZ	MZ076	D1	15965 16178 16187 16223 16325 16362 73 150 199 263 374 489	Motti, 2012
MZ	MZ107	D1	16172 16187 16223 16325 16362 73 263 489	Motti, 2012
MZ	MZ041	D1	16187 16223 16325 16362 16371R 73 263 489 573.1C 573.2C 573.3C	Motti, 2012
MZ	MZ150	D1	16187 16189 16209 16223 16325 16362 55 56 73 263 489	Motti, 2012
MZ	MZ021	D1	16187 16189 16209 16223 16325 16362 55 56 73 185 263 489 499	Motti, 2012
MZ	MZ073	D1	16092 16187 16189 16209 16223 16325 16362 55 56 73 263 489 499	Motti, 2012
MZ	MZ052	D1	16223 16242 16311 16325 16362 73 152 263 489	Motti, 2012
MZ	MZ112	D1	16157 16223 16242 16311 16325 16362 73 152 263 489	Motti, 2012
MZ	MZ058	D1	16223 16242 16311 16325 16362 73 152 263 489 524.1A 524.2C	Motti, 2012
MZ	MZ115	D1	16223 16242 16311 16325 16362 73 152 263 489 524.1A 524.1C	Motti, 2012

RdlS	RdlS24	B	16182.1C 16183C 16189 16217 16361 73 146 152 263	This study
RdlS	RdlS98	B	16182C 16183C 16189 16194 16195	This study
RdlS	RdlS81	B2i	16183C 16189 16207 16217 16291 16360 16501 64 73 263 393d	This study
RdlS	RdlS52	C1	16223 16297 16298 16325 16327 16362 73 249d 263 290d 291d	This study
RdlS	RdlS67	C1	16192 16223 16298 16325 16327 16356 73 195 207 249d 263 290d 291d 325d	This study
RdlS	RdlS70	C1	16086 16223 16327 73 143 249d 263 290d 291d	This study
RdlS	RdlS82	C1	16223 16234 16298 16325 16327 73 249d 263 290d 291d	This study
RdlS	RdlS83	C1	16086 16089 16110 16223 16298 16325 16327 73 185d 249d 258 261 263 324	This study
RdlS	RdlS42	C1b13	16147 16223 16298 16325 16327 16474 73 249d 258 263 290d 291d	This study
RdlS	RdlS103	C1b13	16171 16223 16298 16325 16327 73 249d 258 263 401d	This study
RdlS	RdlS18	C1b13	16223 16249 16298 16325 16327 73 199 249d 263 290d 291d 348 385.1A 388	This study
RdlS	RdlS19	C1b13	16223 16298 16325 16327 73 103 249d 258 263 290d 291d 388.1A 414	This study
RdlS	RdlS21	C1b13	16223 16256 16298 16325 16327 73 146 153 249d 263 290d 291d 303.1T 348 379 388 389 397d 416d	This study
RdlS	RdlS23	C1b13	16223 16298 16325 16327 73 249d 258 263 291d 389	This study
RdlS	RdlS34	C1b13	16223 16298 16325 16327 73 125d 176d 180d 196d 209d 212.1G 228 233.1T 236.1G	This study
RdlS	RdlS40	C1b13	16147 16223 16298 16325 16327 16474 73 249d 258 263 290d 291d 345 389	This study
RdlS	RdlS49	C1b13	16223 16293 16298 16325 16327 73 234 249d 258 263 290d 291d	This study
RdlS	RdlS54	C1b13	16223 16234 16298 16325 16327 16381 73 249d 263 290d 291d	This study
RdlS	RdlS59	C1b13	16223 16266 16294 16298 16325 16327 73 171 249d 258 263 290d 291d	This study
RdlS	RdlS65	C1b13	16223 16298 16325 16327 73 249d 258 263 290d 291d	This study
RdlS	RdlS7	C1b13	16223 16298 16325 16327 73 249d 258 263 389d 401d	This study
RdlS	RdlS84	C1b13	16223 16293 16298 16325 16327 73 249d 258 263 290d 291d	This study
RdlS	RdlS93	C1b13	16223 16298 16325 16327 73 235d 249d 258 263 290d 291d 325d	This study
RdlS	RdlS96	C1b13	16223 16298 16325 16327 73 2A9d 258 263 290d 291d	This study
RdlS	RdlS69	C1d	16223 16298 16325 16327 73 194 195 204 249d 263 290d 291d	This study
RdlS	RdlS3	C1d	16051 16223 16298 16325 16327 73 146 152 194 249d 263 478 489 499 523 525	This study
RdlS	RdlS68	D1	16154 16193 16223 16319 16325 16362 16428 73 143 263	This study
RdlS	RdlS45	D1g	16187 16223 16325 16362 73 263	This study
RdlS	RdlS47	D1g	16178 16187 16223 16325 16362 152d 199 263	This study
RdlS	RdlS53	D1g	16093 16178 16187 16223 16325 16356 16362 73 199C 263G 315.1C 374G	This study
RdlS	RdlS41	D1g	16093 16178 16187 16223 16325 16362 73 199 263 324	This study
RdlS	RdlS100	D1g1b	16187 16223 16245 16325 16362 16390 73 148 152 263	This study

RdlS	RdlS101	D1g1b	16187 16223 16245 16325 16362 16390 73 146 152 263	This study
RdlS	RdlS102	D1g1b	16187 16223 16245 16325 16362 16390 73 146 152 224.1T 263 274 342.1C	This study
RdlS	RdlS10	D1g1b	16153 16187 16223 16245 16325 16362 16390 73 146 151 152 263 274	This study
RdlS	RdlS48	D1g1b	16153 16187 16223 16245 16325 16362 16390 73 146 152 263	This study
RdlS	RdlS71	D1g1b	16086 16088 16153 16187 16223 16245 16325 16362 16390 73 146 151 152 263 291d 325d	This study
RdlS	RdlS73	D1g1b	16187 16189 16223 16245 16325 16362 16390 73 146 152 263	This study
RdlS	RdlS86	D1j	16223 16242 16311 16325 16362 73 152 263	This study
sNQN-wRN	MARG13	A2	16111 16129 16223 16290 16319 16362 64 73 146 153 195 235 263 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG42	A2	16111 16223 16290 16319 16356 16362 64 73 146 153 235 263 291.1A 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG87	A2	16111 16223 16290 16319 16356 16362 64 73 146 153 235 263 291.1A 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG148	A2	16112 16223 16290 16319 16356 16362 64 73 146 153 235 263 291.1A 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG33	A2	16111 16192 16223 16227 16290 16319 16362 64 73 146 152 153 235 263 309.1C 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	ALU2	A2	16111 16156 16223 16263 16290 16319 16362 16438 64 73 146 235 263	This study
sNQN-wRN	ALU7	A2	16111 16223 16290 16294 16319 16362 64 73 146 153 235 263 315.1 419d	This study
sNQN-wRN	ALU8	A2	16223 16290 16319 16362 64 73 146 150 153 195 235 263	This study
sNQN-wRN	ALU5	B	16182C 16183C 16189 16194 16204 16208 16211 16217 16218 297 299	This study
sNQN-wRN	MARG03	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG111	B2i	16183C 16189 16217 73 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG96	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG97	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG124	B2i	16183C 16189 16217 16249 73 153 263 470 499 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG147	B2i	16183C 16189 16217 16249 73 153 263470 499 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MARG48	B2i	16183C 16189 16217 16249 16318 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG69	B2i	16183C 16189 16217 16249 16318 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG70	B2i	16183C 16189 16217 16249 16318 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG106	B2i	16183C 16189 16217 16249 16318 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG114	B2i	16183C 16189 16217 16249 16318 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG120	B2i	16183C 16189 16217 16249 16318 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG09	B2i	16182C 16183C 16189 16217 16249 16289 16294 16390 16391 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG36	B2i	16182C 16183C 16189 16217 16249 16289 16294 16390 16391 73 153 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG150	B2i	16183C 16189 16217 16291 73 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MARG159	B2i	16183C 16189 16217 16456 73 207 263 470 499	de Saint Pierre et al., 2012a

sNQN-wRN	MAR G85	B2i	16183C 16189 16217 16465 73 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G80	B2i	16183C 16189 16217 16465 73 189 207 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G46	B2i	16182C 16183C 16189 16207 16217 16278 73 146 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G02	B2i	16183C 16189 16207 16217 16291 73 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G32	B2i	16183C 16189 16207 16217 16291 73 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G119	B2i	16183C 16189 16207 16217 16291 73 263 470 499	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G134	C1b	16182C 16183C 16189 16223 16298 16311 16325 16327 73 249d 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G56	C1b	16223 16239 16298 16325 16327 73 249d 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G98	C1b	16223 16297 16298 16325 16327 73 249d 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G55	C1b	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G149	C1b	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G145	C1b	16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G81	C1b13	16172 16223 16298 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G25	C1b13	16223 16298 16311 16325 16327 73 249d 258 263 290d 291d 489 493 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	ALU4	C1b13	16093 16223 16266 16298 16325 16327 73 249d 258 263 387.1	This study
sNQN-wRN	ALU6	C1b13	16093 16223 16266 16298 16325 16327 73 249d 258 263 290d 291d	This study
sNQN-wRN	MAR G142	C1d	16051 16223 16274 16298 16311 16325 16327 16533 73 146 194 249d 263 290d 291d 489 523d 524d	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G100	D1	16126 16223 16325 16362 10 55 56 64 73 263 279 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G127	D1	16159 16188 16223 16325 16356 16362 73 263 489 513	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G83	D1g1	16187 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G151	D1g1	16187 16223 16325 16362 73 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G137	D1g1	16187 16223 16325 16362 55 73 152 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G113	D1g1	16187 16223 16325 16362 55 73 152 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G152	D1g1	16187 16223 16325 16356 16362 73 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G110	D1g1a	16187 16223 16325 16362 16390 73 146 152 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G44	D1g1a	16187 16223 16325 16362 16390 73 146 152 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G133	D1g1b	16187 16223 16304 16325 16362 73 143 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G90	D1g1b1	16092 16187 16189 16223 16362 73 143 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G39	D1g1e	16187 16189 16209 16223 16325 16362 55 56 64 73 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G99	D1g1e	16187 16189 16209 16223 16325 16362 55 56 73 146 263 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G102	D1g1f	16178 16187 16223 16325 16362 73 150 199 263 374 489	de Saint Pierre et al., 2012a
sNQN-wRN	MAR G71	D1j	16223 16242 16311 16325 16362 73 152 263 489	de Saint Pierre et al., 2012a

Supplementary Table S2. Group Classification of Individuals Analyzed According to the Birthplace of the Mother or Maternal Grandmother to Show the Composition of Subhaplogroups for Each Region

Geographical groups: North Region (Bolivia, North Argentina and Paraguay), Northwest Neuquén (NW-Nqn), Central-South Neuquén (CS-Nqn), Northeast Patagonia (NE Patagonia; Río Negro,Buenos Aires and La Pampa), South Cuyo (Mendoza and San Luis), Eurasia (España and Rusia), Chile (mainly central Chile).

Individual	Localities	Haplotipe	Group of Haplotipes	Geographical Groups	
Lov27	Lov	A2	A2-B2	North Region	Bolivia, North Argenitna and Paraguay
Lov17	Lov	B2i	A2-B2	NW-Nqn	
Lov18	Lov	B2i	A2-B2	NW-Nqn	
Lov3	Lov	B2i	A2-B2	CS-Nqn	
Lov20	Lov	C1b13	C1	NW-Nqn	
Lov2	Lov	C1b13	C1	NW-Nqn	
Lov26	Lov	D	D1-D4h	NW-Nqn	
Lov13	Lov	D1	D1-D4h	NW-Nqn	
Lov24	Lov	D1	D1-D4h	North Region	
Lov1	Lov	D1g	D1-D4h	NE Patagonia	Río Negro, Buenos Aires and La Pampa
Lov21	Lov	D1g	D1-D4h	NW-Nqn	
Lov5	Lov	D1g	D1-D4h	NW-Nqn	
Lov7	Lov	D1g	D1-D4h	NW-Nqn	
Lov11	Lov	D1g1b	D1-D4h	South Cuyo	Mendoza and San Luis
Lov12	Lov	D1g1b	D1-D4h	NW-Nqn	
Lov16	Lov	D1g1b	D1-D4h	NW-Nqn	
Lov19	Lov	D1g1b	D1-D4h	NW-Nqn	
Lov22	Lov	D1g1b	D1-D4h	NW-Nqn	
Lov8	Lov	D1g1b	D1-D4h	NW-Nqn	
Lov9	Lov	D1g1b	D1-D4h	NW-Nqn	
Lov25	Lov	Dah3a5	D1-D4h	NW-Nqn	
Lov15	Lov	H2a2	H-K-T-J	NW-Nqn	
Lov23	Lov	K1a	H-K-T-J	NW-Nqn	
LOV 28	Lov	K2b1a1	H-K-T-J	Eurasia	España and Rusia
LOV 4	Lov	H2a2a	H-K-T-J	NW-Nqn	
LOV 6	Lov	K1b1+16093	H-K-T-J	NW-Nqn	
RdlS24	RdlS	B	A2-B2	South Cuyo	

RdlS98	RdlS	B	A2-B2	South Cuyo	
RdlS81	RdlS	B2i	A2-B2	NE-Nqn	
RdlS52	RdlS	C1	C1	North Region	
RdlS67	RdlS	C1	C1	North Region	
RdlS70	RdlS	C1	C1	NE-Nqn	
RdlS83	RdlS	C1	C1	CS-Nqn	
RdlS18	RdlS	C1	C1	CS-Nqn	
RdlS21	RdlS	C1	C1	South Cuyo	
RdlS42	RdlS	C1b13	C1	NE-Nqn	
RdlS82	RdlS	C1b13	C1	NE-Nqn	
RdlS19	RdlS	C1b13	C1	CS-Nqn	
RdlS103	RdlS	C1b13	C1	CS-Nqn	
RdlS23	RdlS	C1b13	C1	NE-Nqn	
RdlS34	RdlS	C1b13	C1	Chile	Mainly Central Chile
RdlS40	RdlS	C1b13	C1	NE-Nqn	
RdlS49	RdlS	C1b13	C1	NE-Nqn	
RdlS54	RdlS	C1b13	C1	CS-Nqn	
RdlS59	RdlS	C1b13	C1	CS-Nqn	
RdlS65	RdlS	C1b13	C1	NE Patagonia	
RdlS7	RdlS	C1b13	C1	NW-Nqn	
RdlS84	RdlS	C1b13	C1	NE-Nqn	
RdlS93	RdlS	C1b13	C1	NE-Nqn	
RdlS96	RdlS	C1b13	C1	South Cuyo	
RdlS69	RdlS	C1d	C1	NE-Nqn	
RdlS3	RdlS	C1d	C1	NE-Nqn	
RdlS68	RdlS	D1	D1-D4h	North Region	
RdlS45	RdlS	D1g	D1-D4h	Chile	
RdlS47	RdlS	D1g	D1-D4h	NE-Nqn	
RdlS53	RdlS	D1g	D1-D4h	NE-Nqn	
RdlS41	RdlS	D1g	D1-D4h	NE-Nqn	
RdlS100	RdlS	D1g1b	D1-D4h	NW-Nqn	
RdlS101	RdlS	D1g1b	D1-D4h	NE-Nqn	
RdlS102	RdlS	D1g1b	D1-D4h	NE-Nqn	
RdlS10	RdlS	D1g1b	D1-D4h	South Cuyo	
RdlS48	RdlS	D1g1b	D1-D4h	CS-Nqn	
RdlS71	RdlS	D1g1b	D1-D4h	South Cuyo	
RdlS73	RdlS	D1g1b	D1-D4h	NE Patagonia	
RdlS86	RdlS	D1j	D1-D4h	South Cuyo	
RdlS2	RdlS	H2a2	H-K-T-J	South Cuyo	
RdlS4	RdlS	T2	H-K-T-J	NE Patagonia	
RdlS5	RdlS	T2c1+146	H-K-T-J	NE-Nqn	
RdlS12	RdlS	H2a2	H-K-T-J	Chile	
RdlS16	RdlS	H3p	H-K-T-J	NE-Nqn	

RdlS30	RdlS	H2a2a1g	H-K-T-J	CS-Nqn
RdlS35	RdlS	J1b	H-K-T-J	NE-Nqn
RdlS36	RdlS	H2a2a	H-K-T-J	NE-Nqn
RdlS37	RdlS	H2a2a1g	H-K-T-J	South Cuyo
RdlS43	RdlS	H2a2a1g	H-K-T-J	NE-Nqn
RdlS44	RdlS	H2a2a	H-K-T-J	NE-Nqn
RdlS46	RdlS	T2c1+146	H-K-T-J	NE-Nqn
RdlS50	RdlS	H2a2a2	H-K-T-J	Eurasia
RdlS56	RdlS	H3	H-K-T-J	NE-Nqn
RdlS60	RdlS	H2a2b	H-K-T-J	NE-Nqn
RdlS61	RdlS	H3p	H-K-T-J	NE-Nqn
RdlS62	RdlS	K2a	H-K-T-J	Eurasia
RdlS63	RdlS	H2a2a	H-K-T-J	Chile
RdlS94	RdlS	H2a2a	H-K-T-J	NE-Nqn
RdlS1	RdlS	T2	H-K-T-J	NE Patagonia
RdlS11	RdlS	C1	C1	Chile
RdlS13	RdlS	D	D1-D4h	NE-Nqn
RdlS14	RdlS	B	A2-B2	NE-Nqn
RdlS20	RdlS	B	A2-B2	South Cuyo
RdlS31	RdlS	C1	C1	South Cuyo
RdlS33	RdlS	D	D1-D4h	Chile
RdlS39	RdlS	C	C1	NE-Nqn
RdlS51	RdlS	D	D1-D4h	South Cuyo
RdlS55	RdlS	D	D1-D4h	CS-Nqn
RdlS72	RdlS	C	C1	North Region

Supplementary Table S3. Frequencies of Subhaplogroups for Each Group Used for the Extended Principal Components Analyses

Abrev.: Central-South Andes (c-sAndes), Northern Chile (nChile), Northwestern Argentina (NwA), Southern Brasil (sBr), Chanco and Formosa provinces (Ch-F), Buenos Aires province (BsAs), Chubut province (Chu), Southern Chile (sChile).

	Mitochondrial Haplogroups and Sub-haplogroups															
Groups	**A2**	**B2**	**B2i**	**C1**	**C1b**	**C1b13**	**C1c**	**C1d**	**D1**	**D1g**	**D1g1**	**D1j**	**D4h3**	**N**	**Hipervariable Region sequenced**	**References**
c-sAndes	13.14	63.26	1.22	7.06	4.14	0.00	0.00	2.92	7.54	0.49	0.00	0.24	0.00	411	16051-16362 / 73-249; 16024-576; 16056–16383	Gayá-Vidal et al., 2011; Sandoval et al., 2013; Batai et al 2014
nChile	13.43	61.19	0.00	0.00	7.46	1.49	0.00	0.00	10.45	0.00	1.49	2.99	1.49	67	15878-16569 / 001-576	de Saint Pierre et al., 2012
NwA	14.12	54.80	2.82	1.13	16.38	0.00	0.00	0.56	6.78	0.00	0.00	2.26	1.13	177	16024-576	Cardoso et al., 2013
sBr	73.36	1.09	0.00	20.07	0.00	0.00	0.00	0.00	5.47	0.00	0.00	0.00	0.00	274	16051-16362	Marrero et al., 2007
Ch-F	15.69	42.65	0.00	10.29	0.00	0.00	0.00	2.94	26.96	0.00	0.00	1.47	0.00	204	16051-16391	Cabana et al., 2006;
BsAs	28.26	19.57	0.00	0.00	10.87	4.35	4.35	6.52	9.78	4.35	0.00	8.70	3.26	92	16024-576	Bobillo et al., 2010
Chu	0.00	6.90	13.79	0.00	3.45	17.24	0.00	0.00	0.00	0.00	31.03	0.00	27.59	29	15878-16569 / 001-576	de Saint Pierre et al., 2012
sChile	2.94	0.00	0.00	0.00	32.35	8.82	0.00	2.94	8.82	17.65	2.94	0.00	23.53	34	15878-16569 / 001-576	de Saint Pierre et al., 2012

Figure Captions

Figure 1. Geographical location of the six groups studied including the relevant geographical references mentioned in the text. In the map of the southern cone of South America the Patagonia Region is shown in grey and the red square represents the area of study. In red dots are shown the two localities from North of Neuquén. Abrev.: Mendoza (MZ), southern Neuquén-western Río Negro (sNQN-wRN), Bío-Bío (BB), Araucanía-Los Lagos-Los Ríos (A-LL-LR), Las Ovejas (Lov) and Rincón de los Sauces (RdlS).

Figure 2. Mother and grandmother geographical origin of the individuals from Lov and RdlS. The subhaplogroup of each individual is also shown.

Figure 3. Mitochondrial hierarchical networks of haplogroups D1 (A) and C1 (B) constructed by hand. Networks include individuals from Rincon de Los Sauces (RdlS; orange) and Las Ovejas (Lov; yellow). Subhaplogroups framed in red were defined following Phylotree and Bodner et al. (2012)

Figure 4. Phylogenetic networks of subhaplogroups of D1 (A) and the subhaplogroup C1b13 (B). Abrev.: Mendoza (MZ), southern Neuquén-western Río Negro (sNQN-wRN), Bío-Bío (BB), Araucanía-Los Lagos-Los Ríos (A-LL-LR), Las Ovejas (Lov) and Rincón de los Sauces (RdlS).

Figure 5. Geographical location of the six groups studied together with pie charts highlighting the mitochondrial variants, characteristic from Patagonia, shared among them. Abrev.: Mendoza (MZ), southern Neuquén-western Río Negro (sNQN-wRN), Bío-Bío (BB), Araucanía-Los Lagos-Los Ríos (A-LL-LR), Las Ovejas (Lov) and Rincón de los Sauces (RdlS).

Figure 6. Principal components calculated on the frequencies of subhaplogroups. The size of the circles is proportional to the size of each group. The color of the circles indicates: Red: North of

Neuquén; Light blue: the rest of Argentina; Grey: Center of Chile. Dotted lines show the connections in a neighbor-joining tree calculated on the FSTs indices; significant FSTs are in red lines. Abrev.: Mendoza (MZ), southern Neuquén-western Río Negro (sNQN-wRN), Bío-Bío (BB), Araucanía-Los Lagos-Los Ríos (A-LL-LR), Las Ovejas (Lov) and Rincón de los Sauces (RdlS).

Figure 7. Principal components calculated on the frequencies of subhaplogroups for the Southern Cone of South America. The size of the circles is proportional to the size of each group. The color of the circles indicates: Red: North of Neuquén; Variants of blue: Center of Argentina; Grey: Center of Chile; Black: South Chile; Variants of brown: South Brazil, northern Argentina and Centeral-South Andes. Abrev.: Mendoza (MZ), southern Neuquén-western Río Negro (sNQN-wRN), Bío-Bío (BB), Araucanía-Los Lagos-Los Ríos (A-LL-LR), Las Ovejas (Lov), Rincón de los Sauces (RdlS), Chubut (Chu), Islands from South Chile (sChile), Buenos Aires (BsAs), South Brazil (sBr), Chaco and Formosa (Ch-F), Northwest Argentina (NwA), North Chile (nChile) and Centeral-South Andes (c-sAndes).

Figure 1.

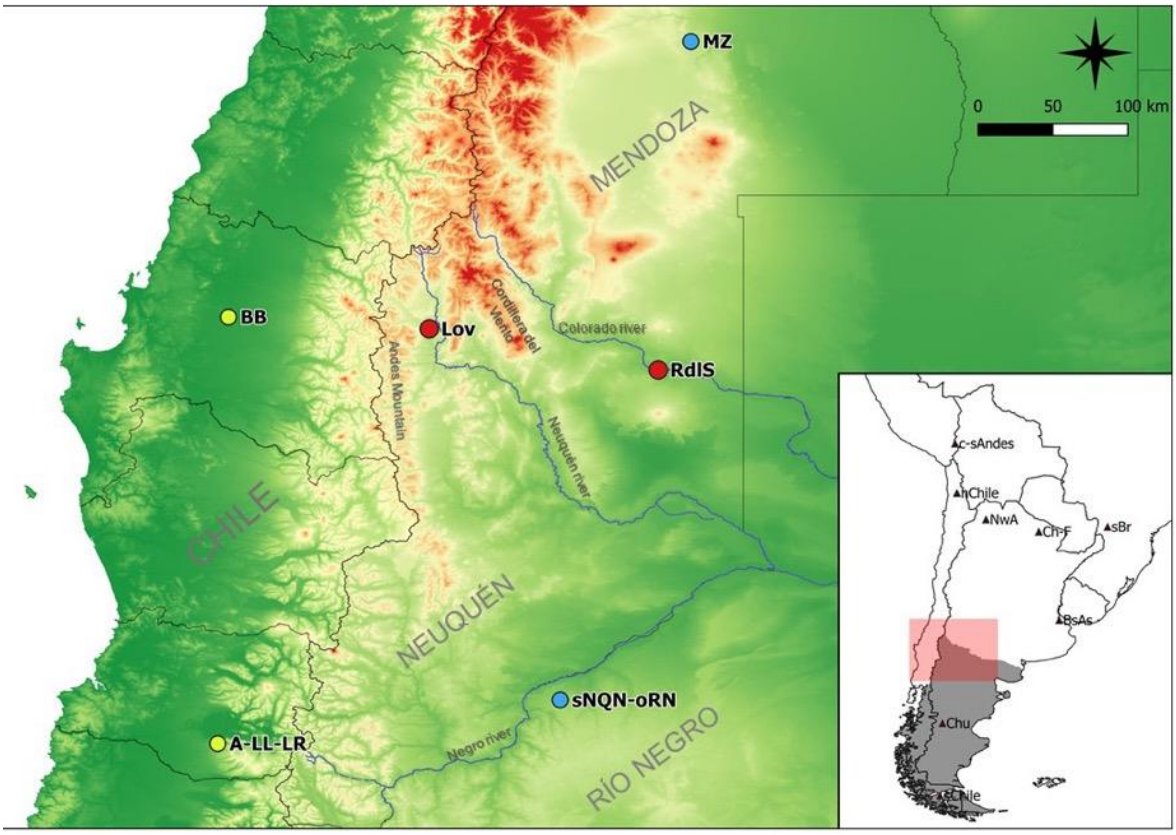

MZ
MENDOZA
0
50
100 km
BB
Lov
Cordillera del Viento
Colorado river
RdlS
Andes Mountain
Neuquén river
CHILE
NEUQUÉN
sNQN-oRN
A-LL-LR
Negro river
RÍO NEGRO
c-sAndes
nChile
NWA
Ch-F
sBr
BsAs
Chu
Chile

Figure 2.

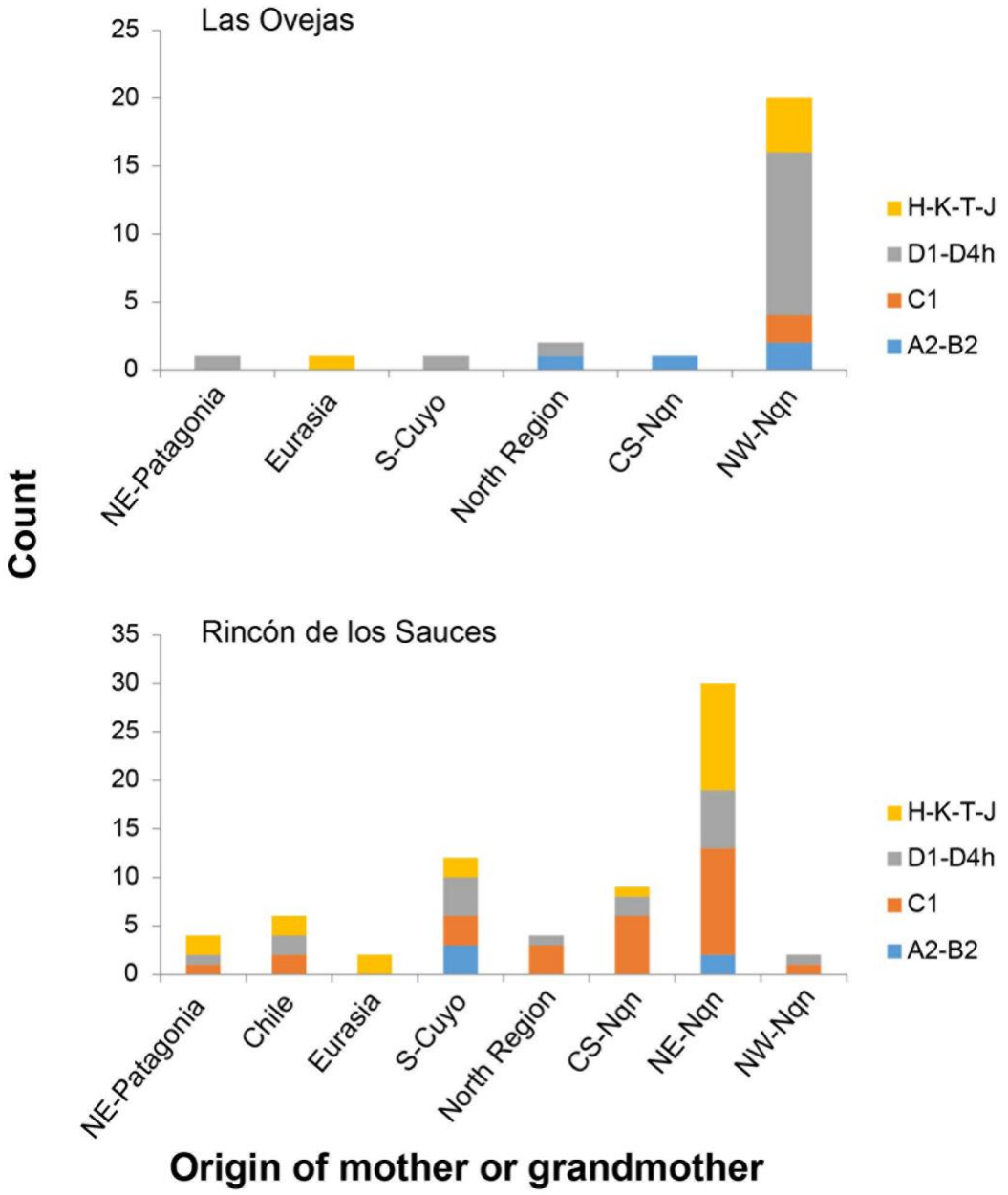
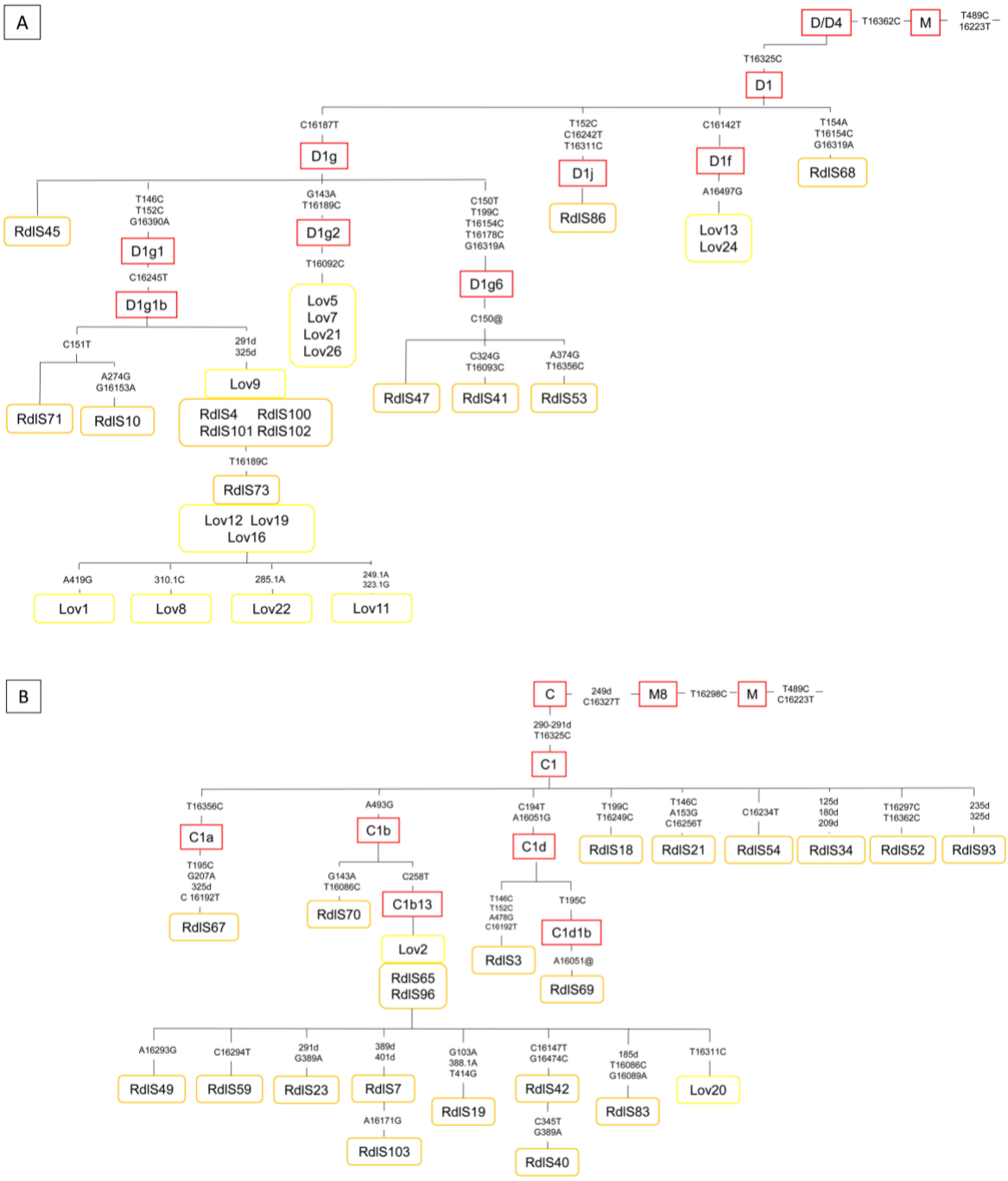


Figure 3.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D/D4
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M
T489C
16223T
T16325C
D1
C16187T
D1g
T152C
C16242T
T16311C
D1j
C16142T
D1f
T154A
T16154C
G16319A
RdlS68
A16497G
Lov13
Lov24
RdlS86
RdlS45
T146C
T152C
G16390A
D1g1
G143A
T16189C
D1g2
C150T
T199C
T16154C
T16178C
G16319A
D1g6
C16245T
D1g1b
T16092C
Lov5
Lov7
Lov21
Lov26
C150@
C151T
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RdlS41
RdlS53
RdlS71
RdlS10
RdlS4 RdlS100
RdlS101 RdlS102
T16189C
RdlS73
Lov12 Lov19
Lov16
A419G
310.1C
285.1A
249.1A
323.1G
Lov1
Lov8
Lov22
Lov11
B
C
249d
C16327T
M8
T16298C
M
T489C
C16223T
290-291d
T16325C
C1
T16356C
A493G
C194T
A16051G
T199C
T16249C
T146C
A153G
C16256T
C16234T
125d
180d
209d
T16297C
T16362C
235d
325d
C1a
C1b
C1d
RdlS18
RdlS21
RdlS54
RdlS34
RdlS52
RdlS93
T195C
G207A
325d
C 16192T
G143A
T16086C
C258T
T146C
T152C
A478G
C16192T
T195C
RdlS67
RdlS70
C1b13
RdlS3
C1d1b
A16051@
Lov2
RdlS69
RdlS65
RdlS96
A16293G
C16294T
291d
G389A
389d
401d
G103A
388.1A
T414G
C16147T
G16474C
185d
T16086C
G16089A
T16311C
RdlS49
RdlS59
RdlS23
RdlS7
RdlS19
RdlS42
RdlS83
Lov20
A16171G
C345T
G389A
RdlS103
RdlS40

Figure 4.

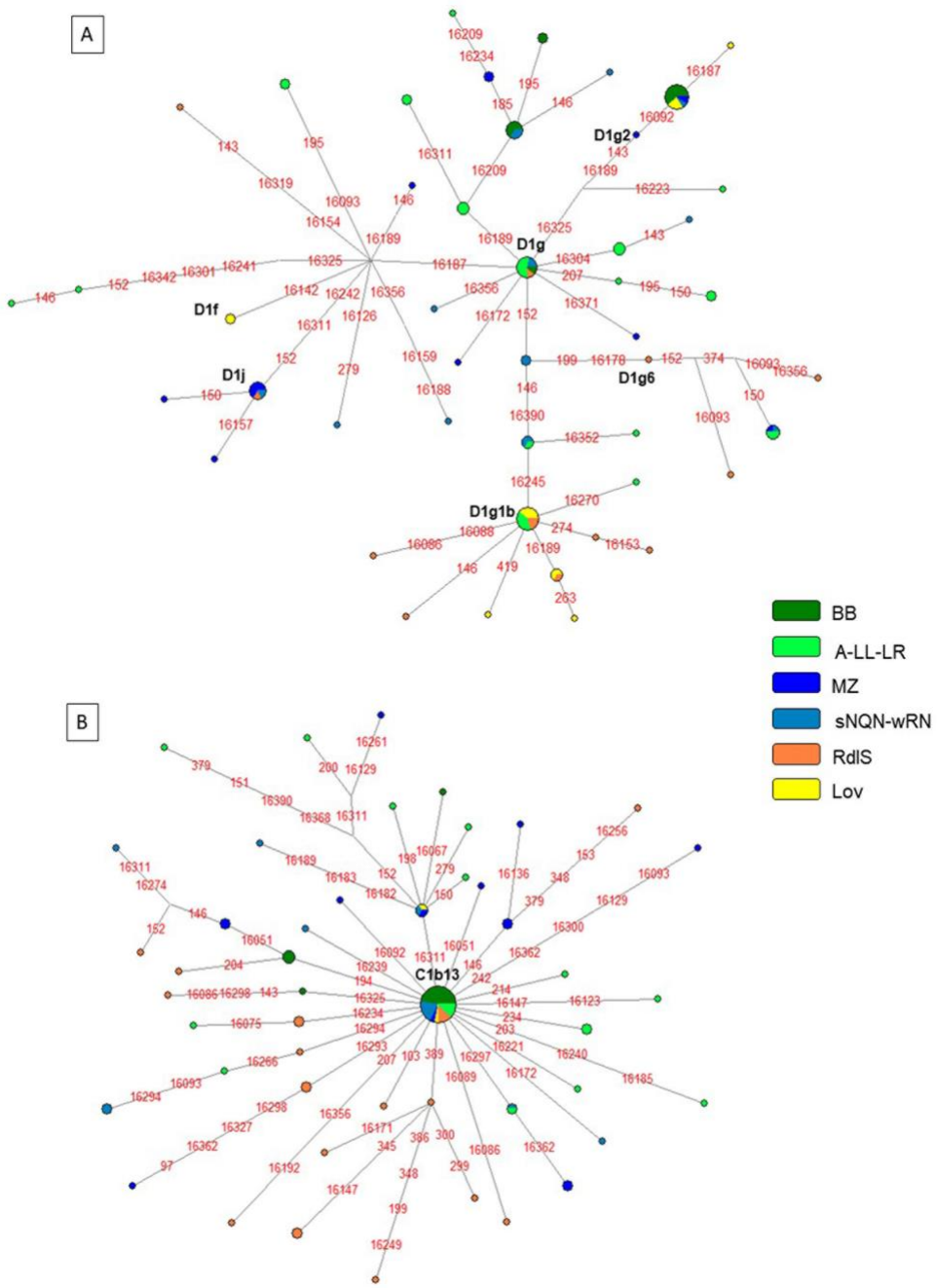
A
D1g2
D1g
D1f
D1j
D1g6
D1g1b
B
C1b13
BB
A-LL-LR
MZ
sNQN-wRN
RdlS
Lov

Figure 5.

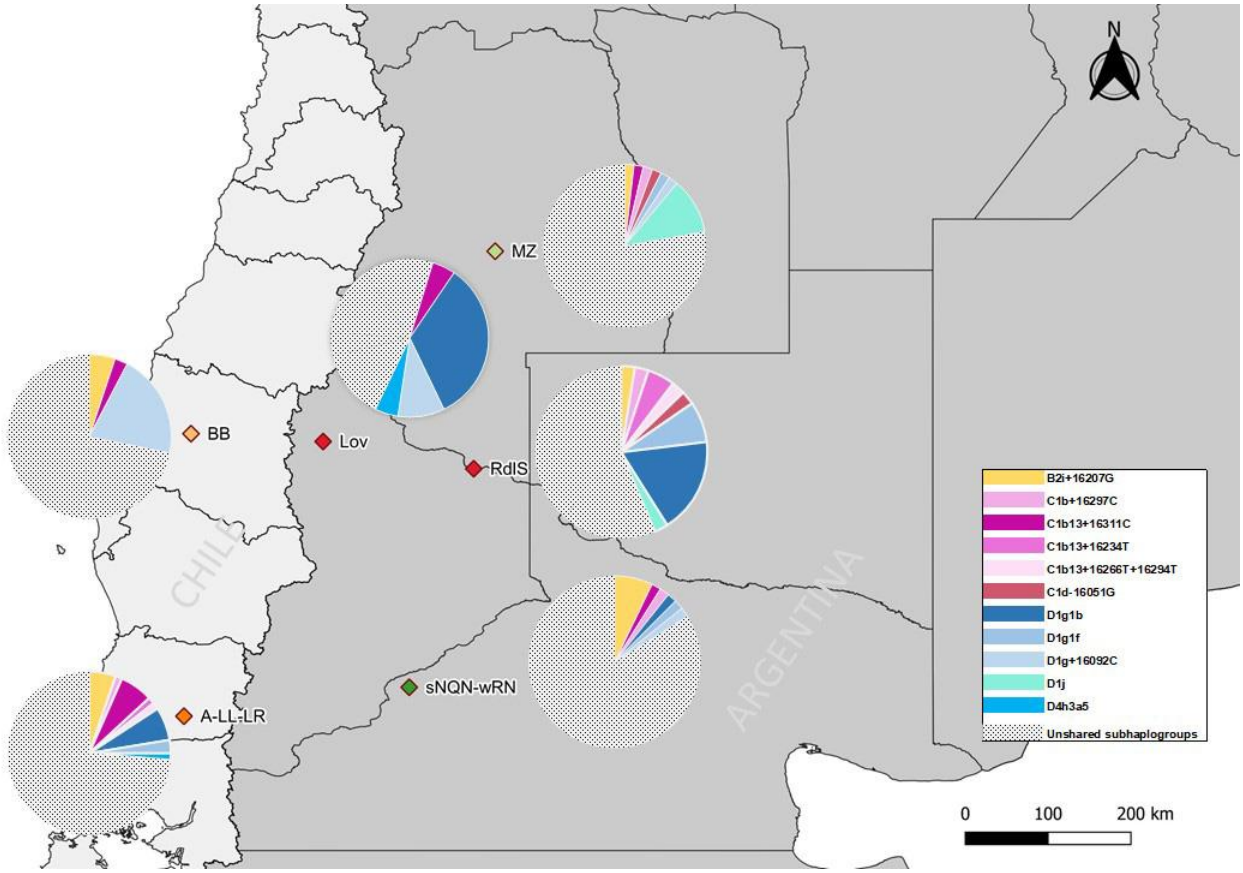

Figure 6.

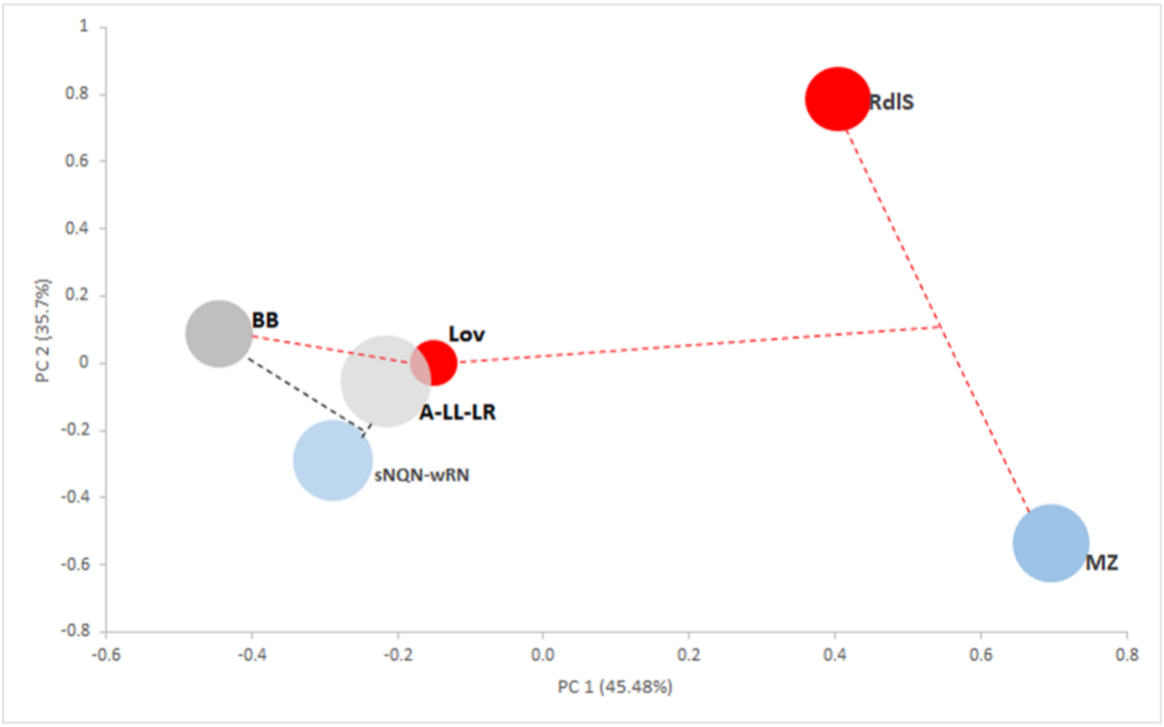

Figure 7.