Global phylogeography and genetic diversity of the zoonotic tapeworm Echinococcus granulosus sensu stricto genotype G1

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- 2 Echinococcus granulosus sensu stricto genotype G1
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62 ABSTRACT

Echinococcus granulosus sensu stricto (s. s.) is the major cause of human cystic 63 echinococcosis worldwide and is listed among the most severe parasitic diseases of humans. To 64 date, numerous studies have investigated the genetic diversity and population structure of E. 65 granulosus s. s. in various geographic regions. However, there has been no global study. Recently, 66 67 using mitochondrial DNA, it was shown that E. granulosus s. s. G1 and G3 are distinct genotypes, but a larger dataset is required to confirm the distinction of these genotypes. The objectives of this 68 study were to: (i) investigate the distinction of genotypes G1 and G3 using a large global dataset; 69 (ii) analyse the genetic diversity and phylogeography of genotype G1 on a global scale using near-70 71 complete mitogenome sequences. For this study, 222 globally distributed E. granulosus s. s. samples were used, of which 212 belonged to genotype G1 and 10 to G3. Using a total sequence 72 length of 11 682 bp, we inferred phylogenetic networks based on the whole E. granulosus s. s. 73 dataset (n = 222), G1 dataset (n = 212) and G1 human samples (n = 41). In addition, the Bayesian 74 phylogenetic and phylogeographic analyses were performed. The latter yielded several statistically 75 significant diffusion routes of genotype G1 originating from Turkey, Tunisia and Argentina. We 76 conclude that: (i) using a considerably larger dataset than employed previously, E. granulosus s. s. 77 G1 and G3 are indeed distinct mitochondrial genotypes; (ii) the genetic diversity of *E. granulosus* s. 78 s. G1 is high globally, with lower values in South America; (iii) the complex phylogeographic 79 patterns emerging from the phylogenetic and geographic analyses suggest that the current 80 distribution of genotype G1 has been shaped by early livestock diffusion events, along with 81 82 intensive animal trade in relatively recent history.

83

84

- 86 *Keywords:*
- 87 Cystic echinococcosis
- 88 *Echinococcus granulosus*
- 89 Genetic variability
- 90 Global phylogeography
- 91 Mitochondrial genome
- 92 Livestock domestication

93 **1. Introduction**

Echinococcus granulosus sensu lato (s. l.) is the causative agent of cystic echinococcosis 94 (CE), which is one of the most important zoonoses worldwide and a significant global public health 95 96 concern (e.g., Eckert et al., 2001; Alvarez Rojas et al., 2014; Marcinkute et al., 2015; Budke et al., 2017). CE is listed amongst the most severe parasitic diseases in humans, ranking second in the list 97 of food-borne parasites globally (FAO/WHO, 2014) and representing one of the 17 neglected 98 99 tropical diseases prioritised by the World Health Organization (WHO, 2015). The life cycle of the parasite involves mainly dogs and wild carnivores as definitive hosts and a wide range of domestic 100 101 and wild mammals, but also humans, as intermediate or accidental hosts (Eckert et al., 2001; Moks 102 et al., 2006; Deplazes et al., 2011; Laurimaa et al., 2015a).

Echinococcus granulosus s. l. exhibits considerable variation in terms of morphology, host 103 range, infectivity to humans, pathogenicity and other aspects (e.g., Eckert et al., 2001; Thompson, 104 2008; Gholami et al., 2011; Romig et al., 2015). Molecular studies have identified and characterised 105 a number of genotypes/species within the E. granulosus s. l. complex (Bowles et al., 1992, 1994; 106 107 Thompson and McManus, 2002; Lavikainen et al., 2003; Thompson, 2008; Saarma et al., 2009; 108 Knapp et al., 2011), which are relatively closely related to other species within the genus Echinococcus (Knapp et al., 2015). The accurate identification and differentiation of genotypes has 109 110 important epidemiological implications and informs about the zoonotic potential of particular genotypes. Earlier, the complex was considered to consist of genotypes G1-G8, G10 and E. felidis 111 (see Bowles et al., 1992, 1994; Lavikainen et al., 2003; Hüttner et al., 2008), however G2 is no 112 longer considered a valid genotype (Kinkar et al., 2017). Currently, the genotypes regarded as 113 distinct species are *E. granulosus* sensu stricto (s. s.; genotypes G1 and G3; Kinkar et al., 2017), *E.* 114 equinus (G4), E. ortleppi (G5) (Thompson and McManus, 2002), whereas the species status of 115 genotypes G6-G10 remains contentious (Moks et al., 2008; Thompson, 2008; Saarma et al., 2009; 116

Knapp et al., 2011, 2015; Lymbery et al., 2015; Nakao et al., 2015). Recently, a new genotype was
discovered in Ethiopia, but its status is not yet clear (Wassermann et al., 2016).

Echinococcus granulosus s. s. (genotypes G1 and G3) is widespread globally, with highly 119 120 endemic foci in South America, the Mediterranean basin and Central Asia, and particularly affects rural livestock-raising areas (Dakkak et al., 2010; Hajialilo et al., 2012; Rostami et al., 2015; Zhang 121 122 et al., 2015; Cucher et al., 2016). Some of the main factors contributing to the persistence of CE 123 include the frequent illegal and home slaughtering of animals for food, feeding raw offal to dogs, low public awareness of the disease, large populations of stray dogs and poor hygiene conditions 124 (Eckert et al., 2001; Torgerson and Budke, 2003; Varcasia et al., 2011; Possenti et al., 2016). 125 126 According to a recent estimate by Alvarez Rojas et al. (2014), E. granulosus s. s. is also the most frequently implicated causative agent of CE of humans (88% of cases) worldwide, and thus 127 deserves particular attention. 128

To date, numerous studies have explored the genetic diversity and population structure of E. 129 130 granulosus s. s. in various geographic regions (Nakao et al., 2010; Casulli et al., 2012; Rostami 131 Nejad et al., 2012; Yanagida et al., 2012; Andresiuk et al., 2013; Yan et al., 2013; Boufana et al., 2014, 2015; Romig et al., 2015; Kinkar et al., 2016; Laurimäe et al., 2016; Hassan et al., 2017). 132 However, there has been no global study. In addition, the analytical power has been low in most 133 134 studies as the analyses have been based largely on short sequences of mitochondrial DNA (mtDNA), most often on a single gene, e.g., the cytochrome c oxidase subunit 1 gene (cox1; 1609 135 bp; Yanagida et al., 2012; Alvarez Rojas et al., 2016; Alvarez Rojas et al., 2017) or partial sequence 136 of the cox1 or nad1 (e.g., Casulli et al., 2012; Andresiuk et al., 2013). Few studies used 137 considerably longer mtDNA sequences (~8270 bp; Kinkar et al., 2016; Laurimäe et al., 2016) and 138 139 demonstrated significantly better phylogenetic resolution. Due to the variable sequence lengths used thus far (a few hundred bp up to \sim 8270 bp), the results from different studies and geographic 140 regions are not directly comparable. Therefore, an analysis of near-complete mitogenome sequences 141

in a large geographical scale is required to gain better insight into the global patterns of diversity and phylogeography. Furthermore, the sequences of relatively short mtDNA regions most commonly used to date cannot unequivocally differentiate genotypes G1-G3 due to limited phylogenetic signal (e.g., Casulli et al., 2012; Andresiuk et al., 2013; Romig et al., 2015). Thus, although short mtDNA sequences have been widely used in phylogeographic studies and to develop methods for identifying genotypes (e. g. Boubaker et al., 2013; Laurimaa et al., 2015b), one has to be cautious when interpreting the results based on short mtDNA sequences.

By contrast, using near-complete mitogenome sequences (11 443 bp), Kinkar et al. (2017) provided evidence that G1 and G3 are distinct mitochondrial genotypes. As a relatively small number of samples was used in Kinkar et al. (2017), a larger sample size would be preferable to confirm the distinction of the two genotypes (G1 and G3). Therefore, in the present study, we (i) investigated the distinction of the *E. granulosus* s. s. genotypes G1 and G3 using a large global dataset (n = 222), and (ii) analysed the genetic diversity and phylogeography of genotype G1 on a world-wide scale using near-complete mitochondrial genome sequences.

156

157 **2. Materials and methods**

158 *2.1 Parasite material*

We sequenced 221 *E. granulosus* s. s. samples and included an additional sequence from Genbank (AB786664; genotype G1 from China; Nakao et al., 2013). Of the 221 samples, 114 were newly sequenced, whereas the rest were from Kinkar et al. (2016 and 2017) and Laurimäe et al. (2016) (Tables S1 and S2). However, additional mtDNA loci were sequenced for these samples in this study. The samples were obtained during routine meat inspections or from hospital cases and were ethanol-preserved at -20°C until further use.

166 2.2 DNA extraction, PCR amplification, sequencing and assembly

Total genomic DNA was extracted from protoscoleces, cyst membranes or adult worms of 167 E. granulosus using the High Pure PCR Template Preparation Kit (Roche Diagnostics, Mannheim, 168 169 Germany), following the manufacturer's protocols. For PCR amplification we used 12 primer pairs described in Kinkar et al. (2017). Sequencing was performed using the same primers as for the 170 initial PCR amplification. Cycle parameters for PCR and sequencing were as described in Kinkar et 171 172 al. (2016). Sequences were assembled using the program CodonCode v6.0.2 and manually curated in BioEdit v7.2.5 (Hall, 1999). All G1 sequences were deposited in the GenBank database under 173 174 accession nos. XXXX-XXXX.

175

176 2.3 Phylogenetic analyses

Phylogenetic networks were calculated for three mtDNA sequence datasets: (1) all samples of *E. granulosus* s. s. (n = 222), (2) sequences representing genotype G1 only (n = 212) and (3) sequences representing genotype G1 from humans (n = 41) using Network v4.6.1.5 (Bandelt et al., 180 1999); http://www.fluxusengineering.com, Fluxus Technology Ltd., 2004. Networks were constructed considering both indels and point mutations.

182 The Bayesian phylogenetic analysis for the whole dataset (n = 222 samples) was performed in the program BEAST 1.8.4 (Drummond et al., 2012) using BEAUti v1.8.4 to generate the initial 183 xml file for BEAST. The general time-reversible nucleotide-substitution model with a proportion of 184 invariable sites and gamma distributed rate variation (GTR+I+G; Tavaré, 1986; Gu et al., 1995) 185 was determined as the best-fit model of sequence evolution using the program PartitionFinder 2.1.1 186 (Guindon et al., 2010; Lanfear et al., 2012, 2016). Exponential growth coalescent prior (Griffiths 187 and Tavaré, 1994) was chosen for the tree, and a strict molecular clock was assumed owing to the 188 intraspecific nature of the data (Drummond and Bouckaert, 2015). The posterior distribution of 189

parameters was estimated by Markov Chain Monte Carlo (MCMC) sampling. MCMC chains were
run for 10 million states, sampled every 1000 states with 10% burn-in. Log files were analysed
using the program Tracer v1.6 (Rambaut et al., 2014). The tree was produced using TreeAnnotator
v1.8.4 and displayed in FigTree v.1.4.3 (Rambaut, 2014).

194

195 *2.4 Population indices*

196 The population diversity indices, such as the number of haplotypes, haplotype diversity and nucleotide diversity, were calculated using the program DnaSP v5.10.01 (Librado and Rozas, 197 2009). Neutrality indices Tajima's D (Tajima, 1989) and Fu's Fs (Fu, 1997) and the pairwise 198 fixation index (Fst) were calculated using the Arlequin 3.5.2.2 software package (Excoffier et al., 199 2005). Indices were calculated for four different datasets representing genotype G1: (a) all 200 201 sequences (n = 212); (b) the three most numerous host species in this study (cattle, sheep and human), (c) five regions (the Americas, Africa, Asia/Australia, Europe and the Middle East), and 202 203 (d) eight countries for which the sample size exceeded 10: Algeria, Argentina, Brazil, Iran, Italy 204 (comprising continental Italy and Sardinia), Spain, Tunisia and Turkey. In addition, the pairwise 205 fixation index was calculated between genotypes G1 and G3.

206

207 *2.5 Bayesian phylogeographic analysis*

The phylogeographic diffusion patterns of genotype G1 were analysed using a Bayesian discrete phylogeographic approach (Lemey et al., 2009). This approach estimates ancestral locations from the set of sampled locations and annotates the discrete location states to tree nodes (Lemey et al., 2009; Faria et al., 2011). The standard Markov model is extended using a Bayesian Stochastic Search Variable Selection (BSSVS) procedure, which offers a Bayesian Factor (BF) test to identify the most parsimonious description of the phylogeographic diffusion process (Lemey et al., 2009).

Specifically, the intial xml file generated in BEAUti in the Bayesian phylogenetic analysis (see 214 section 2.3) was edited according to the 'Discrete phylogeographic analysis' tutorial available on 215 the Beast website (http://beast.bio.ed.ac.uk/tutorials). The analysis was performed in BEAST 1.8.4 216 (Drummond et al., 2012) using the BEAGLE library (Avres et al., 2011). MCMC chains were run 217 for 50 million states, sampled every 5000 states with 10% burn-in. The effective sampling size 218 (ESS) of estimates was assessed using Tracer v1.6 (Rambaut et al., 2014), and the tree was 219 produced using TreeAnnotator v1.8.4 and displayed in FigTree v.1.4.3 (Rambaut, 2014). The 220 program SpreaD3 v0.9.6 (Bielejec et al., 2016) was used to visualize the output from the Bayesian 221 phylogeographic analysis and to calculate the Bayes Factor supports. Three independent runs were 222 conducted and geographic links that yielded BF > 10 in all three runs were displayed. 223

224

3. Results

Near-complete mitogenome sequences representing *E. granulosus* s. s. samples (n = 221) were produced and aligned (length of alignment 11 682 bp). Most sequences were 11 675 bp in length, but some varied from 11 674 bp to 11 678 bp. An additional sequence from GenBank (see section 2.1) was included, totalling 222 sequences in analysis.

230

231 *3.1. The phylogenetic network of E. granulosus s. s.*

The 222 sequences divided into two haplogroups, separated by 37 mutations (Fig. 3). The largest haplogroup included 212 sequences representing genotype G1, whereas the other haplogroup included 10 samples representing genotype G3. The 212 G1 samples were divided into 171 different haplotypes (Fig. 3). The origin and host species of the G1 samples are shown in Figs. 1 and 2 and Tables 1 and S3. To the best of our knowledge, all human G1 samples used in the analysis were autochthonic cases of CE, except for a Finnish sample, which originated from an Algerian patient who was living in Finland. Therefore the origin of the infection is most likelyAlgeria.

240

241 *3.2 Bayesian phylogenetic analysis*

The Bayesian phylogenetic analysis divided *E. granulosus* s. s. samples into two wellsupported clades, corresponding to genotypes G1 and G3 (posterior probability value = 1.00; Fig. 4; Fig. S1). The intraspecific phylogeny of G1 yielded clades with varying support values, of which several clades were well resolved (posterior probability values = 1.00).

246

247 3.3. The phylogenetic network for genotype G1

The phylogenetic network for genotype G1 was highly divergent (Fig. 5). Among the 171 haplotypes, 147 were represented by a single sample, 18 haplotypes included two samples, 5 haplotypes (IRA1, BRA1, TUR1, TUR3, TUN5) included 3 samples and one haplotype (ARB1) included 14 samples. The average number of mutational steps between different G1 haplotypes was 16 and the maximum 32 (e.g., between TUR12 and ALB2).

Multiple haplogroups (monophyletic groups) could be distinguished. Seven such haplogroups (named A-G, respectively) corresponded to the well-supported clusters in the Bayesian phylogenetic tree (posterior probability values = 1.00; see Figs. 4 and 5; see also section *3.2*). Out of the nine haplogroups in grey (Fig. 5), seven were well-supported on the phylogenetic tree (posterior probability values = 1.00; Fig. 5).

In some of the monophyletic clusters in the network, haplotypes clustered together according to geographic origin. For example, three monophyletic groups represented haplotypes only from Tunisia (TUN25, TUN11 and TUN1; TUN26 and TUN6; TUN13, TUN3 and TUN18). Another haplogroup (D) was of Middle-East origin, comprising samples from Turkey (TUR8, TUR21,

TUR18, TUR19) and Iran (IRA11). In addition, one group was of African origin and included 262 samples from Tunisia (TUN5, TUN7) and Algeria (ALG9) and another group was from South-263 America, including haplotypes from Brazil and Argentina (BRA4, ARG2, BRA6). In other 264 monophyletic groups, samples from Eurasia clustered together, some of which comprised 265 haplotypes that were geographically distant from each other, such as an Indian-Iranian group (IND1 266 and IRA16) and a Turkish-Spanish-Iranian group F (TUR12, TUR24, TUR27, TUR4, TUR9, 267 IRA12 and SPA1). Haplogroup G from Eurasia represented haplotypes from Turkey (TUR32, 268 TUR22, TUR11, TUR36, TUR13, TUR28, TUR26, TUR10, TUR31, TUR33, TUR17, TUR7), Iran 269 (IRA1, IRA13, IRA8, IRA18, IRA7, IRA17, IRA4, IRA9), Albania (ALB1, ALB2), Moldova 270 (MOL2) and Romania (ROM1), and haplogroup C represented haplotypes from Iran (IRA19, IRA6 271 and IRA5), Moldova (MOL3), Mongolia (MON1) and Romania (ROM2). 272

The geographically most distant haplotypes that clustered together into haplogroups originated 273 274 from different continents, including two haplotypes from Australia (AUS1 and AUS2) and a haplotype originating from Algeria (ALG4). However, haplotype AUS3 from Australia clustered 275 276 together with 12 haplotypes from Africa (TUN8, TUN30, ALG6, TUN12, ALG10, TUN14, 277 TUN23, TUN9, ALG1, TUN10, ALG3 and ALG11) and the haplotypes from Europe (SPA7, SPA4 and FIN1; A). In addition, five haplotypes from Africa (ALG2, TUN15, MOR1, TUN27, ALG8) 278 clustered with haplotype ARG8 from Argentina, and haplotypes ITA7, ITA6, ITA8, and TUN2 279 from Italy and Tunisia also clustered together. 280

No host-specific pattern was identified, as the majority of monophyletic clusters included samples from different host species. The most numerous host species in this study, cattle and sheep, were genetically closely related and some haplotypes (TUR17, TUN14 and ARB1) included samples from both hosts. As expected, the haplotypes representing 41 samples from humans did not cluster together and were in different haplogroups, together with samples from other hosts. Haplotype TUN5 from Tunisia represented three samples, one from sheep and two from human and

haplotype TUN15 also from Tunisia represented two samples, one from sheep the other fromhuman.

289

290 *3.4 The phylogenetic network of human G1 samples*

The 41 genotype G1 samples from humans represented 37 distinct haplotypes (Fig. 6). Haplotypes from Tunisia and Algeria were frequently closely related (e.g., TUN22 and ALG12), but some were genetically very distant from one another (e.g. ALG7 and TUN27; separated by 30 mutations). Haplotype ALG1 from Algeria was most closely related to haplotype FIN1; FIN1 was from an Algerian CE patient who was living in Finland. Haplotype MON1 representing two samples from Mongolia was within a monophyletic cluster with haplotype ROM2 from Romania and haplotype IRA3 from Iran with haplotype TUN21 from Tunisia.

298

3.5 Diversity and neutrality indices

The overall haplotype diversity index for genotype G1 was very high (Hd = 0.994), while 300 the nucleotide diversity was low ($\pi = 0.00133$; Table 2). The most numerous host species in this 301 302 study – cattle, sheep and human – were represented by high haplotype diversity indices (0.987 to 0.995), whereas nucleotide diversities ranged from 0.00128 to 0.00138. The haplotype diversity 303 indices for genotype G1 from the five geographical regions were also high, ranging from 0.926 to 304 305 0.994, whereas the nucleotide diversities varied from 0.00083 to 0.00136, with samples from 306 America having the lowest values. Of the countries represented in the present analysis, Argentina had the lowest values of haplotype and nucleotide diversities (Hd = 0.832 and π = 0.00057), whilst 307 308 the corresponding values for other countries were higher (ranging from 0.956 to 1.000 and π ranging from 0.115 to 0.00143). 309

Neutrality indices Tajima's D and Fu's Fs were negative and statistically highly significant 310 for genotype G1 (D = -2.77, Fs = -23.80; Table 2). Neutrality indices were similar among host 311 species and in the majority of the regions (Africa, the Americas, Europe and the Middle East). 312 However, neutrality indices were lower and insignificant for Asia and Australia. Among the 313 countries included, both neutrality indices were negative and statistically significant for Algeria, 314 Argentina, Tunisia and Turkey, while only Tajima's D (-2.03) was significant for Iran. The 315 neutrality indices calculated for Brazil, Italy and Spain were all negative, and statistically 316 insignificant. 317

318

319 *3.6. Population differentiation*

The Fst value between genotypes G1 and G3 was very high (0.711; p < 0.00001). By contrast, 320 321 low Fst values were observed between cattle, sheep and human samples of G1 (Fst < 0.05; Table 3) and between most of the regions of G1 in this study (Africa, Asia and Australia, Europe and the 322 Middle East), ranging from 0.022 to 0.068 (Table 4). However, higher Fst values (ranging from 323 0.186 to 0.216) were detected between the Americas and the other regions. Among countries, the 324 highest Fst values were seen between Argentina and the Eurasian (Iran, Italy, Spain and Turkey) 325 and African countries (Algeria and Tunisia), ranging from 0.269 to 0.359, while the value was 326 slightly lower between Argentina and Brazil (0.124; Table 5). The Fst values between the remaining 327 countries were mostly less than 0.100. Statistically insignificant values were observed between 328 329 Europe and Asia-Australia (Table 4) and between Algeria and Tunisia (Table 5).

330

331 *3.7. Bayesian phylogeographic analysis*

The Bayesian discrete phylogeographic analysis yielded 18 statistically significant spatial diffusion routes for genotype G1, of which 11 had a BF value of 10 to 100, whereas the BF value was very high (>100) for seven routes (Fig. 7). A total of seven routes originated from Turkey, two
of which had very high statistical support (BF > 100; between Turkey and Iran and Turkey and
Greece); six originated from Tunisia, three of which had BF values >100 (between Tunisia and
Italy, Tunisia - Algeria and Tunisia - Argentina). Argentina was the ancestral location to Brazil (BF
> 100), Mexico and Chile, while Iran was ancestral to India. Algeria was identified as the origin of
the sample from a human from Finland.

340

341 4. Discussion

The results of this study based on 222 near-complete E. granulosus s. s. mitogenome 342 sequences from a worldwide distribution confirmed that genotypes G1 and G3 are indeed distinct 343 genotypes, as reported recently by Kinkar et al. (2017) with a significantly smaller sample size (n =344 345 23). The analysis of the much larger dataset used in the present study also positioned genotypes G1 346 and G3 into distinct haplogroups, separated by 37 mutations (Fig. 3). This distinction was also well supported by the Bayesian phylogenetic analysis (Fig. 4) and by the high Fst value (0.7nn; p < p347 0.00001) between genotypes G1 and G3. As genotypes G1 and G3 represent distinct mitochondrial 348 lineages and G1 is more widespread with a larger spectrum of hosts, it is possible that there are 349 epidemiological differences between these genotypes. Although this proposal has not yet been 350 explored, the use of up-to-date molecular methods to identify and distinguish these genotypes will 351 be the prerequisite to test this hypothesis. However, sequencing a large portion of the mitochondrial 352 353 genome is often not feasible in most laboratories, such that establishing a set of diagnostic nucleotides to confidently assign samples to genotypes G1 and G3 is needed (ongoing project). 354

The results of the present study demonstrated an extremely high global haplotype diversity within genotype G1 (Fig. 5); the 212 samples analysed represented a total of 171 haplotypes (overall haplotype diversity 0.994; Table 2). Haplotype diversities within genotype G1 were high

for different host species, regions and countries (with values being mostly between 0.970 and 1.000; 358 Table 2), whereas Fst values were low (mostly < 0.1; Tables 3-5), pointing to a high genetic 359 diversity and low genetic differentiation between G1 subpopulations globally, possibly due to rapid 360 361 radiation. However, the South- and Central-American samples (since only one sample was from Mexico, we use henceforth South America) showed slightly lower values of haplotype diversities 362 (particularly Argentina; Hd = 0.832; Table 2) and higher values of Fst (ranging from 0.186 to 0.216) 363 between the Americas and the other regions; Table 4), indicating lower genetic diversity and 364 moderate genetic differentiation of samples from South America compared with those from Africa 365 and Eurasia. This finding is also supported by the phylogenetic network wherein the South-366 367 American samples formed a haplogroup (B) with a dominant central haplotype (Fig. 5), suggesting a bottleneck event in the past, while significant negative values of neutrality indices (D = -2.201, Fs 368 = -13.284; Table 2) indicated a population expansion in South America. A possible explanation for 369 370 this observation is the relatively recent arrival to and sudden expansion of domestic animals (cattle and sheep) in South America during the 15th and 16th Centuries (Rodero et al., 1992) compared with 371 372 the domestication history in Africa and Eurasia, extending thousands of years BC (Zeder, 2008; Lv 373 et al., 2015). However, as Argentina contributed more to the lower Hd value for South America, another possible reason could be that a relatively large number of the Argentinian samples (24 of 374 31) originated from the same geographical area (the Buenos Aires province in Argentina). 375 However, the samples from Turkey used in this study also originated from one area in the East 376 (Erzurum and Elazig provinces), but yielded very high haplotype diversity (Hd = 0.991; Table 2). 377 Therefore, the results could reflect a more recent arrival and sudden expansion of E. granulosus s. s. 378 genotype G1 in South America. 379

In addition to the South-American haplogroup B, there were multiple other groups where samples clustered together according to their geographical origin; for example, some of the African samples (Fig. 5). However, the opposite was also observed, and numerous well-supported clusters

on the phylogenetic tree comprised samples from various geographic locations (e.g., in haplogroup 383 A, in which African, Australian and European samples clustered together). These observed 384 phylogeographical patterns (along with the low Fst values in Eurasia and Africa) might be the 385 consequence of an extensive livestock trade that has facilitated the dispersal of the parasite over 386 vast geographic areas. Demographic analysis also supported this hypothesis: high haplotype 387 diversity coupled to relatively low nucleotide diversity values observed in this study (Hd = 0.994, π 388 = 0.00133 for the overall population) suggest rapid demographic expansion, supported by 389 390 significant negative values of neutrality indices Tajima's D (-2.771) and Fu's Fs (-23.802), particularly evident among subpopulations with larger sample sizes (the whole dataset, hosts, 391 African and the Middle Eastern region, Turkey; Table 2). Similar results reflecting populations 392 under expansion have been reported in previous studies in various geographic regions (e.g., Nakao 393 et al., 2010; Casulli et al., 2012; Yanagida et al., 2012; Kinkar et al., 2016; Laurimäe et al., 2016; 394 395 Hassan et al., 2017).

In this study, samples from humans did not cluster together and were frequently positioned 396 with samples from various livestock species (e.g., sheep and goat in group C; sheep and cattle in 397 groups A and F; see Figs. 4 and 5). Furthermore, some of the samples from humans were relatively 398 closely related to samples from wildlife species, such as dingo (group A) and wild boar (group E). 399 Interestingly, the aforementioned human samples were of African origin, whereas the samples from 400 dingo and wild boar were from Australia and Spain, respectively (Fig. 5). The results clearly 401 demonstrate a highly efficient transmission cycle of genotype G1 among different host species 402 403 (livestock, wildlife and humans) globally. This statement is further supported by the low Fst values among cattle, sheep and human samples (Table 3), suggesting that no particular haplotype is more 404 virulent to humans than any other within genotype G1. However, the Fst values point to a slightly 405 higher genetic similarity between sheep and human samples (Fst = 0.025) compared with cattle and 406 407 human samples (Fst = 0.046). Interestingly, the majority of the *E. granulosus* s. s. cysts obtained

from cattle are reported as sterile whereas a high fertility rate is characteristic of sheep and human infections (e.g. McManus and Thompson, 2003; Andresiuk et al., 2013; Elmajdoub and Rahman, 2015; Kamelli et al., 2016). The higher genetic similarity between samples of human and sheep origin could indicate better G1 transmission between human and sheep, compared with human and cattle.

As a large portion (29 of 41) of the G1 samples from human studied here originated from Africa, it is not surprising that most of these clustered together in the phylogenetic network (see Fig. 6). The sample from a CE patient in Finland who originated from Algeria, clustered together with another human sample from Algeria and the link between Algeria and Finland was also supported by phylogeographic analysis (Fig. 7), suggesting that the individual was most likely infected in Algeria. The genetic diversity among samples from humans was very high (Hd = 0.995), almost equal to values calculated for cattle and sheep (Hd = 0.992 and 0.987, respectively; Table 2).

The Bayesian phylogeographic analysis revealed a number of statistically significant migration 420 421 routes which seemed to follow the spread of livestock animals from the centre of domestication 422 during Neolithic times (Zeder, 2008; Lv et al., 2015; Fig. 7). One ancestral location of genotype G1 was Turkey, from which several migration routes originated. The Fertile Crescent of the Middle 423 East is considered as one of the earliest centres of livestock domestication (mainly cattle, sheep, 424 425 pigs and goats) from where the animals were later distributed east- and westwards during Neolithic times (Bruford et al., 2003; Zeder, 2008; Chessa et al., 2009; Lv et al., 2015; Rannamäe et al., 426 427 2016). The phylogeographic results of this study could reflect the early spread of livestock from this region along with E. granulosus s. s. genotype G1. Although the possible ancestral location of E. 428 granulosus s. s. in the Middle East has been suggested before (e. g. Nakao et al., 2010; Casulli et 429 430 al., 2012; Yanagida et al., 2012; Kinkar et al., 2016; Hassan et al., 2017), the discrete Bayesian phylogeographic approach used here provided statistical support for this diffusion pattern. In 431 addition, the migration routes from Tunisia to Morocco and Algeria point to a westward movement 432

of genotype G1 in North Africa which is also in accordance with the supposed direction of early
dispersal of domesticated animals (cattle, sheep and goat) in this area (Gifford-Gonzalez and
Hanotte, 2011).

Another location from which several diffusion routes originated was Tunisia: among others, 436 three routes showed a possible migration of genotype G1 from Tunisia to Argentina, Australia and 437 Turkey which could be linked to human/livestock migration in later history. It is possible that 438 during the colonization of Tunisia by the Ottoman Empire (founded by the Turkish) from the 16th to 439 19th Centuries, domestic animals infected with genotype G1 were transported between these 440 regions, and later to other parts of the world, which could also result in Tunisia being one of the 441 centres of radiation, together with Turkey. During the same period (the 15th and 16th Centuries), 442 sheep and other livestock were introduced to the Americas by Spanish and British colonizers. 443 However, some animals that arrived to the Americas could have had an African origin as some of 444 445 the livestock species (mostly pigs and goats) were taken aboard on the Canary Islands, which were colonized by people from North Africa (Rodero et al., 1992; Rando et al., 1999; also discussed in 446 447 Alvarez Rojas et al., 2017), possibly explaining the significant diffusion route between Tunisia and 448 Argentina. The ancestral position of Argentina could indicate its possible origin for the other American samples (Brazil, Chile and Mexico). The connection between Tunisia and Australia could 449 also be linked to relatively recent history: it is thought that the sources of Australian sheep could be 450 Spain and/or North Africa, as Merinos raised in North Africa arrived in Australia in the beginning 451 of the 19th Century, as discussed by Jenkins (2005). 452

In conclusion, this is the first study to explore the global patterns of genetic diversity and phylogeography of *E. granulosus* s. s. using near-complete mitogenome sequences. We show that: (i) using a considerably larger dataset than employed previously, *E. granulosus* s. s. genotypes G1 and G3 are clearly distinct mitochondrial genotypes; (ii) the genetic diversity within genotype G1 is very high worldwide, with slightly lower values in South America; (iii) the observed complex

458	phylogeographic patterns emerging from the phylogenetic and -geographic analyses suggest that the
459	current distribution of E. granulosus s. s. genotype G1 has been shaped by the early livestock
460	diffusion events, along with intensive animal trade in the relatively recent history.

462 **Conflict of interest**

- 463 Authors declare no conflict of interest.
- 464

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Fig. 1. Geographic locations of *Echinococcus granulosus* sensu stricto genotype G1 samples (n =
212) analysed in this study.

736

Fig. 2. Geographic locations of *Echinococcus granulosus* sensu stricto genotype G1 samples from
humans (n = 41) used in this study.

739

Fig. 3. Phylogenetic network of *Echinococcus granulosus* sensu stricto samples based on 11 682 bp of mtDNA. Small black circles are median vectors (i.e. hypothetical haplotypes: haplotypes not sampled or extinct). The larger haplogroup (n = 212) corresponds to the mitochondrial genotype G1 and the smaller haplogroup (n = 10) to G3. The small circles and triangles in the haplogroups represent haplotypes. The number on the line connecting the haplogroups indicates the mutational steps between genotypes G1 and G3.

746

Fig. 4. Bayesian phylogenetic tree inferred from 222 *Echinococcus granulosus* sensu stricto samples. The larger clade (n = 212) corresponds to the mitochondrial genotype G1 and the smaller (n = 10) to G3. Posterior probability values >0.95 are indicated at the nodes. The asterisks indicate haplotypes obtained from humans. Seven clades depicted in blue, yellow, red, green, pink, purple, orange and named A–G, respectively, illustrate clades that received the posterior probability value >0.95 and in which the sample size was equal or higher than 5. Note that the lengths of two branches are reduced (dashed line); for the figure with actual branch lengths, see Fig. S1.

754

Fig. 5. Phylogenetic network of *Echinococcus granulosus* sensu stricto G1 samples based on 11 682
bp of mtDNA. Circles represent haplotypes obtained from livestock and wild animals, triangles
represent haplotypes of human origin. Haplotype colours represent different geographical regions:

purple - Africa, green - America, orange - Asia and Australia, blue - Europe, dark red - the 758 Middle East (please note that colours indicated on the right corner of the figure refer to geographic 759 locations of haplotypes, not haplogroups). Haplotype names represent their geographical origin: 760 ALB - Albania, ALG - Algeria, ARG - Argentina, AUS - Australia, BRA - Brazil, CHI - Chile, 761 CHN - China, FIN - Finland (patient from Algeria), FRA - France, GRE - Greece, IND - India, 762 IRA - Iran, ITA - Italy, KAZ - Kazakhstan, MEX - Mexico, MOL - Moldova, MON - Mongolia, 763 MOR – Morocco, ROM – Romania, SPA – Spain, TUN – Tunisia, TUR – Turkey. Host species are 764 indicated with letters inside the haplotypes (C - cattle, S - sheep, H - human, P - pig, G - goat, D -765 dingo, W – wild boar, B – buffalo). The small number inside haplotypes indicates the frequency of 766 the haplotype. Numbers on the lines represent the number of mutations (single mutations are not 767 marked with a number). 768

769

770 Fig. 6. Phylogenetic network of *Echinococcus granulosus* sensu stricto G1 human samples based on 11 682 bp of mtDNA. Triangles represent haplotypes. Haplotype colours represent different 771 772 geographical regions: purple – Africa, orange – Asia, blue – Europe and dark red – the Middle East. 773 Haplotype names represent different geographical origins: ALG - Algeria, CHN - China, FIN -Finland (Algerian patient), IRA - Iran, ITA - Italy, KAZ - Kazakhstan, MON - Mongolia, ROM -774 Romania, SPA – Spain, TUN – Tunisia. The number inside the triangles indicate the frequency of 775 the haplotype. Numbers on the lines represent the number of mutations (single mutations are not 776 marked with a number). 777

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Fig. 7. Statistically significant diffusion routes inferred from the Bayesian phylogeographic analysis based on 212 *Echinococcus granulosus* sensu stricto genotype G1 samples (11 682 bp of mtDNA). Black lines represent significant links (BF > 10), whereas black lines with red outlines represent highly significant links (BF > 100). **Fig. S1.** Bayesian phylogenetic tree inferred from 222 *Echinococcus granulosus* sensu stricto samples. The larger clade (n = 212) corresponds to the mitochondrial genotype G1 and the smaller (n = 10) to G3. Posterior probability values >0.95 are indicated at the nodes. The asterisks indicate haplotypes obtained from humans. Seven clades depicted in blue, yellow, red, green, pink, purple, orange and named A-G, respectively, illustrate clades that received the posterior probability value >0.95 and in which the sample size was equal or higher than 5. This is essentially the same as Fig. 4, but with actual branch lengths.

791

				U					5		5
794		Origin	Sheep	Cattle	Human	Goat	Swine	Wild boar	Dingo	Buffalo	Total
795	1.	Turkey	28	14							42
796	2.	Tunisia	17	4	17						38
797	3.	Iran	16	3	2	2					23
798	4.	Argentina	16	14			1				31
799	5.	Brazil		14							14
800	6.	Spain	6		2	3	1	1			13
801	7.	Algeria			12						12
802	8.	Italy	6	2	1	1					10
803	9.	Chile		6							6
804	10.	Australia							3		3
805	11.	Greece	3								3
806	12.	Mongolia			3						3
807	13.	Moldova	2	1							3
808	14.	Romania		1	1						2
809	15.	Albania	2								2
810	16.	Finland (Alg)			1						1
811	17.	France		1							1
812	18.	Kazakhstan			1						1
813	19.	China			1^{a}						1
814	20.	India								1	1
815	21.	Mexico					1				1
816	22.	Morocco		1							1
817	Tot	al	96	61	41	6	3	1	3	1	212

Host data for 212 *Echinococcus granulosus* sensu stricto G1 isolates analysed in this study.

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^a Sequence was obtained from GenBank (AB786664; Nakao et al., 2013).

Diversity and neutrality indices for Echinococcus granulosus sensu stricto G1 samples based on 11 682 bp mtDNA sequences.

	Divers	ity			Neutrality	
	n	Hn	$Hd \pm S.D.$	$\pi \pm S.D.$	D	Fs
Total	212	171	0.994 ± 0.002	0.00133 ± 0.00004	-2.77109 ^a	-23.80242 ^b
Host						
Cattle	61	52	0.992 ± 0.005	0.00138 ± 0.00007	-2.56626 ^a	-24.20117 ^a
Sheep	96	74	0.987 ± 0.006	0.00128 ± 0.00005	-2.65309 ^a	-24.12005 ^a
Human	41	37	0.995 ± 0.007	0.00130 ± 0.00008	-2.61502 ^a	-18.96890 ^a
Region						
Africa	51	43	0.993 ± 0.006	0.00136 ± 0.00007	-2.50107 ^a	-20.46636 ^a
Asia & Australia	9	8	0.972 ± 0.064	0.00099 ± 0.00014	-1.16779	-0.73526
Europe	35	31	0.993 ± 0.009	0.00136 ± 0.00008	-2.40214 ^a	-12.30737 ^b
America	52	34	0.926 ± 0.031	0.00083 ± 0.00009	-2.20130 ^b	-13.28433 ^b
Middle East	65	55	0.994 ± 0.004	0.00132 ± 0.00007	-2.60935 ^a	-24.21632 ^a
Country	10	10	1 000 0 001	0.00142+0.00014	1.00(10)	0.170.400
Algeria	12	12	1.000±0.034	0.00143 ± 0.00014	-1.9861 <i>3</i> °	-3.17349°
Argentina	31	19	0.832 ± 0.070	0.00057 ± 0.00014	-2.38545°	-5.29367
Brazil	14	12	0.956 ± 0.045	0.00115 ± 0.00012	-1.31585	-1.67741
Iran	23	19	0.980 ± 0.020	0.00120 ± 0.00011	-2.03201 ^b	-4.14849
Italy	10	9	0.978 ± 0.054	0.00126 ± 0.00014	-1.32335	-0.77495
Tunisia	38	30	0.987 ± 0.009	0.00132 ± 0.00008	-2.25318 ^b	-8.60682 ^c
Turkey	42	36	$0.991 {\pm} 0.008$	0.00137 ± 0.00009	-2.48392 ^b	-15.01834 ^a
Spain	13	11	0.974 ± 0.039	0.00124 ± 0.00012	-1.61222	-0.92526

Spain13110.974±0.0390.00124±0.00012-1.61222-0.92526Abbreviations: number of isolates examined (n), number of haplotypes (Hn), haplotype diversity (Hd), nucleotide diversity (π), Tajima's D (D), Fu's Fs (Fs), and standard deviation (S.D.).

^a Highly significant p value ($p \le 0.001$).

^b Highly significant p value ($p \le 0.001$) ^c Significant p value (p < 0.01).

Pairwise fixation index (Fst) values between *Echinococcus granulosus* sensu stricto genotype G1
hosts based on 11 682 bp of mtDNA.

		~ .	~1	~~
		Cattle	Sheep	Human
3	Cattle	-		
4	Sheep	0.01171^{a}	-	
5	Human	0.04620^{a}	0.02477	^a _
	^a Signifi	cant p valu	e (p < 0.	05).

Pairwise fixation index (Fst) values between Echinococcus granulosus sensu stricto genotype G1 838 regions based on 11 682 bp of mtDNA. 839

Africa	Asia & Au	s Europe	The Americas	Middle East
-				
0.02603^{a}	-			
0.02844^{a}	0.02243	-		
0.18581 ^a	0.21568 ^a	0.19073 ^a	-	
0.06808^{a}	0.04671^{a}	0.02998^{a}	0.20726 ^a	-
	Africa - 0.02603 ^a 0.02844 ^a 0.18581 ^a 0.06808 ^a	Africa Asia & Aux - 0.02603 ^a - 0.02844 ^a 0.02243 0.18581 ^a 0.18581 ^a 0.21568 ^a 0.06808 ^a 0.04671 ^a	Africa Asia & Aus Europe - - 0.02603 ^a - 0.02844 ^a 0.02243 0.18581 ^a 0.21568 ^a 0.06808 ^a 0.04671 ^a	AfricaAsia & Aus EuropeThe Americas $ 0.02603^a$ $ 0.02844^a$ 0.02243 $ 0.18581^a$ 0.21568^a 0.19073^a 0.06808^a 0.04671^a 0.02998^a 0.20726^a

Significant p value (p < 0.05). 846

Pairwise fixation index (Fst) values between *Echinococcus granulosus* sensu stricto genotype G1
countries based on 11 682 bp of mtDNA.

	Algeria	Argentina	ı Brazil	Iran	Italy	Tunisia	Turkey	Spain
Algeria	-							
Argentina	a 0.32670 ^a	-						
Brazil	0.08251^{a}	0.12434 ^a	-					
Iran	0.08940^{a}	0.33548 ^a	0.12860 ^a	-				
Italy	0.04580^{a}	0.35853 ^a	0.10146 ^a	0.10366 ^a	-			
Tunisia	0.00410	0.26940^{a}	0.07992 ^a	0.08233^{a}	0.05166 ^a	-		
Turkey	0.06763^{a}	0.27984 ^a	0.09946 ^a	0.01280^{a}	0.07387^{a}	0.06480^{a}	-	
Spain	0.02989^{a}	0.34402^{a}	0.10144^{a}	0.08996 ^a	0.06351^{a}	0.04593^{a}	0.06133	a _
Signific	ont n vol	$u_0 (n < 0)$	15)					

859 ^a Significant p value (p < 0.05).

Table S1

The list of G1 samples from the Americas partially published previously in Laurimäe et al. (2016) and Kinkar et al. (2017).

Lab code in Tartu	Haplotype in this study (11 682 bp)	Haplotype in Laurimäe et al. (2016; 8279 bp)	Haplotype in Kinkar et al. (2017; 11 443 bp)
Al	ARB1	ARG1	
A2	ARG1	ARG3	
A10	ARG2	ARG11	
A13	ARG3	ARG13	ARG1
A17	ARG4	ARG5	
A19	ARG5	ARG16	
A21	ARG6	ARG8	
A23	ARB1	ARG1	
A29	ARB1	ARG1	
A30	ARB1	ARG1	
A35	ARB2	AB1	
A40	ARG7	ARG1	
A41	ARG8	ARG14	
A42	ARG9	ARG2	
A43	ARG10	ARG1	
A47	ARB1	ARG1	
A50	ARB1	ARG1	
A52	ARB1	ARG1	
A53	ARB1	ARG1	
A54	ARB1	ARG1	
A55	ARB1	ARG1	
A57	ARG11	ARG12	
TŠ6	CHI1	CHI2	
TŠ13	CHI2	CHI1	
TŠ14	CHI1	CHI2	
TŠ15	CHI3	CHI4	
TŠ16	CHI4	CHI3	
TŠ18	CHI2	CHI1	CHI1
H172	BRA2	BRA5	
H408	BRA1	BRA3	
H424	BRA6	BRA2	
H429	BRA1	BRA3	

H442	BRA9	BRA6
H567	ARB2	AB1
H574	BRA10	BRA1
H575	BRA5	BRA4
H585	BRA1	BRA3
P66	ARG12	ARG17
P67	ARG13	ARG17
P68	ARB1	ARG1
P69	ARG14	ARG1
P76	ARG16	ARG6
8G	MEX1	MEX1

Table S2

The list of G1 samples from Eurasia and Africa partially published previously in Kinkar et al. (2016 and 2017).

Lab code in Tartu	Haplotype in this study (11 682 bp)	Haplotype in Kinkar et al. (2016; 8274 bp)	Haplotype in Kinkar et al. (2017; 11 443 bp)
V8	GRE1	GRE1	
HS4	ROM1	ROM1	
Fin16	FIN1	FIN1	FIN1
IT 10	ITA2	ITA6	
AC3	ITA4	ITA3	
AC4	ITA4	ITA3	
2G	SPA1	SPA2	
12G	SPA2	SPA3	
ALB3	ALB1	ALB1	
ALB4	ALB2	ALB2	ALB1
5455	FRA1		FRA3
P2	SPA3	SPA4	
P15	SPA5	SPA5	
P16	SPA6	SPA6	
P21	SPA7		SPA5
P47	SPA8	SPA9	
P51	SPA9	SPA10	
P61	SPA11	SPA1	
S 2	TUR2	TUR1	
S 9	TUR3	TUR3	
S 13	TUR4	TUR31	
S 14	TUR5	TUR4	
S 15	TUR3	TUR3	
S 16	TUR3	TUR3	
S 19	TUR6	TUR5	
S 20	TUR7	TUR6	
S30	TUR8	TUR11	
S31	TUR9	TUR12	
S33	TUR10	TUR14	
S53	TUR11	TUR20	
S69	TUR12	TUR25	
S77	TUR13	TUR26	

S78	TUR14	TUR27	
S99	TUR17	TUR35	
S104	TUR18	TUR37	
S107	TUR19	TUR39	
S111	TUR21	TUR40	
S112	TUR22	TUR41	
S117	TUR23	TUR44	
S119	TUR24	TUR45	
S120	TUR17	TUR35	
S121	TUR25	TUR46	
S124	TUR26	TUR48	
S135	TUR28	TUR51	
S136	TUR29	TUR52	
S138	TUR30	TUR53	
S142	TUR32	TUR54	
S144	TUR33	TUR55	
S146	TUR34	TUR56	
S149	TUR35	TUR58	
S154	TUR36	TUR62	
U66	TUN10		TUN1
MI2	IND1		IND2
IR19	IRA7		IRA4

Lab code in	Haplotype	Host	Origin	GenBank accession nr
Tartu			0	
V8	GRE1	Sheep	Greece	
HS4	ROM1	Cattle	Romania	
Fin16	FIN1	Human	Finland, Algerian patien	t
IT3	ITA1	Cattle	Italy. South	
IT10	ITA2	Cattle	Italy, North	
HIP9	ITA3	Human	Italy Pavia	
AC3	ITA4	Sheep	Italy Sicily island	
AC4	ITA4	Sheep	Italy, Sicily island	
2G	SPA1	Human	Spain	
20 7G	ROM2	Human	Romania	
12G	SPA2	Wild boar	Spain	
ALB3	ALB1	Sheep	Albania Tirana	
ALB4	ALB2	Sheep	Albania Tirana	
4150	MOR1	Cattle	Morocco Sidi Kacem	
5455	FRA1	Cattle	France Oloron-Sainte-N	farie
6200	MOL1	Sheen	Moldova Centre	
6214	MOL2	Cattle	Moldova Centre	
6187	MOL3	Sheen	Moldova South	
P2	SPA3	Sheep	Central Spain	
P3	SPA4	Sheep	Central Spain	
P4	SPA4	Sheep	Central Spain	
P15	SPA5	Sheep	Central Spain	
P16	SPA6	Sheep	Central Spain	
P21	SPA7	Sheep	Central Spain	
P47	SPA8	Pig	Spain Segovia	
P51	SPA9	Goat	Central Spain	
P52	SPA10	Goat	Central Spain	
P53	SPA9	Goat	Central Spain	
P61	SPA11	Human	Spain, Madrid	
U3	TUN1	Sheep	Tunisia, Sousse	
U8	TUN2	Sheep	Tunisia, Sousse	
U11	TUN3	Sheep	Tunisia, Sousse	
U17	TUN4	Sheep	Tunisia, Sousse	
U30	TUN5	Sheep	Tunisia, Sousse	
U32	TUN6	Sheep	Tunisia, Sousse	
U33	TUN7	Sheep	Tunisia, Sousse	
U44	TUN8	Sheep	Tunisia, Sousse	
U57	TUN8	Sheep	Tunisia, Sousse	
U62	TUN9	Sheep	Tunisia, Sousse	
U66	TUN10	Sheep	Tunisia, Kairouan	
U80	TUN10	Sheep	Tunisia, Kairouan	
U82	TUN11	Sheep	Tunisia, Kairouan	
U110	TUN12	Sheep	Tunisia, Kairouan	
U117	TUN13	Sheep	Tunisia, Kasserine	
U118	TUN14	Sheep	Tunisia, Kasserine	
U120	TUN15	Sheep	Tunisia, Gafsa	

Table S3Data for the 211 *Echinococcus granulosus* sensu stricto G1 isolates sequenced in this study.

$ \begin{array}{ccccc} U154 & TUN16 & Cattle & Tunisia, Monastir \\ U167 & TUN17 & Cattle & Tunisia, Kasserine \\ U183 & TUN17 & Cattle & Tunisia, Kasserine \\ S1 & TUR1 & Sheep & Turkey, Elazig \\ S2 & TUR2 & Sheep & Turkey, Elazig \\ S1 & TUR1 & Sheep & Turkey, Elazig \\ S1 & TUR1 & Sheep & Turkey, Elazig \\ S12 & TUR1 & Sheep & Turkey, Elazig \\ S13 & TUR4 & Sheep & Turkey, Elazig \\ S14 & TUR5 & Sheep & Turkey, Elazig \\ S16 & TUR3 & Sheep & Turkey, Elazig \\ S16 & TUR3 & Sheep & Turkey, Elazig \\ S20 & TUR7 & Cattle & Turkey, Elazig \\ S10 & TUR8 & Cattle & Turkey, Elazig \\ S20 & TUR7 & Cattle & Turkey, Elazig \\ S30 & TUR8 & Cattle & Turkey, Elazig \\ S30 & TUR8 & Cattle & Turkey, Erzurum \\ S31 & TUR9 & Cattle & Turkey, Erzurum \\ S33 & TUR10 & Cattle & Turkey, Erzurum \\ S43 & TUR10 & Cattle & Turkey, Erzurum \\ S43 & TUR11 & Cattle & Turkey, Erzurum \\ S78 & TUR14 & Cattle & Turkey, Erzurum \\ S78 & TUR14 & Cattle & Turkey, Erzurum \\ S104 & TUR16 & Cattle & Turkey, Erzurum \\ S104 & TUR16 & Cattle & Turkey, Erzurum \\ S109 & TUR20 & Sheep & Turkey, Elazig \\ S111 & TUR21 & Sheep & Turkey, Elazig \\ S112 & TUR22 & Sheep & Turkey, Elazig \\ S114 & TUR23 & Sheep & Turkey, Elazig \\ S117 & TUR23 & Sheep & Turkey, Elazig \\ S118 & TUR24 & Sheep & Turkey, Elazig \\ S119 & TUR26 & Sheep & Turkey, Elazig \\ S120 & TUR17 & Sheep & Turkey, Elazig \\ S121 & TUR22 & Sheep & Turkey, Elazig \\ S122 & TUR23 & Sheep & Turkey, Elazig \\ S135 & TUR24 & Sheep & Turkey, Elazig \\ S144 & TUR26 & Sheep & Turkey, Elazig \\ S144 & TUR26 & Sheep & Turkey, Elazig \\ S144 & TUR30 & Sheep & Turkey, Elazig \\ S144 & TUR30 & Sheep & Turkey, Elazig \\ S144 & TUR30 & Sheep & Turkey, Elazig \\ S144 & TUR30 & Sheep & Turkey, Elazig \\ S144 & TUR30 & Sheep & Turkey, Elazig \\ S144 & TUR30 & Sheep & Turkey, Elazig \\ S144 & TUR31 & Sheep & Turkey, Elazig \\ S144 & TUR33 & Sheep & Turkey, Elazig \\ S144 & TUR33 & Sheep & Turkey, Elazig \\ S144 & TUR34 & Sheep & Turkey, Elazig \\ S144 & TUR33 & Sheep & Turkey, Elazig \\ S144 & TUR34 & Sheep & Turkey, Elazig \\ S144 & TUR34 & Sheep & Turkey, Elazig$	U141	TUN14	Cattle	Tunisia, Sousse
U167TUN17CattleTunisia, KasserineU183TUN17CattleTunisia, KasserineS1TUR1SheepTurkey, ElazigS2TUR2SheepTurkey, ElazigS7TUR1SheepTurkey, ElazigS12TUR1SheepTurkey, ElazigS13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS17TUR6CattleTurkey, ElazigS30TUR7CattleTurkey, ElazigS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS77TUR12CattleTurkey, ErzurumS78TUR12CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS107TUR18CattleTurkey, ElazigS110TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS114TUR23SheepTurkey, ElazigS115TUR24SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, Elazig <t< td=""><td>U154</td><td>TUN16</td><td>Cattle</td><td>Tunisia, Monastir</td></t<>	U154	TUN16	Cattle	Tunisia, Monastir
U183TUN17CattleTunisia, KasserineS1TUR1SheepTurkey, ElazigS2TUR2SheepTurkey, ElazigS7TUR1SheepTurkey, ElazigS9TUR3SheepTurkey, ElazigS112TUR1SheepTurkey, ElazigS12TUR3SheepTurkey, ElazigS13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS20TUR7CattleTurkey, ElazigS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS33TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS107TUR16CattleTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR24SheepTurkey, ElazigS114TUR25SheepTurkey, ElazigS	U167	TUN17	Cattle	Tunisia, Kasserine
S1TUR1SheepTurkey, ElazigS2TUR2SheepTurkey, ElazigS7TUR1SheepTurkey, ElazigS9TUR3SheepTurkey, ElazigS12TUR1SheepTurkey, ElazigS13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS20TUR7CattleTurkey, ElazigS30TUR8CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS99TUR16CattleTurkey, ErzurumS104TUR18CattleTurkey, ElazigS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR21SheepTurkey, ElazigS113TUR22SheepTurkey, ElazigS114TUR23SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS112TUR24SheepTurkey, ElazigS113TUR25SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS	U183	TUN17	Cattle	Tunisia, Kasserine
S2TUR2SheepTurkey, ElazigS7TUR1SheepTurkey, ElazigS9TUR3SheepTurkey, ElazigS12TUR1SheepTurkey, ElazigS13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS10TUR6CattleTurkey, ElazigS30TUR6CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS91TUR15CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR21SheepTurkey, ElazigS113TUR20SheepTurkey, ElazigS114TUR21SheepTurkey, ElazigS115TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS112TUR24SheepTurkey, ElazigS113TUR25SheepTurkey, ElazigS114TUR26SheepTurkey, ElazigS115TUR27SheepTurkey, Elazig <td< td=""><td>S1</td><td>TUR1</td><td>Sheep</td><td>Turkey, Elazig</td></td<>	S1	TUR1	Sheep	Turkey, Elazig
S7TUR1SheepTurkey, ElazigS9TUR3SheepTurkey, ElazigS12TUR1SheepTurkey, ElazigS13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS10TUR6CattleTurkey, ElazigS20TUR7CattleTurkey, ElazigS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS107TUR18CattleTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR21SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR23SheepTurkey, ElazigS114TUR24SheepTurkey, ElazigS115TUR23SheepTurkey, ElazigS111TUR24SheepTurkey, ElazigS112TUR23SheepTurkey, ElazigS114TUR24SheepTurkey, ElazigS129TUR27SheepTurkey, Elazig <tr< td=""><td>S2</td><td>TUR2</td><td>Sheep</td><td>Turkey, Elazig</td></tr<>	S2	TUR2	Sheep	Turkey, Elazig
S9TUR3SheepTurkey, ElazigS12TUR1SheepTurkey, ElazigS13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS19TUR6CattleTurkey, ElazigS30TUR8CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR21SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR20SheepTurkey, ElazigS113TUR21SheepTurkey, ElazigS114TUR23SheepTurkey, ElazigS115TUR24SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS118TUR26SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS136TUR28SheepTurkey, Elazig <td>S7</td> <td>TUR1</td> <td>Sheep</td> <td>Turkey, Elazig</td>	S7	TUR1	Sheep	Turkey, Elazig
S12TUR1SheepTurkey, ElazigS13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS19TUR6CattleTurkey, ElazigS20TUR7CattleTurkey, ElazigS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR16CattleTurkey, ErzurumS104TUR17CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS114TUR24SheepTurkey, ElazigS115TUR23SheepTurkey, ElazigS111TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS111TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS144TUR26SheepTurkey, Elazig<	S9	TUR3	Sheep	Turkey, Elazig
S13TUR4SheepTurkey, ElazigS14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS19TUR6CattleTurkey, ElazigS20TUR7CattleTurkey, ElazigS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS33TUR11CattleTurkey, ErzurumS53TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS104TUR18CattleTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS114TUR23SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR26SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS135TUR26SheepTurkey, ElazigS14TUR26SheepTurkey, ElazigS15TUR26SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS136TUR26SheepTurkey, ElazigS141TUR26SheepTurkey, Elazig <td>S12</td> <td>TUR1</td> <td>Sheep</td> <td>Turkey, Elazig</td>	S12	TUR1	Sheep	Turkey, Elazig
S14TUR5SheepTurkey, ElazigS15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS19TUR6CattleTurkey, ElazigS20TUR7CattleTurkey, ElazigS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR16CattleTurkey, ErzurumS107TUR18CattleTurkey, ErzurumS104TUR16CattleTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS114TUR23SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS14TUR31SheepTurkey, ElazigS15TUR28SheepTurkey, ElazigS144TUR30SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR31SheepTurkey, Elazig </td <td>S13</td> <td>TUR4</td> <td>Sheep</td> <td>Turkey, Elazig</td>	S13	TUR4	Sheep	Turkey, Elazig
S15TUR3SheepTurkey, ElazigS16TUR3SheepTurkey, ElazigS19TUR6CattleTurkey, ElazigS20TUR7CattleTurkey, ElazigS30TUR8CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS104TUR17CattleTurkey, ErzurumS107TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS114TUR24SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS136TUR28SheepTurkey, ElazigS136TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, Elazi	S14	TUR5	Sheep	Turkey, Elazig
S16TUR3SheepTurkey, ElazigS19TUR6CattleTurkey, ElazigS20TUR7CattleTurkey, ElazigS30TUR8CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS83TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS111TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS141TUR26SheepTurkey, ElazigS154TUR30SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR32SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR32SheepTurkey, Elaz	S15	TUR3	Sheep	Turkey, Elazig
S19TUR6CattleTurkey, ElazigS20TUR7CattleTurkey, ElazigS30TUR8CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS111TUR20SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS114TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR23SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS154TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS145TUR32SheepTurkey, ElazigS146TUR34SheepTurkey,	S16	TUR3	Sheep	Turkey, Elazig
S20TUR7CattleTurkey, ElazigS30TUR8CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS8TUR14CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR21SheepTurkey, ElazigS114TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR26SheepTurkey, ElazigS135TUR27SheepTurkey, ElazigS136TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS144TUR31SheepTurkey, ElazigS145TUR32SheepTurkey, ElazigS146TUR34SheepTurkey, E	S19	TUR6	Cattle	Turkey, Elazig
S30TUR8CattleTurkey, ErzurumS31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS99TUR15CattleTurkey, ErzurumS104TUR16CattleTurkey, ErzurumS107TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR17SheepTurkey, ElazigS111TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR30SheepTurkey, ElazigS145TUR32SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS147TUR35CattleTurkey, ElazigS148TUR20SheepTurkey	S20	TUR7	Cattle	Turkey, Elazig
S31TUR9CattleTurkey, ErzurumS33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS122TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS137TUR30SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS145TUR30SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS147TUR35CattleTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey	S30	TUR8	Cattle	Turkey, Erzurum
S33TUR10CattleTurkey, ErzurumS53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS122TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR32SheepTurkey, ElazigS145TUR36SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS147TUR35CattleTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS140TUR36SheepTurkey	S31	TUR9	Cattle	Turkey, Erzurum
S53TUR11CattleTurkey, ErzurumS69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS110TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS114TUR23SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS145TUR36SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS147TUR35CattleTurkey, ElazigS148TUR20SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS145TUR36SheepTurkey	S33	TUR10	Cattle	Turkey, Erzurum
S69TUR12CattleTurkey, ErzurumS77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS111TUR20SheepTurkey, ElazigS112TUR21SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS114TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS122TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS145TUR36SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR36SheepTurkey	S53	TUR11	Cattle	Turkey, Erzurum
S77TUR13CattleTurkey, ErzurumS78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS122TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS145TUR36SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR36SheepTurkey,	S69	TUR12	Cattle	Turkey, Erzurum
S78TUR14CattleTurkey, ErzurumS83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS137TUR28SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR30SheepTurkey, ElazigS144TUR31SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS145TUR35CattleTurkey, ElazigS146TUR36SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR36SheepTurkey, E	S77	TUR13	Cattle	Turkey, Erzurum
S83TUR15CattleTurkey, ErzurumS91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS114TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS122TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS145TUR34SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR36SheepTurkey, ElazigS149TUR36SheepTurkey, ElazigS149TUR36SheepTurkey, ElazigS149TUR36SheepTurkey, Elaz	S78	TUR14	Cattle	Turkey, Erzurum
S91TUR16CattleTurkey, ErzurumS99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS113TUR23SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS145TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR36SheepTurkey, ElazigS149TUR36SheepTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustralia<	S83	TUR15	Cattle	Turkey, Erzurum
S99TUR17CattleTurkey, ErzurumS104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS122TUR26SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS145TUR36SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR36SheepTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustralia	S91	TUR16	Cattle	Turkey, Erzurum
S104TUR18CattleTurkey, ErzurumS107TUR19SheepTurkey, ElazigS109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS112TUR23SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS145TUR35CattleTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS149TUR36SheepTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S99	TUR17	Cattle	Turkey, Erzurum
S107TUR19SheepTurkey, ElazigS109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS122TUR26SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR27SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS137TUR28SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S104	TUR18	Cattle	Turkey, Erzurum
S109TUR20SheepTurkey, ElazigS111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR27SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS137TUR28SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS145TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S107	TUR19	Sheep	Turkey, Elazig
S111TUR21SheepTurkey, ElazigS112TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS135TUR27SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS137TUR28SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR35CattleTurkey, ElazigS145TUR32SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S109	TUR20	Sheep	Turkey, Elazig
S112TUR22SheepTurkey, ElazigS117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS145TUR32SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S111	TUR21	Sheep	Turkey, Elazig
S117TUR23SheepTurkey, ElazigS119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS137TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS148TUR35CattleTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S112	TUR22	Sheep	Turkey, Elazig
S119TUR24SheepTurkey, ElazigS120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S117	TUR23	Sheep	Turkey, Elazig
S120TUR17SheepTurkey, ElazigS121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S119	TUR24	Sheep	Turkey, Elazig
S121TUR25SheepTurkey, ElazigS124TUR26SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS145TUR20SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S120	TUR17	Sheep	Turkey, Elazig
S124TUR26SheepTurkey, ElazigS129TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S121	TUR25	Sheep	Turkey, Elazig
S129TUR27SheepTurkey, ElazigS135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S124	TUR26	Sheep	Turkey, Elazig
S135TUR28SheepTurkey, ElazigS136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR34SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S129	TUR27	Sheep	Turkey, Elazig
S136TUR29SheepTurkey, ElazigS138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S135	TUR28	Sheep	Turkey, Elazig
S138TUR30SheepTurkey, ElazigS141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S136	TUR29	Sheep	Turkey, Elazig
S141TUR31SheepTurkey, ElazigS142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S138	TUR30	Sheep	Turkey, Elazig
S142TUR32SheepTurkey, ElazigS144TUR33SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S141	TUR31	Sheep	Turkey, Elazig
S144TUR33SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S142	TUR32	Sheep	Turkey, Elazig
S146TUR34SheepTurkey, ElazigS148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S144	TUR33	Sheep	Turkey, Elazig
S148TUR20SheepTurkey, ElazigS149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S146	TUR34	Sheep	Turkey, Elazig
S149TUR35CattleTurkey, ElazigS154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S148	TUR20	Sheep	Turkey, Elazig
S154TUR36SheepTurkey, ElazigJ1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S149	TUR35	Cattle	Turkey, Elazig
J1AUS1DingoAustraliaJ2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	S154	TUR36	Sheep	Turkey. Elazig
J2AUS2DingoAustraliaJ3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	J1	AUS1	Dingo	Australia
J3AUS3DingoAustraliaOU2TUN18HumanTunisia, Kasserine	J2	AUS2	Dingo	Australia
OU2 TUN18 Human Tunisia, Kasserine	J3	AUS3	Dingo	Australia
	OU2	TUN18	Human	Tunisia, Kasserine

OU3	TUN19	Human	Tunisia, Sidi bouzid
OU5	TUN20	Human	Tunisia, Sidi bouzid
OU6	TUN20	Human	Tunisia, Sidi bouzid
OU7	TUN21	Human	Tunisia, Sidi bouzid
OU9	TUN22	Human	Tunisia, Sidi bouzid
OU10	TUN15	Human	Tunisia, Kasserine
OU12	TUN23	Human	Tunisia. Sidi bouzid
OU13	TUN24	Human	Tunisia, Kasserine
OU14	TUN25	Human	Tunisia, Gafsa
OU15	TUN5	Human	Tunisia, Kasserine
OU16	TUN26	Human	Tunisia Mahdia
OU17	TUN27	Human	Tunisia Kairouan
OU18	TUN5	Human	Tunisia Mahdia
OU20	TUN28	Human	Tunisia, Kairouan
OU21	TUN29	Human	Tunisia, Kairouan
0U23	TUN30	Human	Tunisia, Mahdia
VA1		Goat	Italy Sardinia
VA3		Sheen	Italy, Sardinia
VAS VA6		Sheen	Italy, Sardinia
VAO VA7		Sheen	Italy, Sardinia
VA/		Sheen	Italy, Sardinia
VA14 VA16	CDE1	Sheep	Graage
VAIO VA17	CPE2	Sheep	Greece
VAI/ 7A11	ALC1	Jumon	Algoria
ZATT 7A12	ALG1	Human	Algeria Vhanahla
ZA12	ALG2	Human	Algeria, Kilencina
ZA15	ALG5	Human	Algeria, Boulla
ZA20	ALG4	Human	Algeria, Tipaza
ZA23	ALGS	Human	Algeria, Ain Della
ZA24	ALG6	Human	Algeria, Lagnouat
ZA25	ALG/	Human	Algeria, Ouargia
ZA26	ALG8	Human	Algeria, Ain Defla
ZA2/	ALG9	Human	Algeria, Blida
ZA31	ALGIO	Human	Algeria, Boumerdes
ZA32	ALGII	Human	Algeria, Ain Defla
ZA34	ALG12	Human	Algeria, Ain Defla
Al	ARBI	Cattle	Argentina, 9 de Julio
A2	ARG1	Cattle	Argentina, Castelli
A10	ARG2	Pig	Argentina, Buenos Aires
A13	ARG3	Cattle	Argentina, Balcarce
A17	ARG4	Sheep	Argentina, Tres Arroyos
A19	ARG5	Sheep	Argentina, Tres Arroyos
A21	ARG6	Sheep	Argentina, Tres Arroyos
A23	ARB1	Sheep	Argentina, Mar del Plata
A24	ARB1	Sheep	Argentina, Mar del Plata
A29	ARB1	Sheep	Argentina, Mar del Plata
A30	ARB1	Sheep	Argentina, Mar del Plata
A35	ARB2	Cattle	Argentina, Balcarce
A37	ARB1	Cattle	Argentina, Tres Arroyos
A40	ARG7	Cattle	Argentina, Ayacucho
A41	ARG8	Cattle	Argentina, Balcarce

A42	ARG9	Cattle	Argentina, Balcarce
A43	ARG10	Cattle	Argentina, San Cayetano
A47	ARB1	Sheep	Argentina, Mar del Plata
A50	ARB1	Sheep	Argentina, Mar del Plata
A52	ARB1	Sheep	Argentina, Mar del Plata
A53	ARB1	Sheep	Argentina, Mar del Plata
A54	ARB1	Sheep	Argentina, Tres Arroyos
A55	ARB1	Sheep	Argentina, Tres Arroyos
A57	ARG11	Sheep	Argentina, Tres Arroyos
TŠ6	CHI1	Cattle	Chile, Coquimbo
TŠ13	CHI2	Cattle	Chile, Illapel
TŠ14	CHI1	Cattle	Chile, Illapel
TŠ15	CHI3	Cattle	Chile. Illapel
TŠ16	CHI4	Cattle	Chile, Illapel
TŠ18	CHI2	Cattle	Chile Illapel
H172	BRA2	Cattle	Brazil Cachoeira do Sul
H369	BRA3	Cattle	Brazil Cacapava do Sul
H404	BRA4	Cattle	Brazil Herval
H408	BRA1	Cattle	Brazil Arroio Grande
H474	BRAG	Cattle	Brazil
H429	BR A 1	Cattle	Brazil
H433	ARR1	Cattle	Brazil Sao Gabriel
H439	$RR \Delta 7$	Cattle	Brazil Sao Gabriel
H440	BRA8	Cattle	Brazil Sao Gabriel
H440	BRAG	Cattle	Brazil
H567	ARB2	Cattle	Brazil Alegrete
H574	RRA10	Cattle	Brazil Bagé
H575	BRA10 BRA5	Cattle	Brazil Livramento
П575 Ц585		Cattle	Brazil Alagrata
II J 6 J 1	ID A 1	Shoon	Iran Colostan
IC 11 ID 12		Shoop	Iran, Golestan
IK 12 ID 12		Sheep	Iran, Golestan
IK 15 ID 14		Sheep	Iran, Golestan
IK 14 ID 17		Sheep	Iran, Golestan
IK 1/	IRAS	Sheep	Iran, Mazandaran
IK 18 ID 10		Sheep	Iran, Mazandaran
IK 19 ID 21	IKA/	Sheep	Iran, Mazandaran
IK 21 ID 22		Sheep	Iran, Tehran
IK 22	IRA2	Sheep	Iran, Tenran
IK 23	IRA2	Sheep	Iran, Tenran
IR 24	IRA9	Sheep	Iran, Tehran
IR 27	IRA10	Sheep	Iran, Tehran
IR 29	IRAII	Sheep	Iran, Tehran
IR 31	IRA12	Sheep	Iran, Istahan
IR 32	IRA13	Sheep	Iran, Isfahan
IR 33	IRA14	Sheep	Iran, Isfahan
IR 35	IRA15	Goat	Iran, Isfahan
IR 46	IRA3	Human	Iran, Isfahan
IR 47	IRA3	Human	Iran, Isfahan
IR 49	IRA16	Cattle	Iran, Isfahan
IR 51	IRA17	Cattle	Iran, Isfahan

IR 52	IRA18	Cattle	Iran, Isfahan
P66	ARG12	Cattle	Argentina
P67	ARG13	Cattle	Argentina
P68	ARB1	Cattle	Argentina
P69	ARG14	Cattle	Argentina
P70	ARG15	Cattle	Argentina
P76	ARG16	Sheep	Argentina
J86	MON2	Human	Mongolia
J88	MON1	Human	Mongolia
J91	MON1	Human	Mongolia
SO212	ARG17	Sheep	Argentina, Neuquen
N1	IRA19	Goat	Iran, Lorestan
B20	KAZ1	Human	Kazakhstan
8G	MEX1	Pig	Mexico
MI2	IND1	Buffalo	India



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Highlights

- 11 682 bp of mtDNA was analysed for 222 *E. granulosus* s. s. samples globally
- G1 and G3 are distinct mitochondrial genotypes
- The genetic diversity of *E. granulosus* s. s. G1 is extremely high globally
- The main diffusion routes of G1 originated from Turkey, Tunisia and Argentina
- Livestock trade has greatly influenced the present-day diversity of genotype G1

Global phylogeography of E. granulosus s. s. genotype G1

