

THIRD COLLOQUE
CYSTIC ECHINOCOCCOSIS
2025

**NGS APPROACH FOR
ECHINOCOCCUS GRANULOSUS
GENOTYPING :
IMPLEMENTATION OF A
PROTOCOL FOR SYSTEMATIC
TYPING AT THE NATIONAL
REFERENCE CENTER
ECHINOCOCCOSIS**

CNR **Echinococcoses**

UNIVERSITÉ
MARIE & LOUIS
PASTEUR

CHU
BESANÇON

CHRONO
ENVIRONNEMENT



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CONTEXT :

WHY THIS PROJECT ?

NRC-E OBJECTIVES :

- Epidemiological research for a better understanding of patients contamination (clinical latency)
- Link between geographical events of contamination and genotype

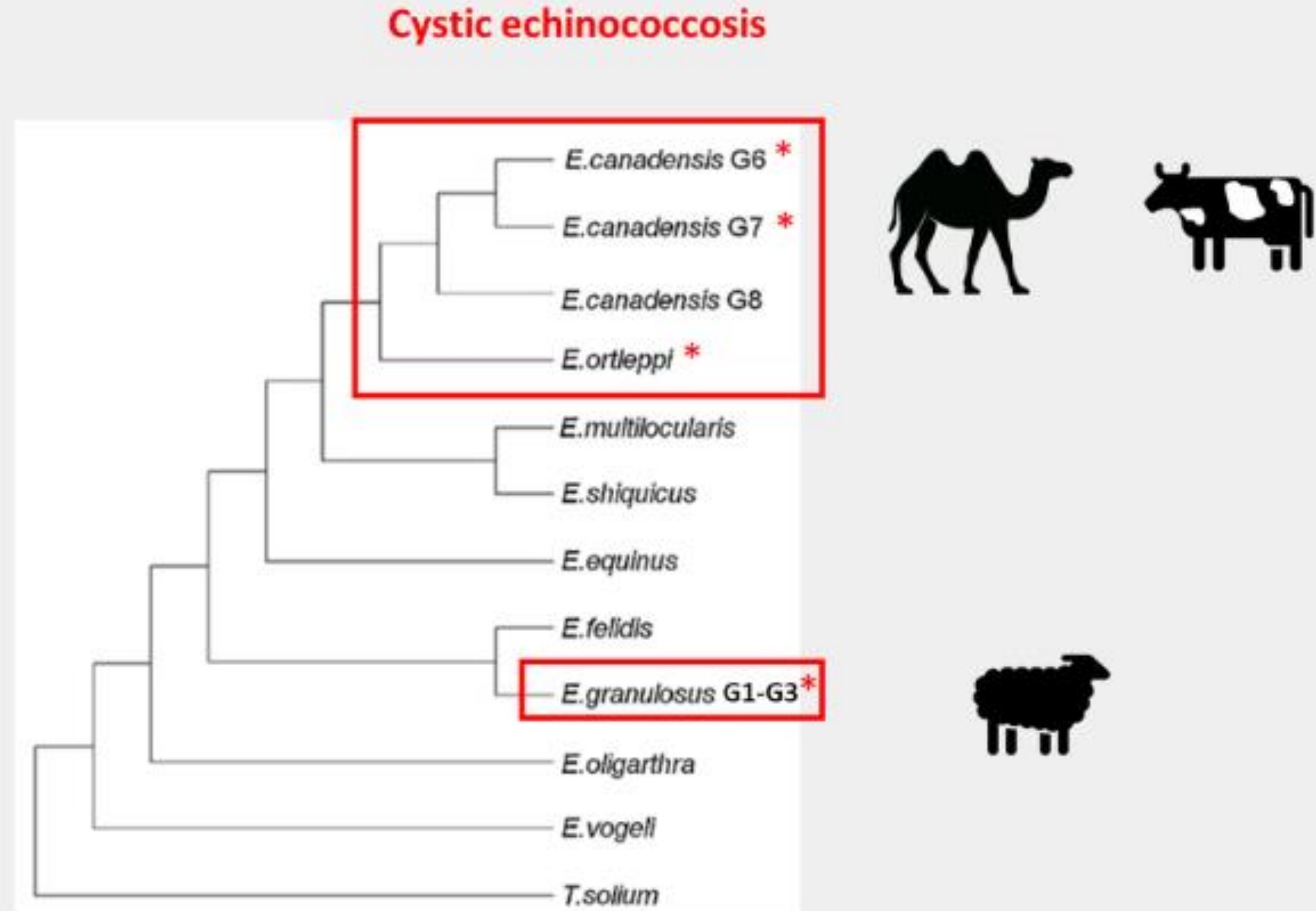
AIM OF THE PROJECT :

Implementation of a systematized protocol of genotyping patients referred to the NRC-E by :

- Trace the origin of the contamination
- Link between genotypes and pathogenicity

CONTEXT :

- TAXONOMY:
Complex of
Echinococcus
granulosus



*described in Human

CONTEXT :

- TAXONOMY:

Complex of *Echinococcus granulosus*

- GENETIC DATA:

Mitochondrial genome : 17461 bp (Nakao et al., 2006)

- GENOTYPE DISTINCTION:

1 to 4 mitochondrial genes (i.e. : CYTB, COX1, NAD5) (Bowles et al., 1993, Kinkar et al., 2018)

- HAPLOTYPES:

Global cohort of **23 samples : ++ haplotypes** (fig. 1) (Kinkar et al., 2017) **vs.** **13 haplotypes** based on full mitogenome of global cohort of **31 *E. multilocularis* samples** (fig. 2) (Bohard et al., 2023)

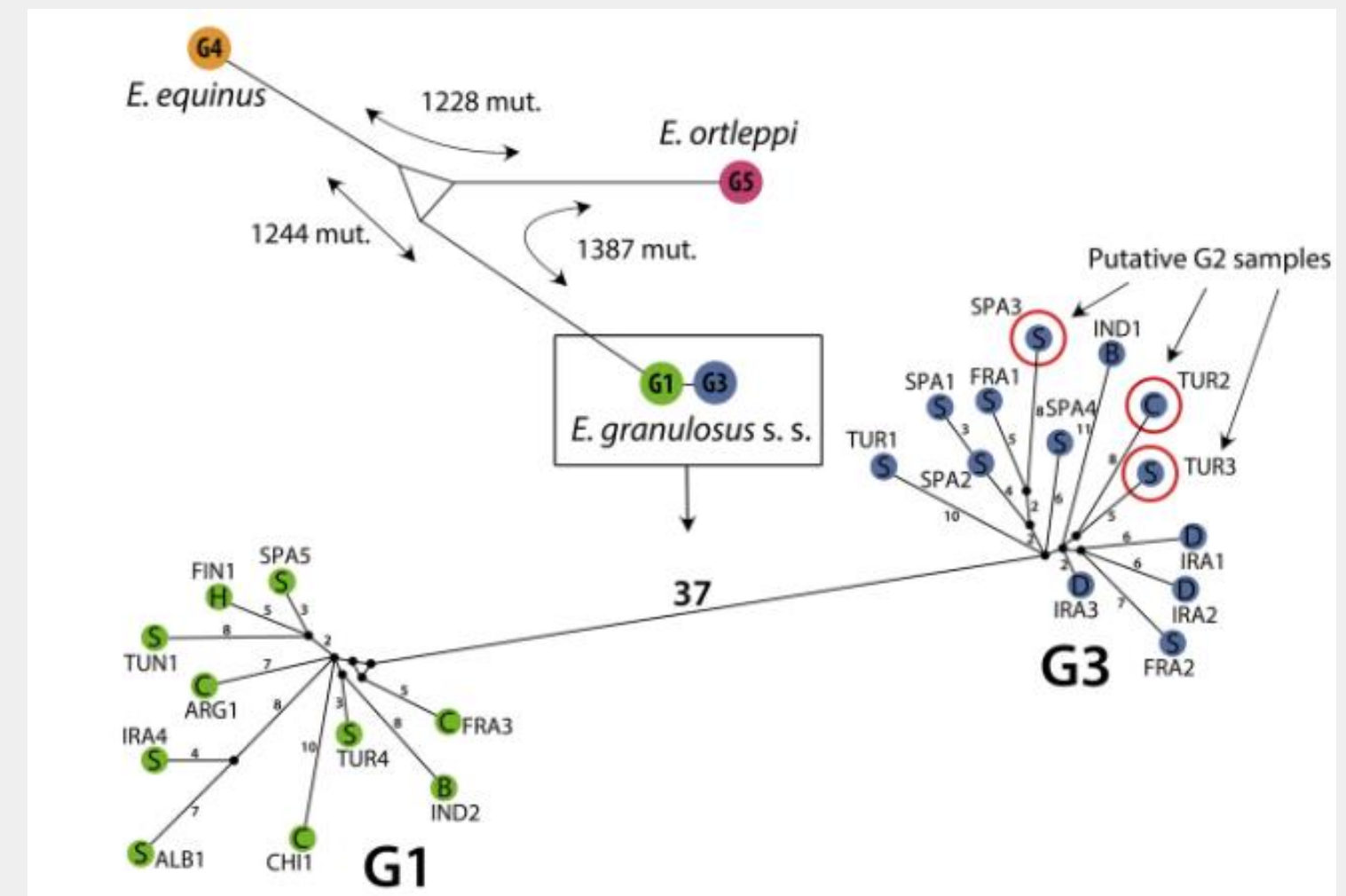


Fig.1 : Haplotype network obtained from 23 samples of *E. granulosus* sensu stricto “near-full mitogenome” (Kinkar et al., 2017)

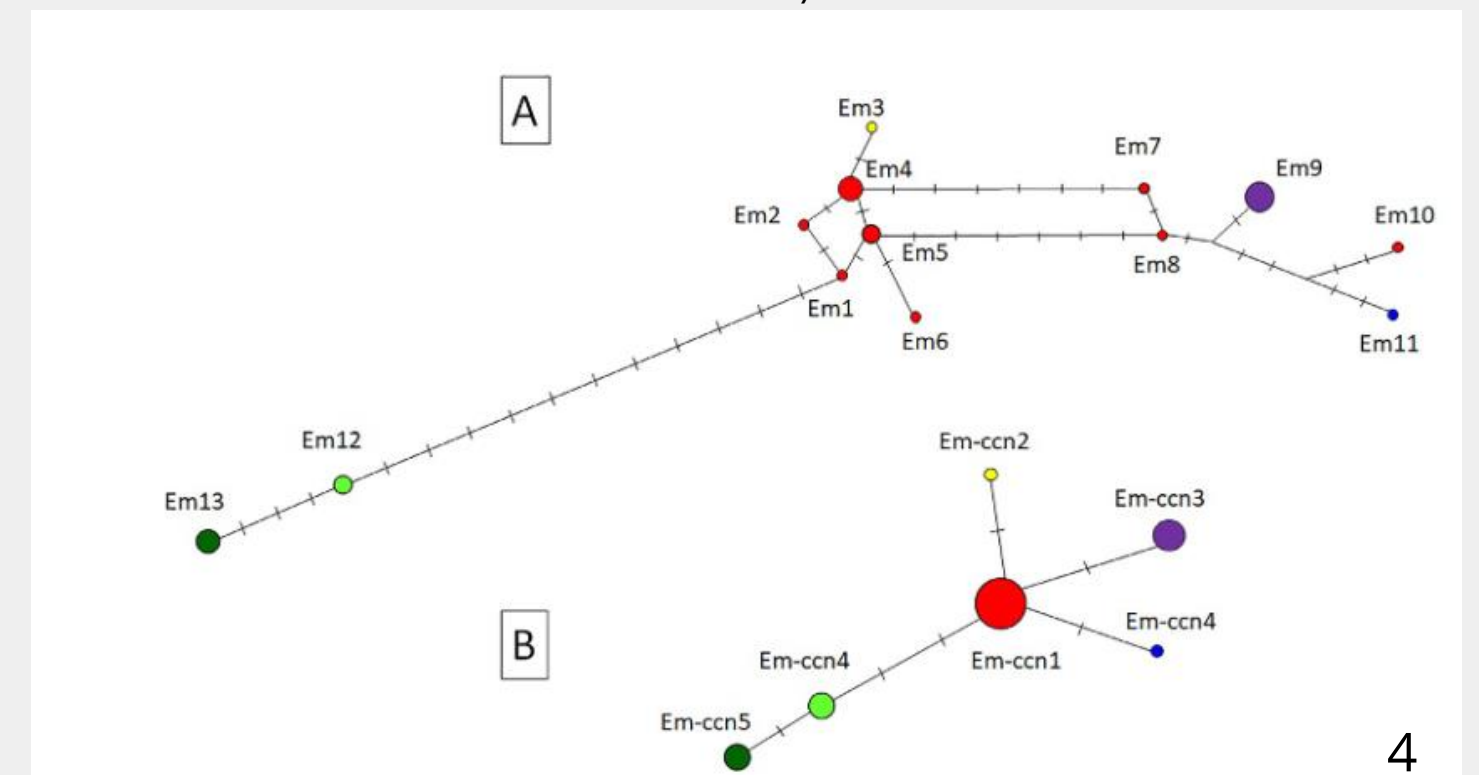
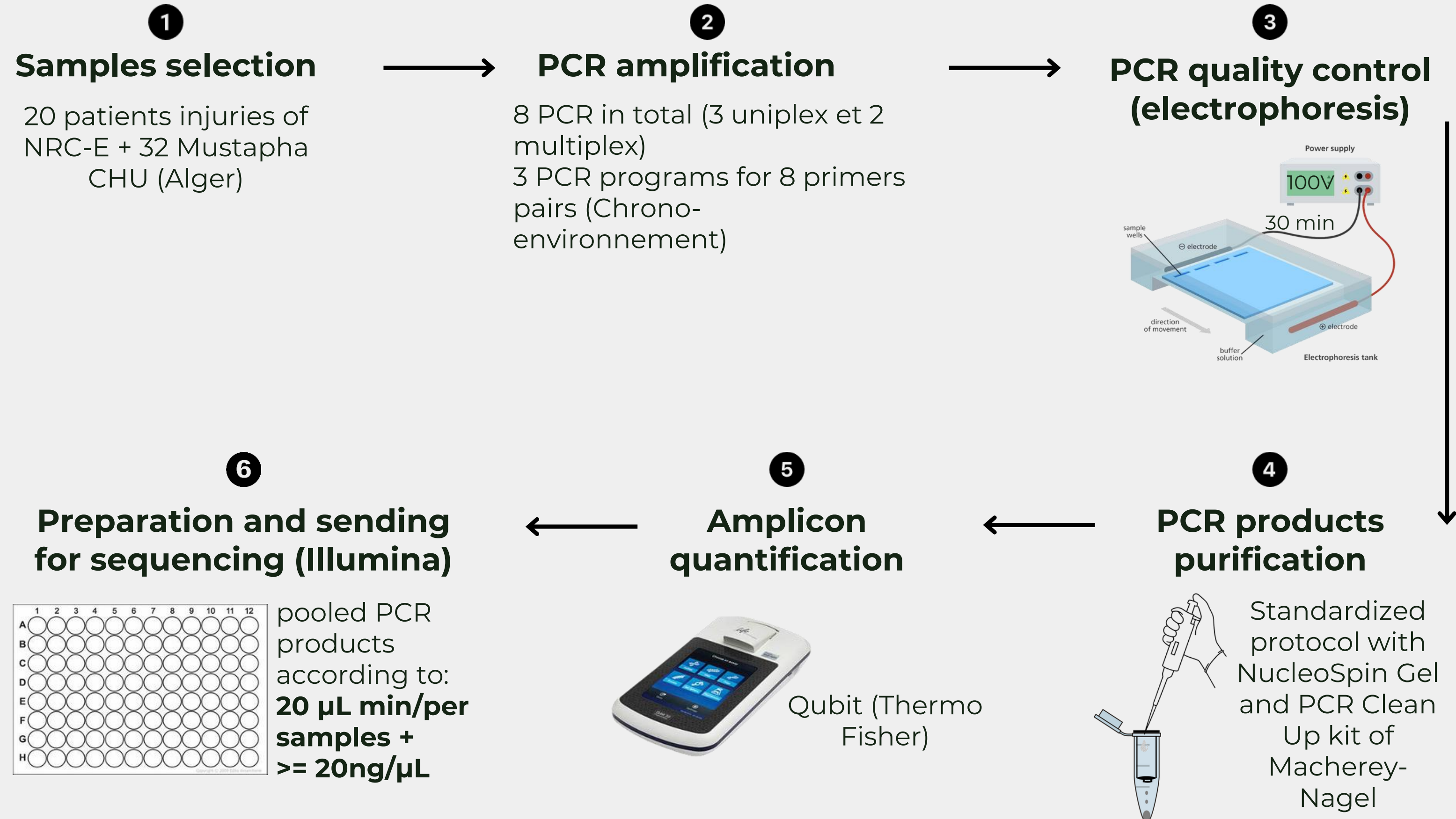


Fig. 2 : Haplotype network obtained from 31 *E. multilocularis* samples full mitogenome. (Bohard et al., 2023)

MATERIALS AND METHODS:

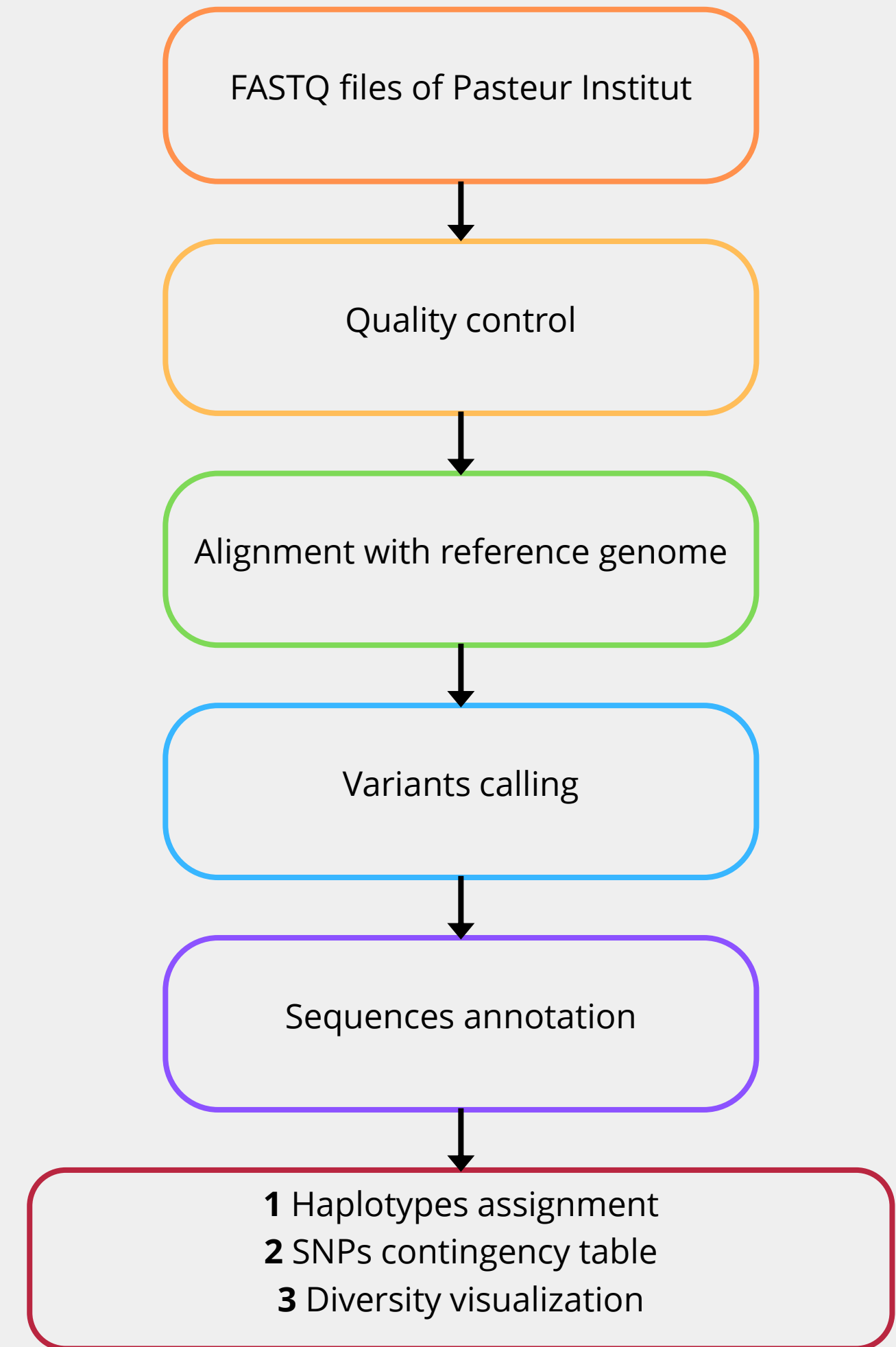
molecular biology



MATERIALS AND METHODS:

bio-informatics

- Bio-informatic workflow systematized
- Several steps to analyse raw data → usable data (tables and graphics)



RESULTS:

• Numbers of mutations :

On average 17 mutations/sequence (based on 13,000 bp)

• Numbers of haplotypes :

56 haplotypes for 61 patients injuries

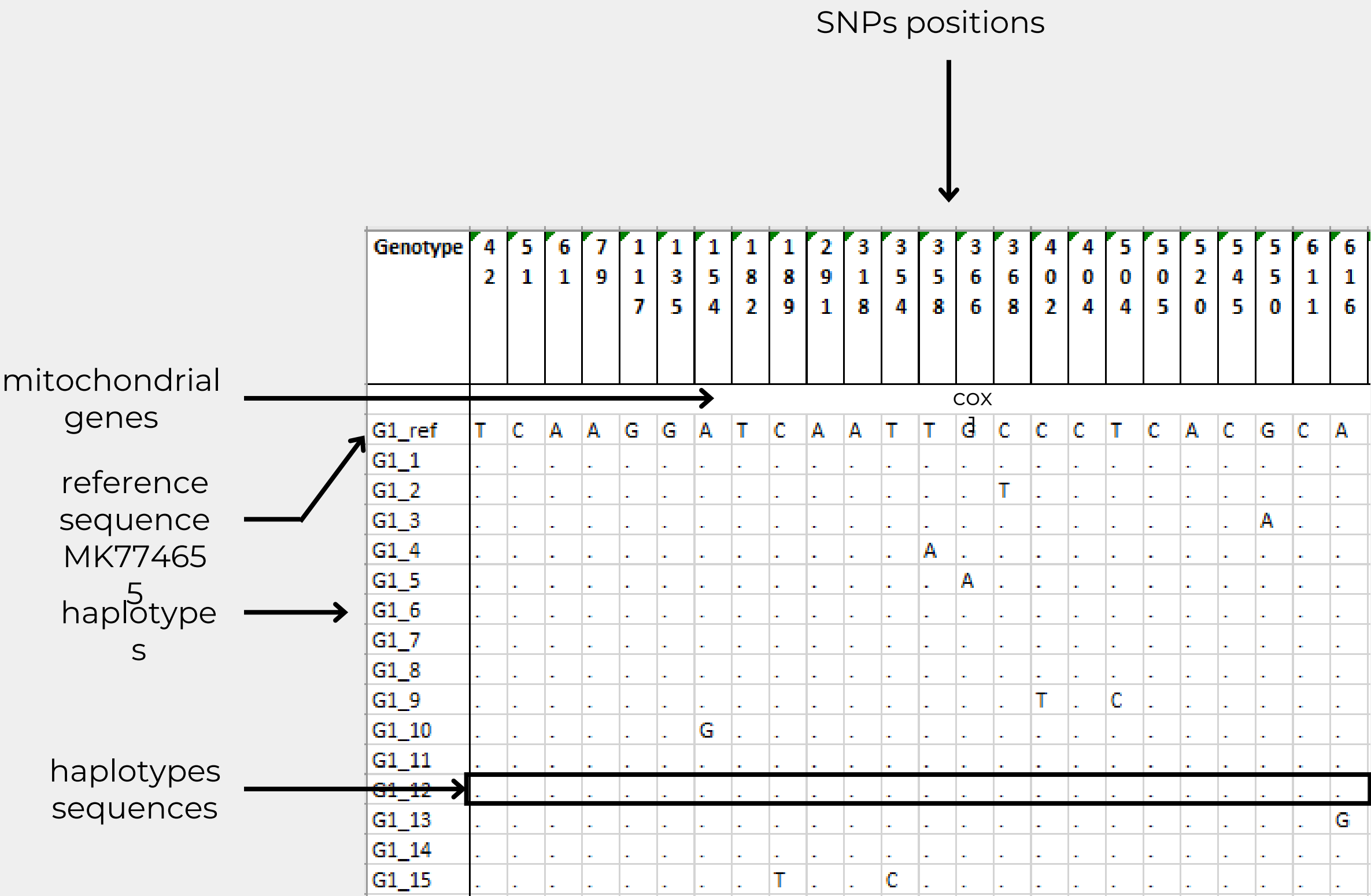


Fig.3 : Extract of summary table show the identify haplotypes from the analyse of *E.granulosus* samples.

RESULTS:

- Samples highlighted in yellow = Algerian patients → **geographical trend present** but **not obvious/clear**
- **Sampling** may be not representative of the reality (1 sample for some countries)
- **Complex** and significant genetic diversity
- **Distinction** between genotypes **G1** and **G3**

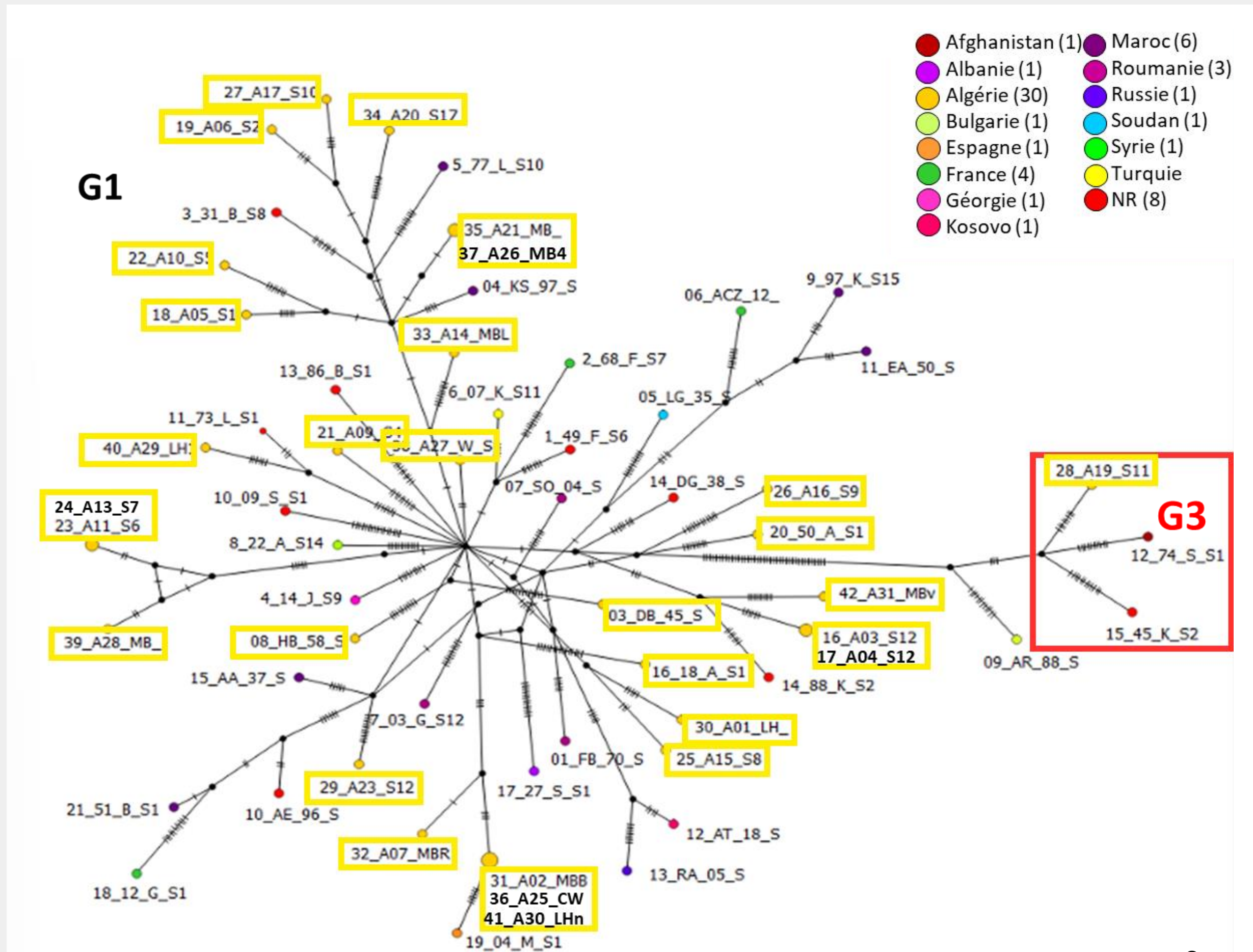


Fig.4 : Haplotype network showing the genetic distance of mitogenome between samples of *E. granulosus* based on patients origin.

TAKE HOME MESSAGES:

- Genetic structure is complexe for *E. granulosus* s.s but already described
→ selection of genes ?
- The protocol (molecular biology + bio-informatic) is functional and validated
→ twice a year
- Bio-informatic part is systematized
- Some improvements to do → haplotypes assignment

OUTLOOK:

- Algerian samples cohort show variability within regions at a local scale of Algeria
→ informations about hometown ?
- Integration of clinical and epidemiological data to improve understanding of the contamination for patients care
- Nuclear genome : clinical form vs. genotype

THANK YOU FOR LISTENING!