**High-resolution phylogeography of zoonotic tapeworm Echinococcus granulosus sensu stricto genotype G1 with an emphasis on its distribution in Turkey, Italy and Spain.**

Liina Kinkar, Teivi Laurimäe, Sami Simsek, Ibrahim Balkaya, Adriano Casulli, Maria Teresa Manfredi, Francisco Ponce-Gordo, Antonio Varcasia, Antti Lavikainen, Luis Miguel González, Steffen Rehbein, Joke van der Giessen, Hein Sprong, Urmas Saarma\*

\* Corresponding author: Department of Zoology, Institute of Ecology and Earth Sciences, University of Tartu, Vanemuise 46, 51014 Tartu, Estonia. E-mail: Urmas.Saarma@ut.ee

**Supplementary Information**

**Table S1.** Diversity and neutrality indices for *E. granulosus* s. s. genotype G1 in Europe based on 1674 bp (*cox1*) of mtDNA. The Southern European samples (South Eur) included all samples except Turkish and Finnish (Algerian).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Diversity |  |  |  | Neutrality |  |
|  | n | Hn | Hd ± S.D. | π± S.D. | *D* | Fs |
|  Total*Origin* Turkey Spain Italy South Eur*Host* Cattle Sheep | 9169107214243 | 493773122426 | 0.920 ± 0.0230.939 ± 0.0190.867 ± 0.1070.524 ± 0.2090.786 ± 0.0960.937 ± 0.0240.905 ± 0.039 | 0.00196 ± 0.000190.00202 ± 0.000210.00143 ± 0.000480.00051 ± 0.000250.00159 ± 0.000430.00171 ± 0.000200.00217 ± 0.00031 | -2.49144\*\* -2.30562\* -1.96119\* -1.35841 -2.13632\*-2.11559\*\*-2.28186\*\* | -26.27676\*\*-26.23723\*\*-9.51463\*\*-9.21700\*\*-26.54614\*\*-26.41819\*\*-26.02824\*\*  |

Abbreviations: 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.).

\*\*Highly significant P value (P < 0.000001).

\* Significant P value (P < 0.05).

**Table S2.** Diversity and neutrality indices for *E. granulosus* s. s. genotype G1 in Europe based on 351 bp (*cox1*) of mtDNA. The Southern European samples (South Eur) included all samples except Turkish and Finnish (Algerian).

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Diversity |  |  |  | Neutrality |  |
|  | n | Hn | Hd ± S.D. | π± S.D. | *D* | Fs |
|  Total*Origin* Turkey Spain Italy South Eur*Host* Cattle Sheep | 9169107214243 | 11841586 | 0.596 ± 0.0430.621 ± 0.0420.533 ± 0.180-0.486 ± 0.1240.677 ± 0.0490.520 ± 0.070 | 0.00219 ± 0.000250.00231 ± 0.000280.00171 ± 0.00067-0.00174 ± 0.000540.00271 ± 0.000400.00176 ± 0.00031 | -1.43098\*-0.83662-1.56222--1.28742-0.83916-1.16481 | -7.065-3.396-1.964--2.365-3.514-2.720 |

Abbreviations: 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.).

\*\*Highly significant P value (P < 0.000001).

\* Significant P value (P < 0.05).

**Table S3.** Pairwise fixation index (Fst) values between *E. granulosus* s. s. genotype G1 subpopulations based on mtDNA datasets of different length. The Southern European samples (South Eur) included all samples except Turkish and Finnish (Algerian).

|  |  |  |
| --- | --- | --- |
|  | 1 | 2 |
| **8274 bp (mtDNA)**1. Turkey2. Italy3. Spain 4. South Eur**1674 bp (full *cox1*)**1. Turkey2. Italy3. Spain4. South Eur**351 bp (partial *cox1*)**1. Turkey2. Italy3. Spain4. South Eur | 0.02008 0.04064\* 0.016420.004430.008680.01272\*0.109340.070720.03297 | 0.00447 -0.3714-0.03960 |

 \* Significant P value (P < 0.05).