Y-chromosome haplotypes and clan structure of the Sherpa of the Solukhumbu (Nepal): preliminary ethnogenetic considerations

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Abstract The present-day Sherpa are thought to descend from a small number of ancestors that settled in Nepal several centuries ago, coming from the Eastern Tibetan region of Kham. A generally accepted ethnographic theory involves the out-of-Kham migration of four proto-clans between the 15th and 16th centuries. Traditional Sherpa society is still divided into clans, called ru, which are patrilinearly transmitted. Ru therefore roughly correspond to the surnames of Western societies: males of the same ru are expected to share identical Y-chromosome haplotypes. However, multiple origins of ru and/or frequent gene flow of male lineages from neighbouring populations can complicate the genealogical structure. In the present work, 25 male Sherpas of the Solukhumbu district were typed for the 17 Y-chromosomal short tandem repeats included in the AmpF/STR® Yfiler™ kit. Seventeen different haplotypes were found; 12 were unique. A phylogenetic tree was then drawn from the pairwise mutational distance matrix with a neighbour-joining algorithm. Branching reliability was also assessed through bootstrap analysis. Two macro-clusters of haplotypes were found, ascribable on the whole to two out of four of the presumed Tibetan proto-ru, the Thimm and the Minyagpa. However, the Minyagpa macro-cluster was found to be bipartite in terms of haplogroups, being composed by two distinct haplotype clusters. Clustering of the contributors by birthplace was also performed, suggesting a differential ru spatial distribution between upper Khumbu and lower Solu. Khumbu seems predominantly populated by newer clans and putative descendants of the Thimm proto-ru, whereas Solu is mostly inhabited by members of the Minyagpa proto-ru.

Key words: Sherpa, clan structure, Solukhumbu, Y-STRs, AmpF/STR Yfiler

Introduction

The Sherpa are a Tibeto-Burman ethnic group from the Nepalese Himalayas, best known for their exceptional mountaineering skills as porters and guides. From the genetic point of view, Sherpa constitute a population isolate. Likely causes of isolation (Arcos-Burgos and Muenke, 2002) are ethnic, cultural, linguistic, religious, and geographical confinement. Sherpa DNA has been studied in detail in order to investigate the potential association between genes and adaptation to high altitude (Malacrida et al., 2007; Dromo et al., 2008). Sherpa villages and communities are scattered over an extremely wide area, ranging from the Helambu region, 72 km north-east of Kathmandu, to the Darjeeling district, in West Bengal. The core of the Sherpa’s earliest settlement area lies in the neighbouring regions of Solu and Khumbu (Von Fürer-Haimendorf, 1964), located in the north-eastern Nepalese administrative districts of Solukhumbu and Okhaldhunga (Figure 1).

Traditional Sherpa society is divided into patrilineal clans, although the number of clans is debated: it ranges from 12 to 24 (Table 1), depending on the author (Von Fürer-Haimendorf, 1964; Oppitz, 1968; Krämer and Sherpa, 2002; Wangmo, 2005). The Sherpa word for clan is ru, which means ‘bones,’ since Sherpas actually believe that bones pass from father to son, thus establishing the natural propensities of a man. This pseudo-genetic paternal inheritance was considered superior to that of the mother, whose contribution is only transmitting the flesh, or sха (Wangmo, 2005). Ru are neither castes nor social classes, but rather wide familial clans with common roots in a certain village or in a common, and often legendary, ancestor (Fantin, 1973; Childs, 1997). After all, as in every human society, the addition of a heritable element facilitates identification and also marks lineages, providing a label of membership (King and Jobling, 2009). Sherpa can overall be considered as an endogamic ethnic group, yet exogamy between ru is compulsory: marrying within the same ru is forbidden and considered incestuous (Presciutti et al., 2010).
Sherpa tradition tells that all of the present Sherpa ru descend from some ancient Tibetan clans that came to Nepal from Eastern Tibet about 500 years ago. Many alternative stories about the very first arrival of the Sherpa to the Nepalese valleys exist, and most of these should probably be regarded as mere legends (Brower, 1991). There is not even agreement about the route of migration from Tibet to Solukhumbu, nor the exact Nepal entrance point (Von Fürer-Haimendorf, 1964).

Nevertheless, most Sherpa tales trace back the coming of their ancestors from the Salmo Gang (Zal mo sgang) area of Kham, in Eastern Tibet, during the 15th–16th centuries (Brower, 1991). The Salmo Gang area is presently part of the modern Ganzi Tibetan Autonomous Prefecture of the Chinese Sichuan Province. Significantly, the word sherpa itself is composed of two Tibetan words (shar, east and pa, person), together meaning 'Easterners,' and could thus be reflecting this migration (Stevens, 1993). The pioneering work of Oppitz (1968), derived from the analysis of a few written clan ancestry records retrieved in Solu, provides firmer historical evidence for the Kham homeland hypothesis, yet still has to face the dubious historical authenticity of the documents (Wangmo, 2005). On the whole, authors usually agree the broad terms of Oppitz’s reconstruction (Von Führer-Haimendorf, 1964; Brower, 1991; Krämer and Sherpa, 2002; Wangmo, 2005) that have already dealt with this issue (Table 1). An exact genealogy of modern ru cannot be traced for certain, since written sources are scarce and incomplete and oral tradition sometimes reports contrasting theories. Unfortunately, the degree of complexity has been increased over the years by the later arrival of other groups of Tibetan immigrants, particularly from the bordering Tingri area, after the first migration. The members of these more recent groups are also organized in patrilinear ru and are now considered as pure Khumbu Sherpa, even if none of them came from Kham nor had any kind of written tradition concerning its genealogy (Sherpa, 2007).

The four proto-ru were the Lama-serwa (or simply Lama), the Chakpa (or Chiawa), the Minyagpa, and the Thimmi. Probably, each proto-ru gave birth to several sub-clans through time, in accordance with the Sherpa assertion of their Tibetan ancestry. Indeed, Sherpa regard some of the present ru as brother-clans: this is probably due to their common descent from the same proto-ru. The supposed genealogy of present Sherpa ru and their relationship with the four proto-clans can be summarized based on a comparison of the works of the four main works (Von Führer-Haimendorf, 1964; Oppitz, 1968; Krämer and Sherpa, 2002; Wangmo, 2005) that have already dealt with this issue (Table 1). An exact genealogy of modern ru cannot be traced for certain, since written sources are scarce and incomplete and oral tradition sometimes reports contrasting theories. Unfortunately, the degree of complexity has been increased over the years by the later arrival of other groups of Tibetan immigrants, particularly from the bordering Tingri area, after the first migration. The members of these more recent groups are also organized in patrilinear ru and are now considered as pure Khumbu Sherpa, even if none of them came from Kham nor had any kind of written tradition concerning its genealogy (Sherpa, 2007).

Except for its two pseudoautosomal regions found at the telomeric ends, the Y chromosome is exclusively inherited from father to son as an entire haplotype of physically linked loci. The portion of the chromosome which does not undergo homologous recombination is called the non-
recombining region of the Y (NRY) and comprises male-specific genes only, known as holandric genes. The recent characterization of many new Y-chromosome markers has contributed to increasing their usefullness for studies of genetic anthropology, which, until recently, lagged far behind mitochondrial DNA and maternal lineage studies (Crawford, 2007). DNA polymorphisms of the NRY have already proved to be a useful tool for tracing ancient patrilinear lineages (Jobling and Tyler-Smith, 2003; Kwak et al., 2005; King and Jobling, 2009): all patrilinear relatives share the same NRY haplotype and thus inheritance, with absence of recombination, leads to the perpetration of polymorphisms through a simple paternal transmission pathway (Ljubković et al., 2008). The most widely used kind of NRY polymorphisms for phylogeny of recently diverged paternal lineages are the short tandem repeats (STRs). Y-STRs are highly polymorphic markers and thanks to a high level of variability due to variation in repeat number they can reveal further variation within haplogroups (Kwak et al., 2005). Isonymous individuals are expected to carry the same Y haplotype: observed incongruity can be ascribed to new mutational events, adoptions, illegitimacy, or polyphyletic origin of the surname.

In this work, the 17 AmpF/STR Yfiler polymorphic loci (Mulero et al., 2006) were amplified in a sample of 25 male Solukhumbu Sherpa. Haplogroups were also predicted and the emerging genetic tree was compared with ethnogenealogical hypotheses.

In other words, the present research is aimed at a preliminary definition of the true kinship and clan structure of the Sherpa population. The approach followed is that of establishing any existing correspondence between the Y-STR haplotypes and traditional patrilineal Sherpa clans.

### Materials and Methods

**Samples**

Buccal swab samples were collected from 25 male volunteers with Whatman® OmniSwabs. Each ejectable head was put in a 1.5 ml sterile extraction tube. The sampling procedure was approved by the Social and Ethics Committee of the Department of Environmental Medicine and Public Health (EMPH), Padua University.

16 samples were collected in spring 2008, during a meeting of the Sherpa community held in Namche Bazaar, the main village of Khumbu Valley, and 9 samples were collect-
ed in spring 2009 in the villages of Namche, Kunde, and Khumjung. All individuals freely donated their saliva, after signing an informed consent form that explained the purpose of DNA analysis in the present research. The volunteers were questioned about their ru affiliation, age, birthplace, and dwelling place. All of the contributors reported as being unrelated to one another and those sharing the same ru were actually unaware of any kind of biological relationship between them.

Samples were packaged and transported to Padua (Italy) within 7 days and processed in the Forensic Genetics Laboratory of the Department of Environmental Medicine and Public Health (Legal Medicine Unit), Padua University. The laboratory achieved quality control certification by the Y chromosome Haplotype Reference Database (YHRD) on 23 November 2000 (YHRD c.n. YC000052).

DNA extraction

DNA extraction from buccal swabs was performed using the QIAGEN QIAmp® DNA Microkit according to the manufacturer’s instructions (Qiagen, 2010). About 30–50 µg of DNA were recovered in 30 µl of final solution.

Multiplex PCR

Multiplex polymerase chain reaction (PCR) was performed on 0.5–1.0 ng of target DNA for each sample using the AmpF/STR® Yfiler™ PCR Amplification Kit, in accordance with the protocols described in its User’s Manual (Applied Biosystems, 2006). The AmpF/STR® Yfiler™ Kit amplifies 17 Y-STR loci: they consist of the 9-marker Eurothe 11-marker Scientific Working Group DNA Analysis Methods (SWGDAM) recommended Y-STR panel (minHt plus DYS438 and DYS439) and the additional highly polymorphic loci DYS437, DYS448, DYS456, DYS458, DYS635, and Y-GATA-H1. Allele nomenclature follows ISFG recommendations (Gusmao et al., 2006). The locus DYS385 was excluded from further analysis, as its two twin loci show indistinguishable alleles.

PCR reaction was performed in a GeneAmp® PCR System 9700 following the manufacturer’s instructions (Applied Biosystems, 2010) except for minimal modifications of the final reaction volume, which was 12.5 µl (9.5 µl of master mix + 3.0 µl of DNA solution) instead of 25.0 µl. In addition, six supplementary amplification cycles were performed for some samples. PCR thermocycling parameters were the following: initial hot-start incubation step at 95°C for 11 min, 30 amplification cycles (denaturing at 94°C for 1 min, annealing at 61°C for 1 min, and extension at 72°C for 1 min) and final extension at 60°C for 80 min.

Electrophoresis

Amplified STRs were separated by capillary electrophoresis using an ABI Prism® 3130 Genetic Analyzer (Applied Biosystems). GeneScan-500 Internal Lane Size Standard LIZ-500 was the internal standard of choice. The size of the PCR products was classified with GeneMapper v.2 software, with the Yfiler Allelic Ladder (Applied Biosystems) as comparison.

Data analysis

The genetic distance for each pair of haplotypes was calculated as the sum, over all loci, of the absolute difference in the number of STRs. Genetic distances were then reported in a pairwise distance matrix. Further data analysis was performed with Arlequin v. 3.5.1.2 software (Excoffier and Lischer, 2010). Allelic frequencies, allelic ranges, haplotype diversity (Nei, 1987), and gene diversity per locus (h) were also calculated. A phylogenetic tree was extrapolated from the pairwise distance matrix, with a neighbour-joining (NJ) algorithm. Statistical reliability of branching nodes was assessed through bootstrap (Felsenstein, 1985), performing 100 repetitions. The tree was finally drawn with the TreeGen tool (CBRG, 2012). Multi-copy marker DYS385 was excluded from the phylogenetic analysis, as its two loci, DYS385a and DYS385b, were indistinguishable from each other and thus the result from these was not informative.

After haplotype typology, haplogroup was predicted for each sample with the free Haplogroup Predictor tool v. 21 (Athey, 2007). The software identifies the most probable haplogroup, assigning a prediction confidence score expressed as a percentage. Haplogroups obtaining the highest score were chosen and will subsequently be reported.

Results and Discussion

First, statistics of general genetic interest for the Sherpa population were calculated. 17 different haplotypes were found out of 25 samples: 5 of these were shared and 12 were unique. The allelic profiles of the haplotypes are listed in full in Table 2: neither null alleles nor duplicated loci were found. DYS448 showed the 20.2 microvariant in samples M1 and M12. Allelic ranges and frequencies, along with gene diversity, are also schematically reported (Table 3).

Prediction of haplogroups identified three main groups (Table 2): 9 individuals belong to haplogroup Q (M10, M11, M16, M17, M18, M20, M21, M24, M29), 6 to haplogroup Elb, subclade Elb1 (M4, M6, M13, M23, M26, M27), 9 to haplogroup R1 (M1, M3, M12, M14, M15, M19, M25 are R1a; M8, M28 are R1b; M19 had an equal score between R1a and R1b). Individual M22 alone belongs to haplogroup H. Probability scores for each predicted haplogroup are reported in Table 2 as well. Overall haplotype diversity for the Sherpa population assumes a value of 0.9633 ± 0.0208. Haplotype diversities previously reported for a mixed Nepalese and two Tibetan population samples are respectively 0.9970 (Parkin et al., 2007), 0.999 (Tian-Xiao et al., 2009) and 0.9981 (Gayden et al., 2010). Since haplotype diversity of Sherpas is not so different from neighbouring populations, it can be supposed that their ancestors had substantial diversity in their male lineages.

The NJ tree (Figure 2) represents the presumable kinship of the 25 typed Sherpa. In addition, the tree reports the stated ru kinship of each contributor, the proto-ru and the predicted haplogroup. Unfortunately, contributors M1 and M8 simply asserted themselves to be ‘Sherpa’ and of ‘Tibetan origin’, respectively. The topology of the phylogenetic tree clearly presents two main macro-clusters of haplotypes, branched with a bootstrap value of 100 (Figure 2). The first macro-cluster results further partitioned into two minor haplotype
Table 2. The 17 amplified haplotypes and their extended profiles

<table>
<thead>
<tr>
<th>Sample id</th>
<th>M1</th>
<th>M3</th>
<th>M4</th>
<th>M6</th>
<th>M8</th>
<th>M10</th>
<th>M11</th>
<th>M13</th>
<th>M14</th>
<th>M16</th>
<th>M17</th>
<th>M19</th>
<th>M21</th>
<th>M22</th>
<th>M27</th>
<th>M28</th>
<th>M29</th>
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<tbody>
<tr>
<td>Absolute frequency</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
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<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Relative frequency</td>
<td>0.08</td>
<td>0.04</td>
<td>0.12</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
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<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
</tr>
</tbody>
</table>

DYS19  | 15 | 15 | 14 | 14 | 15 | 14 | 14 | 14 | 15 | 14 | 16 | 14 | 16 | 14 | 15 | 14 |
DYS389-I | 13 | 13 | 10 | 10 | 14 | 12 | 12 | 10 | 13 | 12 | 12 | 14 | 12 | 12 | 10 | 13 |
DYS389-II | 29 | 29 | 27 | 27 | 30 | 28 | 28 | 27 | 29 | 28 | 28 | 30 | 30 | 29 | 28 | 28 |
DYS391 | 10 | 11 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 | 10 |
DYS392 | 11 | 7  | 11 | 11 | 7  | 14 | 14 | 11 | 7  | 14 | 14 | 7  | 14 | 10 | 11 | 7  |
DYS393 | 13 | 13 | 14 | 14 | 13 | 13 | 12 | 14 | 13 | 13 | 12 | 13 | 12 | 14 | 13 | 13 |
DYS397 | 14 | 14 | 14 | 14 | 14 | 15 | 14 | 14 | 16 | 14 | 14 | 15 | 14 | 14 | 14 | 15 |
DYS399 | 12 | 12 | 11 | 12 | 12 | 13 | 12 | 12 | 12 | 12 | 12 | 12 | 11 | 11 | 11 | 12 |
DYS448 | 20.2 | 19 | 19 | 19 | 18 | 21 | 20 | 19 | 19 | 21 | 20 | 18 | 21 | 18 | 19 | 19 |
DYS456 | 16 | 16 | 14 | 14 | 17 | 15 | 15 | 13 | 16 | 15 | 16 | 15 | 16 | 15 | 14 | 16 |
DYS458 | 16 | 16 | 15 | 15 | 17 | 17 | 18 | 15 | 16 | 17 | 18 | 17 | 17 | 15 | 15 | 16 |
DYS635 | 21 | 21 | 21 | 21 | 21 | 21 | 20 | 20 | 21 | 21 | 20 | 20 | 20 | 20 | 20 | 20 |

Haplogroup | R1a | R1a | E1b1 | E1b1 | R1b | Q | Q | E1b1 | R1a | Q | Q | Q | R1a/R1b | Q | H | E1b1 | R1b | Q |
Prediction % score | 42.0 | 98.9 | 84.8 | 96.7 | 90.3 | 94.8 | 95.9 | 99.3 | 98.4 | 94.0 | 52.8 | 32.0/30.0 | 99.2 | 99.3 | 98.0 | 91.1 | 92.7 |

Table 3. Allelic frequencies, allelic range, gene diversity per locus and G-W index at the 17 Y-STR loci

<table>
<thead>
<tr>
<th>DYS</th>
<th>19</th>
<th>389-I</th>
<th>389-II</th>
<th>390</th>
<th>391</th>
<th>392</th>
<th>393</th>
<th>437</th>
<th>438</th>
<th>439</th>
<th>448</th>
<th>456</th>
<th>458</th>
<th>635</th>
<th>GATAH4.1</th>
<th>385</th>
<th>Mean</th>
</tr>
</thead>
<tbody>
<tr>
<td>No. of alleles</td>
<td>3</td>
<td>4</td>
<td>4</td>
<td>3</td>
<td>2</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>2</td>
<td>3</td>
<td>4</td>
<td>5</td>
<td>4</td>
<td>2</td>
<td>2</td>
<td>8</td>
<td>3.5</td>
</tr>
<tr>
<td>Allelic range</td>
<td>2</td>
<td>4</td>
<td>3</td>
<td>4</td>
<td>1</td>
<td>7</td>
<td>2</td>
<td>2</td>
<td>1</td>
<td>2</td>
<td>3</td>
<td>4</td>
<td>3</td>
<td>1</td>
<td>1</td>
<td>8</td>
<td>3.1</td>
</tr>
<tr>
<td>Gene diversity h</td>
<td>0.553</td>
<td>0.727</td>
<td>0.750</td>
<td>0.347</td>
<td>0.153</td>
<td>0.717</td>
<td>0.640</td>
<td>0.410</td>
<td>0.420</td>
<td>0.397</td>
<td>0.717</td>
<td>0.723</td>
<td>0.777</td>
<td>0.453</td>
<td>0.453</td>
<td>0.853</td>
<td>0.568</td>
</tr>
</tbody>
</table>

Haplogroup R1a R1a E1b1 E1b1 R1b Q Q E1b1 R1a Q Q R1a/R1b Q H E1b1 R1b Q
Prediction % score 42.0 98.9 84.8 96.7 90.3 94.8 95.9 99.3 98.4 94.0 52.8 32.0/30.0 99.2 99.3 98.0 91.1 92.7

No. of alleles 3 4 4 3 2 4 3 3 2 3 4 5 4 2 2 8 3.5
Allelic range 2 4 3 4 1 7 2 2 1 2 3 4 3 1 1 8 3.1
Gene diversity h 0.553 0.727 0.750 0.347 0.153 0.717 0.640 0.410 0.420 0.397 0.717 0.723 0.777 0.453 0.453 0.853 0.568
clusters, named Cluster I and II, that are mostly composed by individuals affiliated to ru all descending from the Minyagpa proto-clan (Thaktok, 5 individuals; Pinasa, 2 individuals; Gardza, 2 individuals; Gole, 2 individuals; Chuserwa, 1 individual). The Minyagpa proto-clan could therefore have comprised ancestors with two different Y-chromosome lineages, consistently with the two different haplogroups predicted, Q and R1, that respectively characterize Cluster I and Cluster II. Moreover, the Thaktok ru, being common to both Clusters I and II, is indeed still heterogeneous in terms of Y haplotypes and haplogroups. A similar polyphyletic origin for the Minyagpa clan is thus quite plausible. On the other hand, individual M29 falls as outsiders in Cluster I, since he belongs to the Chakpa lineage and not to the Minyagpa one. Similarly, the Tibetan contributor M8 and the Lama ru member M19, are part of Cluster II but they do not belong to the Minyagpa proto-ru. In fact, Lama and Chakpa ru were expected to form two distinct clusters, since they are numbered among the four original Tibetan proto-ru and are described as unsplit clans. Moreover, M25, a Goparma from the Thimmi proto-clan, unexpectedly figures in Cluster II. In order to explain these discrepancies, illegitimacies, adoptions, and personal data uncertainty should be considered.

The second macro-cluster, named Cluster III, comprises members of the Salaka (2 individuals) and Paldorje (1 individual) ru: both clans belong to the Thimmi proto-ru group (Table 1). Cluster III also comprises 3 individuals belonging to the Chuserwa and Tsangup ru, that Oppitz (1968) and Wangmo (2005) regard as recent clans and unrelated to the four Kham proto-ru. Nevertheless, the genetic evidence could be revealing an unreported kinship of these two ru with the Thimmi proto-ru. Moreover, Cluster III is mainly composed by haplotypes belonging to the E1b1 haplogroup. Cluster III could be then regarded as the putative Thimmi proto-ru tree cluster. In addition, assuming the authenticity of the reconstructed genealogies (Oppitz, 1968), several marriages between members of the Minyagpa, Chakpa, and Thimmi clans seem to have taken place during the 15th century (Figure 3). As discussed above, kinship incongruities observed in some NJ tree branches might thus be linked to events of haplotype interchange that occurred among the families of the Sherpa ancestors.

In fact, there is only one clustering outlier represented by M22, a Pinasa Sherpa, thus coming from proto-ru Minyagpa, with the unique property of belonging to the H haplogroup.

Samples were further grouped by considering the birthplaces of contributors. Home villages were located on a map (Figure 1) and assigned either to the Khumbu Valley (North cluster) or to the Solu and Okhaldunga area (South cluster) (Table 4). This kind of approach was undertaken as a preliminary evaluation of two contrasting hypothesis, the
‘Khumbu first’ and the ‘Solu first’ theories, that describe the history of Sherpa settlement in the Solukhumbu area. Briefly, authors supporting the ‘Khumbu first’ theory agree that Sherpa entered Nepal from a high mountain pass, notably the Nangpa La, and immediately settled Khumbu. In particular, they state that the Thimmi proto-clan originally settled in the Bhote Kosi valley, in Western Khumbu (Oppitz, 1968; Krämer and Sherpa, 2002), while Minyagpa families at first settled in the Phortse village area, also in Khumbu, but later on moved to the Solu lowlands (Oppitz, 1968; Krämer and Sherpa, 2002). Moreover, Lama and Chakpa people supposedly went straight to Solu and directly settled there (Krämer and Sherpa, 2002).

On the other hand, the ‘Solu first’ theory suggests that the settlement of the Sherpa in Nepal did not even begin in Khumbu. In fact, the higher Khumbu valley was probably settled only after Solu, since at the time of their arrival prolonged periods of frost still sequestered its cultivable lands. Frost periods faded only with the ending of Little Ice Age, due to major climate changes (Muehlisch, 1998). Moreover, in Khumbu only “mixed” Sherpa settlements are found, whereas in Solu true Sherpa-clan territories and villages can be identified, even nowadays (Muehlisch, 1996). This fact again strongly supports that the first Sherpa settlement area was indeed Solu.

Indirectly, the statement of Krämer and Sherpa (2002) about Lama and Chakpa families heading straight to Solu supports the ‘Solu first’ hypothesis as well. Genealogies provided by Oppitz (1968) too suggest that upper Khumbu was more recently and primarily settled by newcomers coming from the bordering Tingri region. Newcomers were then accepted and integrated by Sherpa already resident in their society (Muehlisch, 1998).

Interpretation of genetic evidence and ru spatial distribution seems favourable to elements of both theories: it suggests that all but two (71.4%) of the Thimmi cluster members, which also comprises most of the new ru, were born in upper Khumbu and eight out of nine (88.9%) members of the major Minyagpa cluster were born in the Southern Solu and Okhaldhunga areas (Table 4). An ancient proto-clan settlement area could thus be roughly identified both for the Thimmi (Khumbu Valley) and for at least one family branch of the Minyagpa (Solu).

In summary, three main clusters of haplotypes were found, ascribable on the whole to two of the presumed proto-clans, the Thimmi and the Minyagpa Tibetan ru. Chakpa and Lama appeared as sub-clans of the Minyagpa rather than self-standing families. Ethnogenetic findings about the clan structure of the Sherpa, do not in fact contradict the reported theories and also confirm an interesting association between Y-haplotypes and social kinship. The oral Sherpa tradition indeed gave birth to a family identification system similar to the one adopted by societies with a formalized patrilineal transmission of surnames. A major weakness of the present preliminary research is the small sample size. As it stands, members of every ru were not typed and consequently some clans are still missing from the tree. However, the preliminary results strongly encourage the ongoing pursuit of ethnogenetic research on Sherpa history: it is likely that Sherpa true clan genealogy and history will be fully elucidated by future sampling campaigns, aimed at enlarging the sample size, and in loco investigations. Moreover, among our future intentions stands out the achievement of a distinct sampling campaign.

Table 4. Birth-village, ru and proto-ru

<table>
<thead>
<tr>
<th>Sample id</th>
<th>Birthplace</th>
<th>Ru</th>
<th>Proto-ru</th>
<th>MST Cluster</th>
</tr>
</thead>
<tbody>
<tr>
<td>Khumbu area</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>M4</td>
<td>Nangma</td>
<td>Salaka</td>
<td>T</td>
<td>I (71.4%)</td>
</tr>
<tr>
<td>M23</td>
<td>Namche</td>
<td>Chuserwa</td>
<td>n</td>
<td></td>
</tr>
<tr>
<td>M6</td>
<td>Shigatse</td>
<td>Paldorje</td>
<td>T</td>
<td></td>
</tr>
<tr>
<td>M21</td>
<td>Khumjung</td>
<td>Chuserwa</td>
<td>n</td>
<td>II (11.1%)</td>
</tr>
<tr>
<td>M1</td>
<td>Namche</td>
<td>?</td>
<td>?</td>
<td>III (71.4%)</td>
</tr>
<tr>
<td>M3</td>
<td>Namche</td>
<td>Thaktok</td>
<td>M</td>
<td></td>
</tr>
<tr>
<td>M22</td>
<td>Namche</td>
<td>Thaktok</td>
<td>M</td>
<td></td>
</tr>
<tr>
<td>M12</td>
<td>Namche</td>
<td>Lhukpa</td>
<td>n</td>
<td></td>
</tr>
<tr>
<td>M25</td>
<td>Kunde</td>
<td>Goparma</td>
<td>T</td>
<td></td>
</tr>
<tr>
<td>M28</td>
<td>Namche</td>
<td>Lhukpa</td>
<td>n</td>
<td></td>
</tr>
<tr>
<td>M10</td>
<td>Gepchuka</td>
<td>Gole</td>
<td>M</td>
<td>I (28.6%)</td>
</tr>
<tr>
<td>M14</td>
<td>Gepchuka</td>
<td>Gole</td>
<td>M</td>
<td>II (88.9%)</td>
</tr>
<tr>
<td>M15</td>
<td>Gepchuka</td>
<td>Gole</td>
<td>M</td>
<td></td>
</tr>
<tr>
<td>M19</td>
<td>Beni</td>
<td>Lama</td>
<td>L</td>
<td></td>
</tr>
</tbody>
</table>

Samples are grouped both by geographical provenance (Khumbu vs. Solu and Okhaldhunga area) and by NJ cluster affiliation (clusters I, II, and III). The last column reports percentages of cluster members born in the corresponding geographical area.
campaign in some Sichuan prefectures, where the legendary Sherpa homeland should lie, in order to assess potential genetic similarity between the Solukhumbu Sherpa and the autochthonous population. Promisingly, in the present Dartsedo (Kangding) County, in the balkanized area of the so-called Western Sichuan Ethnic Corridor (Sun, 1990), a small ethnic group called Minyag is still dwelling (Ikeda, 1998). Some authors sustain that the Minyag people of Sichuan could be the descendants of some dynasty that from 1038 to 1227 CE ruled a North Minyag kingdom northeast of Lake Kokonor, also identified as part of Xi-Xia or Tangut Kingdom, in what later became the Tibetan province of Amdo (Stein, 1951; Balikci, 2008). Sichuan Minyag possibly migrated to their current dwelling area after the Mongols conquered the former Minyag kingdom in 1227.

Surprisingly, it is curious to find that the Namgyal dynasty of the Sikkim kings, the Chogyals, also claims to descend from a Minyag clan member, named Guru Tashi. Oral histories report that, during the 13th century, Guru Tashi left his homeland in Kham Minyag and, via Lhasa, eventually crossed a Himalayan pass and reached the Chumbi Valley in Sikkim. This strong analogy with Sherpa oral traditions about their migration route along with the quite common recurrence of the Minyag appellation in apparently unrelated ethnic groups, definitely represent an interesting research trail that should be further investigated.

In conclusion, in the firm belief that in the end only a multidisciplinary research approach can yield an exhaustive explanation of the true origin of the Solukhumbu Sherpa, we plan to draw together a team capable of juxtaposing clues from linguistics, social sciences, and ethnociology to the genetic data.

Acknowledgments

Revealing ethnogistory through the juxtaposed investigation of manuscripts, oral tradition, and genetic pedigrees is a captivating and engrossing path: the authors wish to thank everybody who, like them, became fascinated with the Solukhumbu Sherpa tradition and especially all the Sherpa volunteers that contributed in person to the present research. The authors are also grateful to the University of Padua for a grant (no. CPDR100470).

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