

# Characterizing genetic diversity of *Trichinella* spp. in European regions by microsatellites analysis

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## Collaborations

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UMR BIPAR, Anses, Ecole Nationale Vétérinaire d'Alfort, INRA, University Paris-Est, Animal Health Laboratory

----- data currently under analysis and / or manuscript in preparation-----

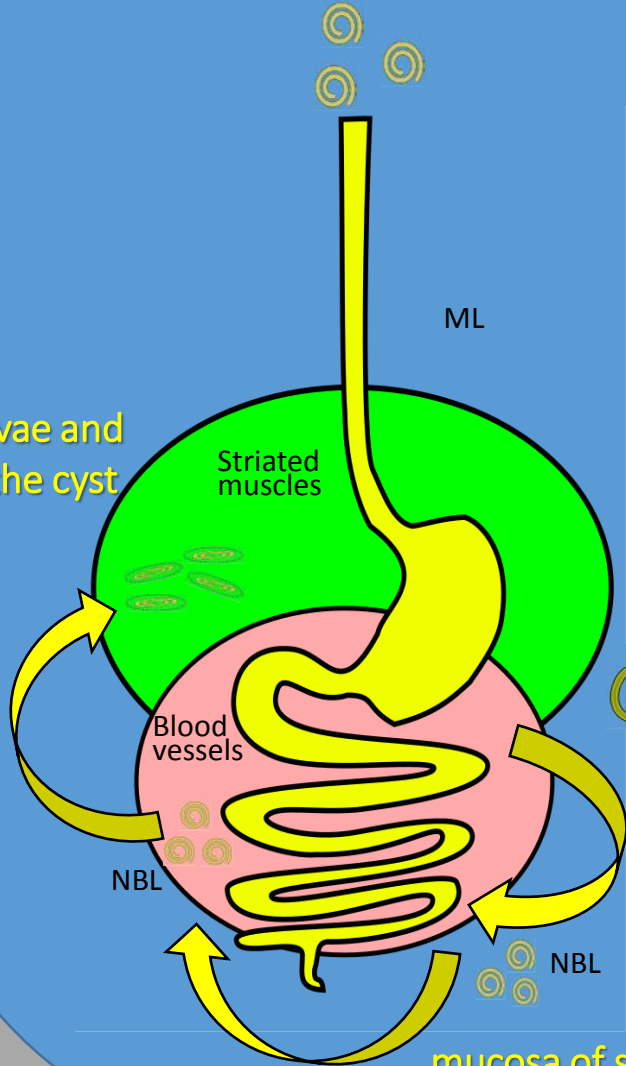
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- Hosts
- Human
  - Pig
  - rat
- 
- Lynx
  - Wolf
  - Raccoon dog
  - Red fox
  - Wild boar
  - Wolverine
  - Pine marten
  - Bear
  - Badger
  - Polecat
  - Otter

striated muscles:  
Settlement of larvae and  
development of the cyst



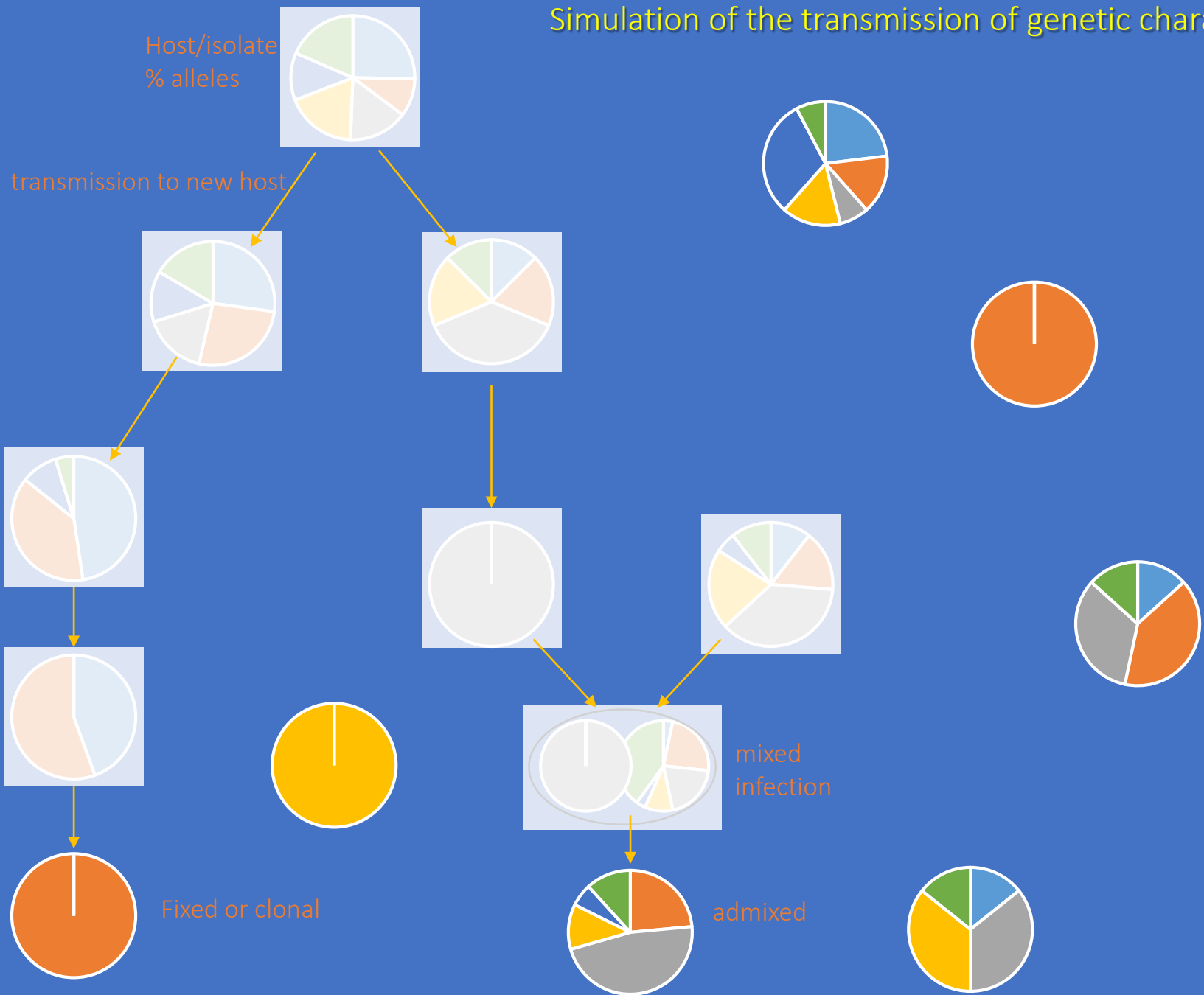
small intestine:  
maturation of adults  
genetic recombination

mucosa of small intestine:  
deposition of nbl, enter the circulation  
degree of kinship  
half sibling - sibling

Genetic variability

- Host
- ML number
- Immune response
- Number of adults
- Sex ratio
- NBL production etc.

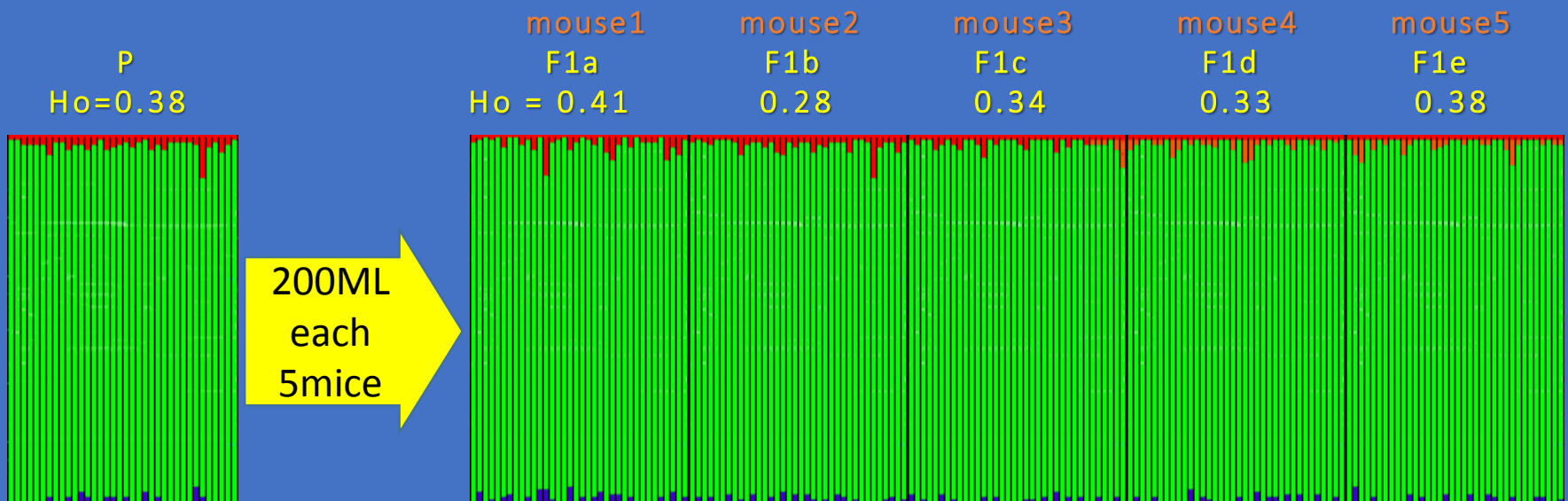
# Simulation of the transmission of genetic characters



# Bayesian analysis of multilocus genotype - 1

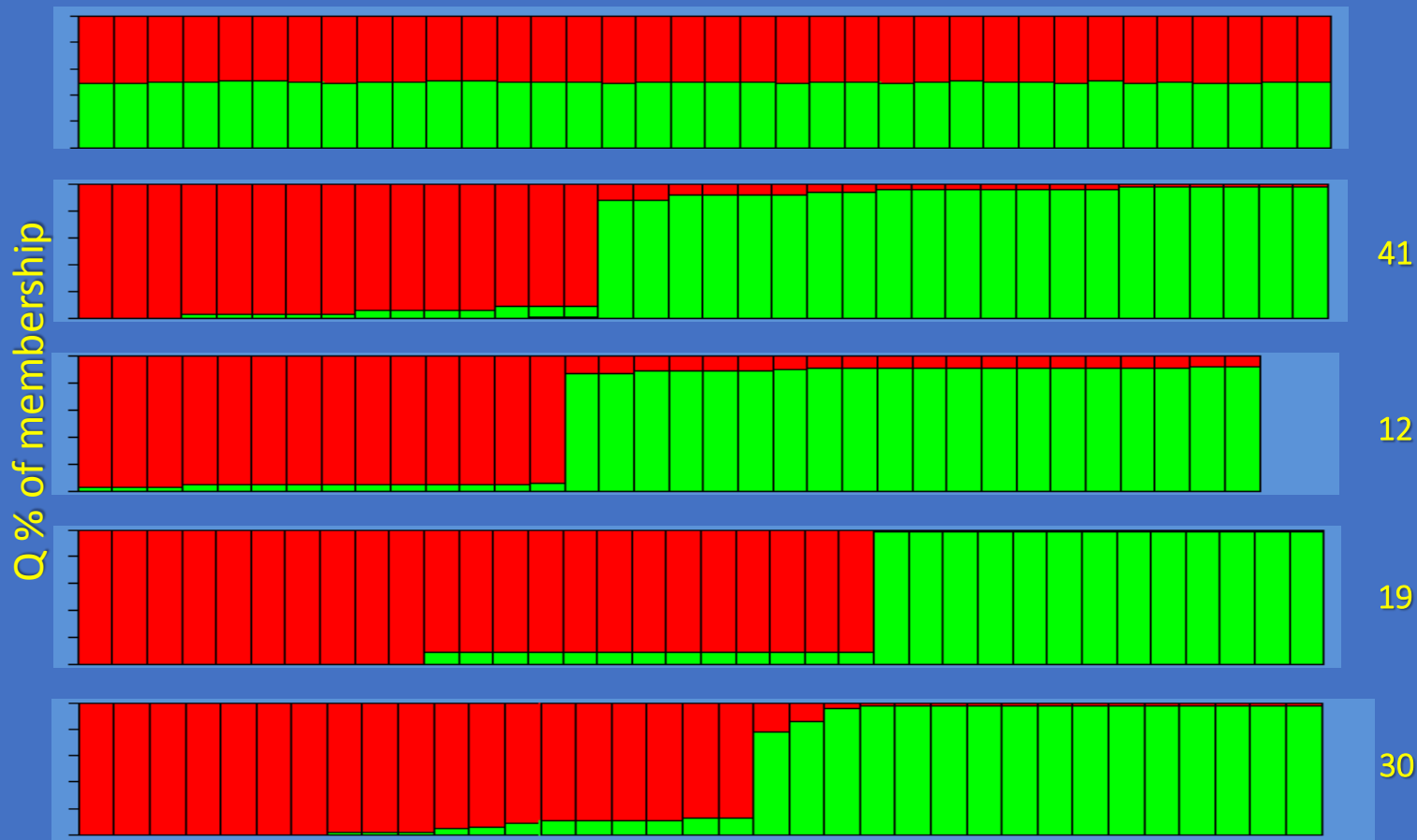
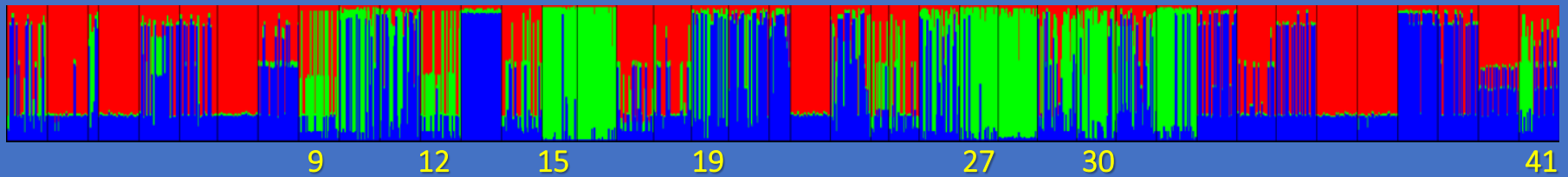
Genetic structure of parental and F1 generations in laboratory test

Bayesian analysis,  $K = 3$ , based on 7 polymorphic microsatellite loci  
36 individuals (small vertical rectangles) each generation  
The color represents the probability of sharing group membership



# Bayesian analysis of multilocus genotype - 2

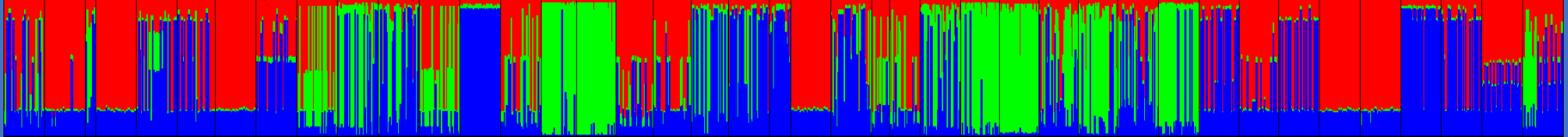
Mixed infections in Extremadura *T. spiralis* isolates



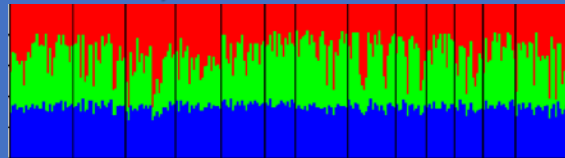
# Bayesian analysis of multilocus genotype - 3

Genetic structure of wild isolates from European regions

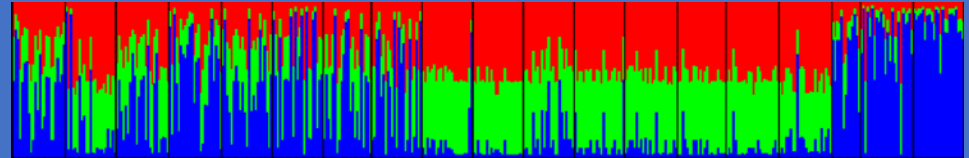
Extremadura (Spain), *T. spiralis*



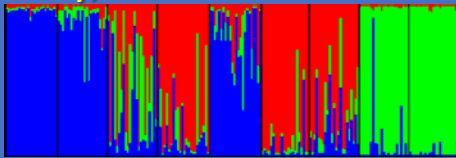
Sardinia, *T. britovi*



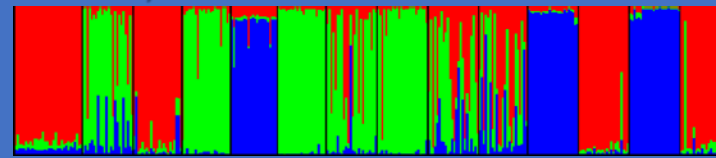
Corsica, *T. britovi*



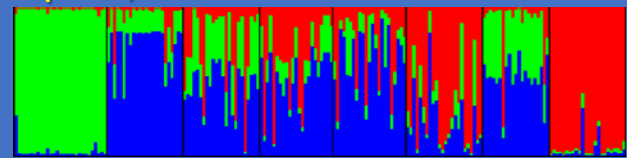
Italy, *T. britovi*



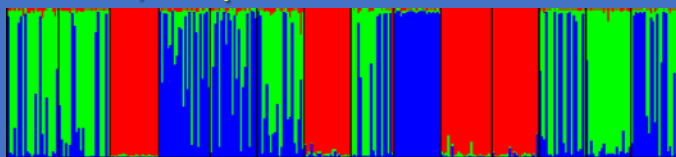
France, *T. britovi*



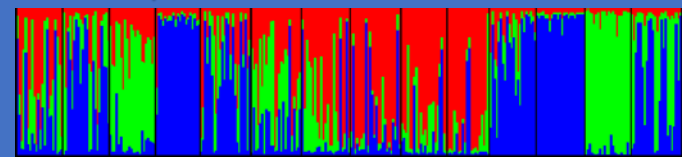
Spain, *T. britovi*



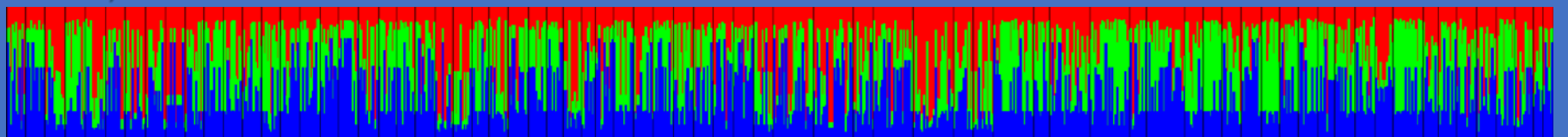
Poland, *T. spiralis*



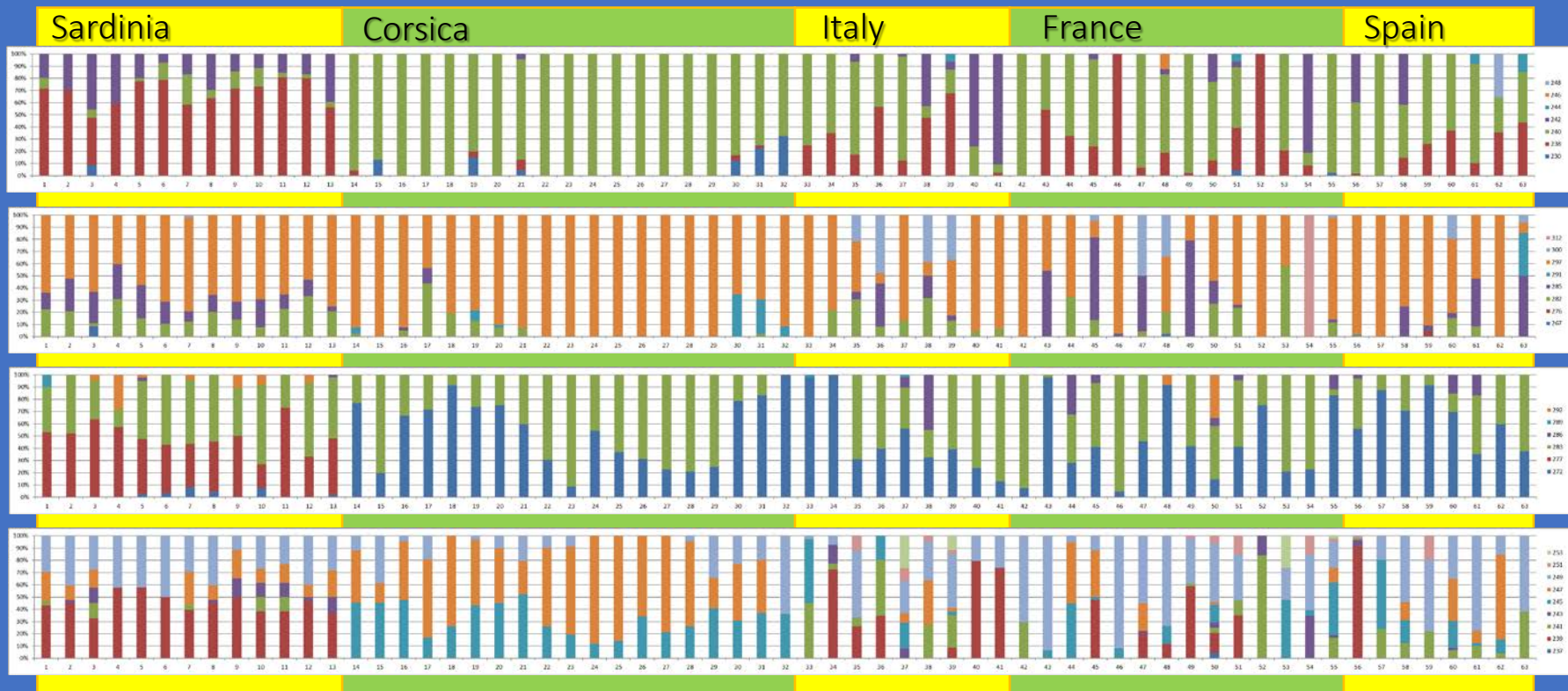
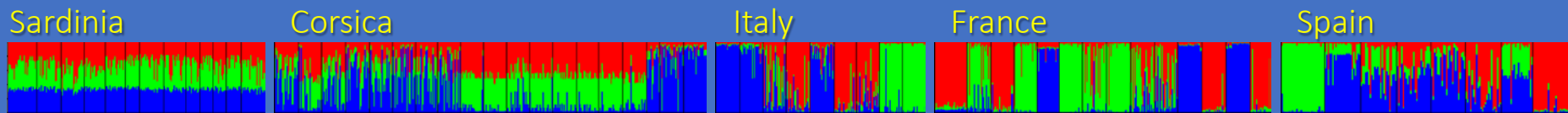
Poland, *T. britovi*



Latvia, *T. britovi*

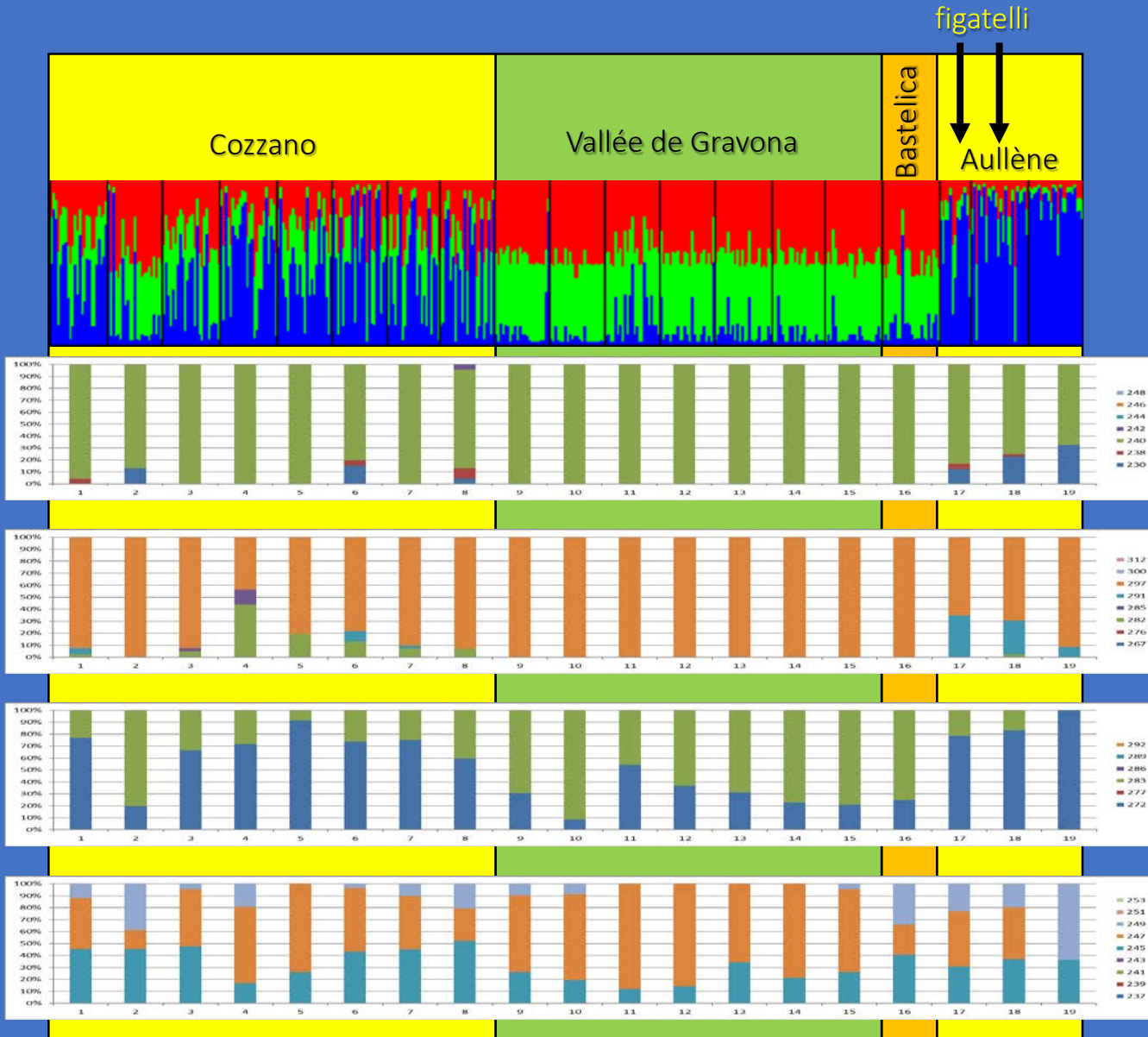


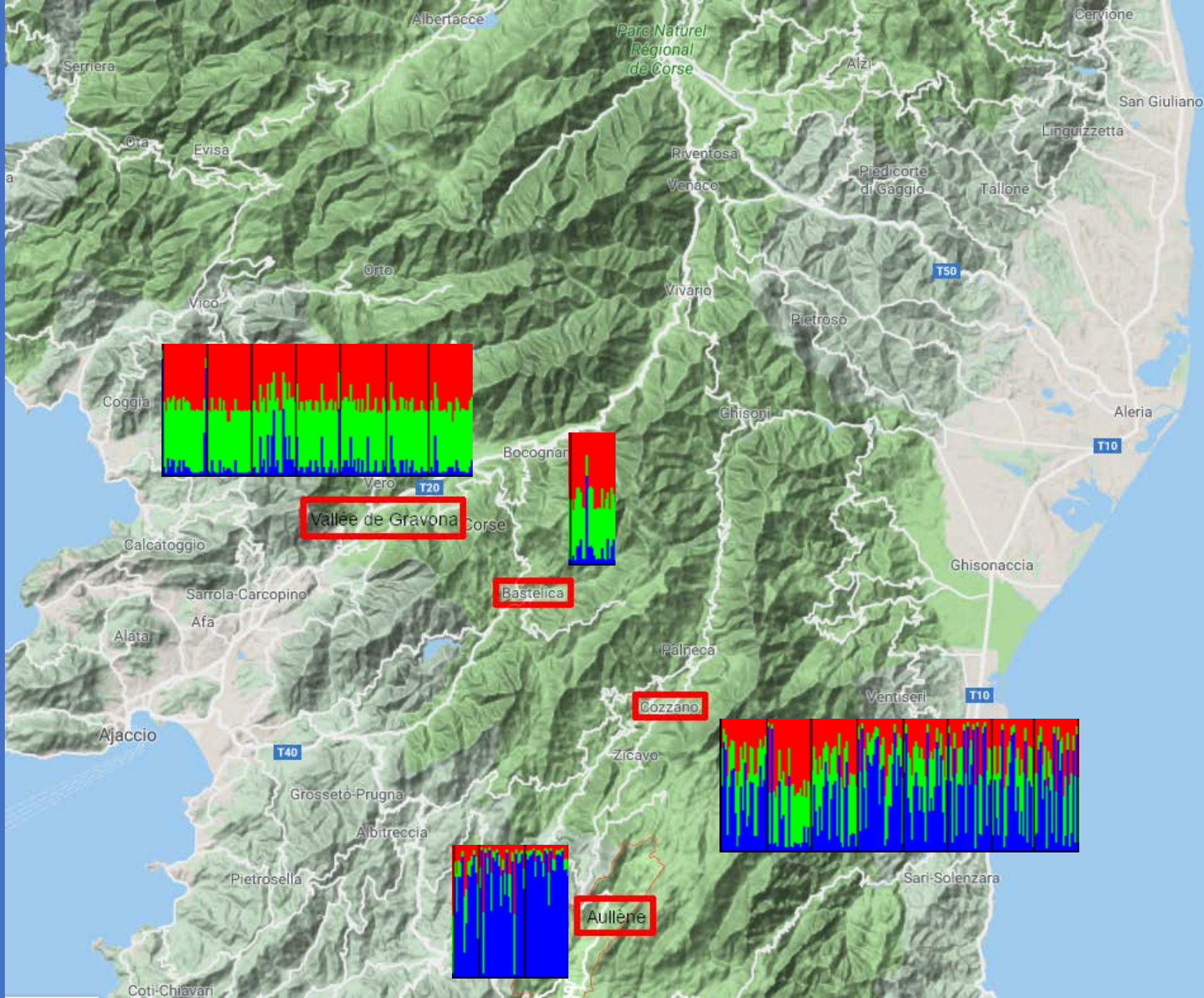
# Genetic variability and alleles analysis as a tool for epidemiological investigation on trichinellosis outbreak occurred in Nice (France)





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# Conclusions

- The isolates are characterized by, alleles and their frequencies, and this makes them useful for tracing the origin of an outbreak
- The genetic structure of isolates helps to define the geographical boundaries of gene pools
- The genetic structure of isolates is a new tool in epidemiological investigation
- The genetic structure shown in wild animals suggests prevalence in that region

## Collaborations

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