

Molecular characterization of *Fasciola hepatica* from Algerian and Sardinian isolates using mitochondrial DNA and relationships with other areas of the world.

M. CHAOUADI¹, F. SCARPA², I. AZZENA^{2,3}, P. COSSU², KH. HARHOURA⁴, M. AISSI⁴, F. TAZEROUTI¹, G. GARIPPA², P. MERELLA², M. CASU², D. SANNA³

¹ Laboratory of Biodiversity and Environment: Interactions and Genomes, Faculty of Biological Sciences, University of Sciences and Technology Houari Boumediene, Alger, Algeria.

² Department of Veterinary Medicine, University of Sassari, Sassari, Italy.

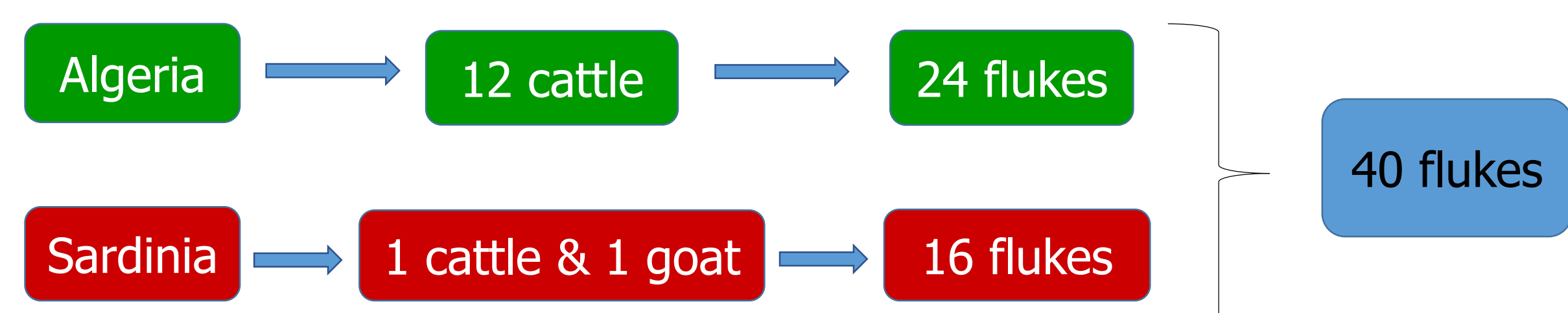
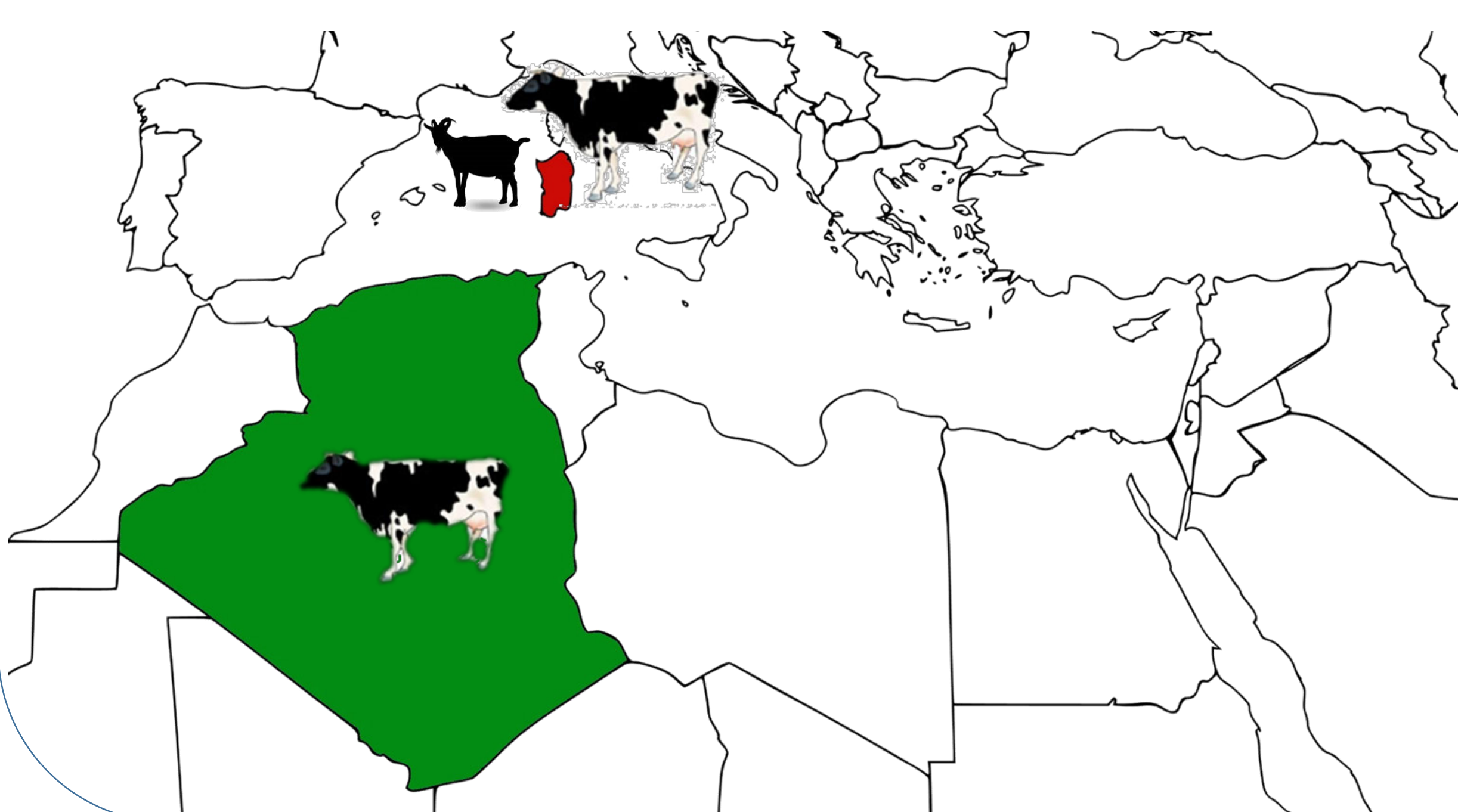
³ Department of Biomedical Sciences, University of Sassari, Sassari, Italy.

⁴ Laboratory of Animal Health and Production, Superior National Veterinary School Rabie Bouchama, Alger, Algeria.

INTRODUCTION

Fasciolosis caused by *Fasciola hepatica* is a hepatobiliary parasitosis affecting herbivores and humans. Despite its economic impact on livestock of Mediterranean countries, a few molecular studies have been conducted on Algerian and Sardinian *Fasciola* flukes. Molecular characterization is essential for the understanding of genetic variability, origin, evolution and expansion of this parasite.

MATERIAL AND METHODS



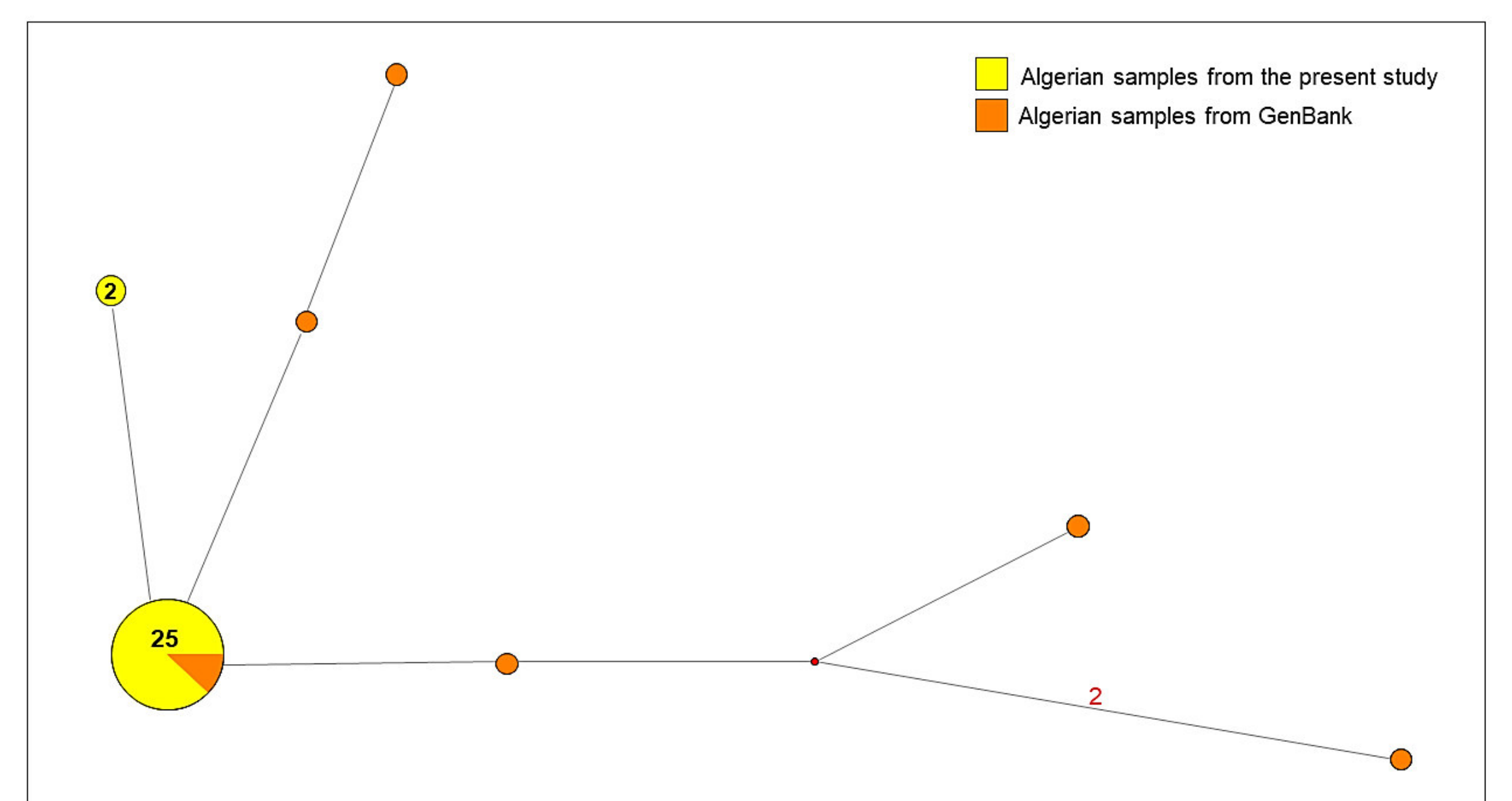
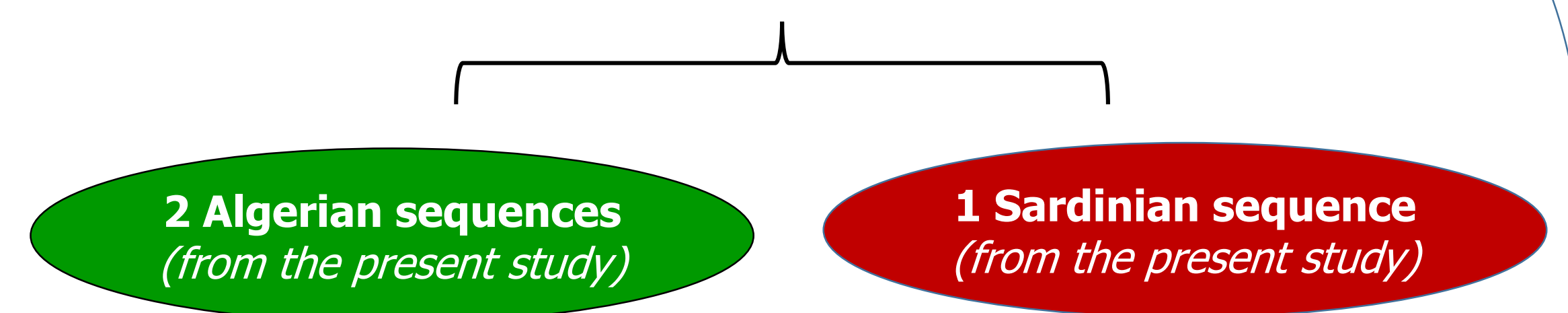
- PCR of the mitochondrial Cytochrome c Oxidase sub. I (COI) gene.
- Phylogenetic and phylogeographic analyses of COI sequences isolated in the present study along with those of *F. hepatica* from all over the world available in GenBank.

RESULTS AND CONCLUSIONS

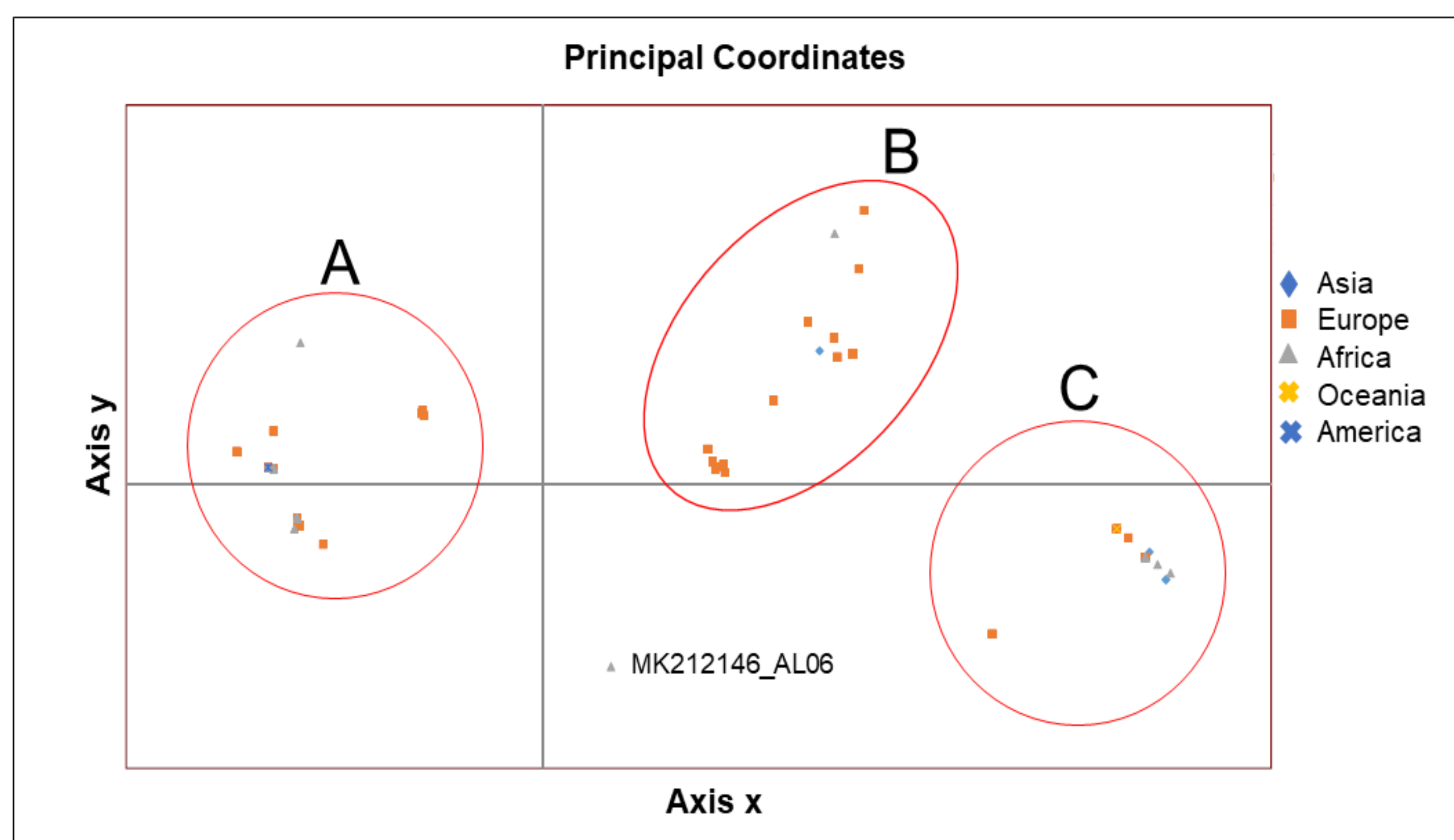


- The 40 flukes analyzed were genetically identified as *Fasciola hepatica*.
- Two new COI lineages for *F. hepatica* were identified in Algerian and Sardinian cattle.
- The other COI sequences from the present study belonged to the most frequent worldwide-diffused haplotype.
- The phylogenetic analysis revealed a genetic similarity between *F. hepatica* isolates from different parts of the world.
- Overall, 3 groups of COI sequences were identified by the Principal Components Analysis (PcoA), with no correlation between genetic structuring and geographic origin of flukes.

Two new COI haplotypes for *F. hepatica*



Median-joining network analysis that includes COI Algerian sequences from the present study along with those from GenBank. The number of mutations between sequences that are greater than 1 are reported on network branches. The number of individuals showing the same haplotype that is greater than 1 is reported inside the spots.



PCoA that shows the genetic differentiation among populations due to the base differences per site found in the dataset. Percentage of variation explained by the first three axes for the COI dataset: 1st = 40.96, 2nd = 13.80, 3rd=9.31.

	N	bp	S	H	hd	π
Algerian samples (present study)	24	441	1	2	0.159	0.00036
Algerian samples (whole dataset)	32	441	7	7	0.393	0.00271
Total COI dataset	187	441	42	32	0.753	0.00664

A very low level of genetic variability among Algerian samples, is the possible consequence of the recent introduction of *F. hepatica* in the country from Europe.

The low levels of genetic variation among isolates from all continents are consistent with a common origin for flukes worldwide distributed.