

# Genetic structure of European invasive populations of two *Xylosandrus* species

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# Two ambrosia beetles

*Xylosandrus crassiusculus*: 2003 in Italy

*Xylosandrus compactus*: 2011 in Italy



*Xylosandrus compactus*



*Xylosandrus crassiusculus*

# Two ambrosia beetles

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*Xylosandrus compactus*: 2011 in Italy

A biology favouring invasion

- Minute species (< 3mm)
- Live inside galleries



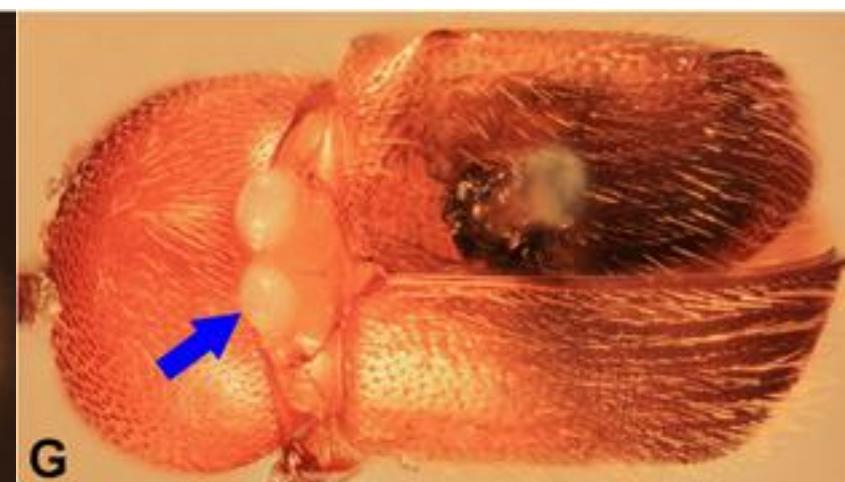
# Two ambrosia beetles

*Xylosandrus crassiusculus*: 2003 in Italy

*Xylosandrus compactus*: 2011 in Italy

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- Minute species (< 3mm)
- Live inside galleries
- Xylomycetophagous
  - Symbiotic fungi
  - Broad host range



*X. crassiusculus'* mycangium

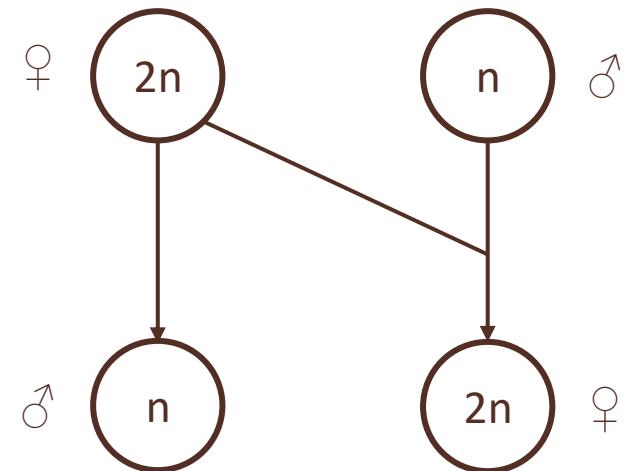
# Two ambrosia beetles

*Xylosandrus crassiusculus*: 2003 in Italy

*Xylosandrus compactus*: 2011 in Italy

A biology favouring invasion

- Minute species (< 3mm)
- Live inside galleries
- Xylomycetophagous
  - Symbiotic fungi
  - Broad host range
- Arrhenotokous + Sib-mating
  - 1 ♀ ⇒ 1 population
  - No mate-finding problem
  - No inbreeding depression



# Two main goals

## Understand their invasion history

- Identify source population(s)
- Identify invasion pathway
- Using two genetic markers
  - Mitochondrial marker: COI (+ Genbank)
  - Nuclear markers: SNPs via RAD sequencing



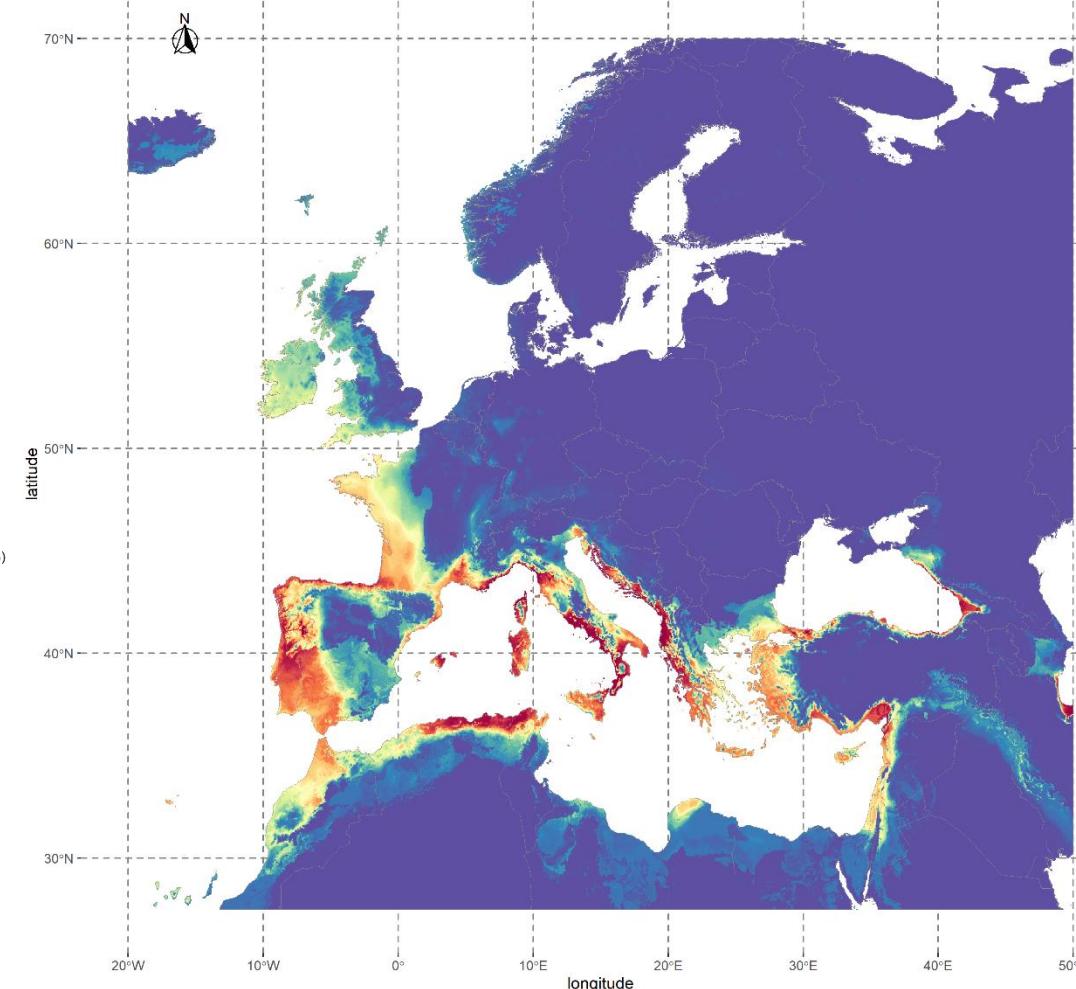
# Two main goals

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  - Nuclear markers: SNPs via RAD sequencing

## Predict suitable areas

- Species Distribution Modelling (SDM)
  - Published for *X. compactus* (Urvois et al. 2021)
  - Failed for *X. crassisculus* ⇒ Could be solved with genetics!



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Climate change impact on the potential geographical distribution of two invading *Xylosandrus ambrosia* beetles

T. Urvois M. A. Auger-Rozenberg, A. Roques, J. P. Rossi & C. Kerdelhue

*Scientific Reports* 11, Article number: 1339 (2021) | Cite this article

681 Accesses | 2 Citations | 1 Altmetric | Metrics

# *X. compactus'* genetic structure

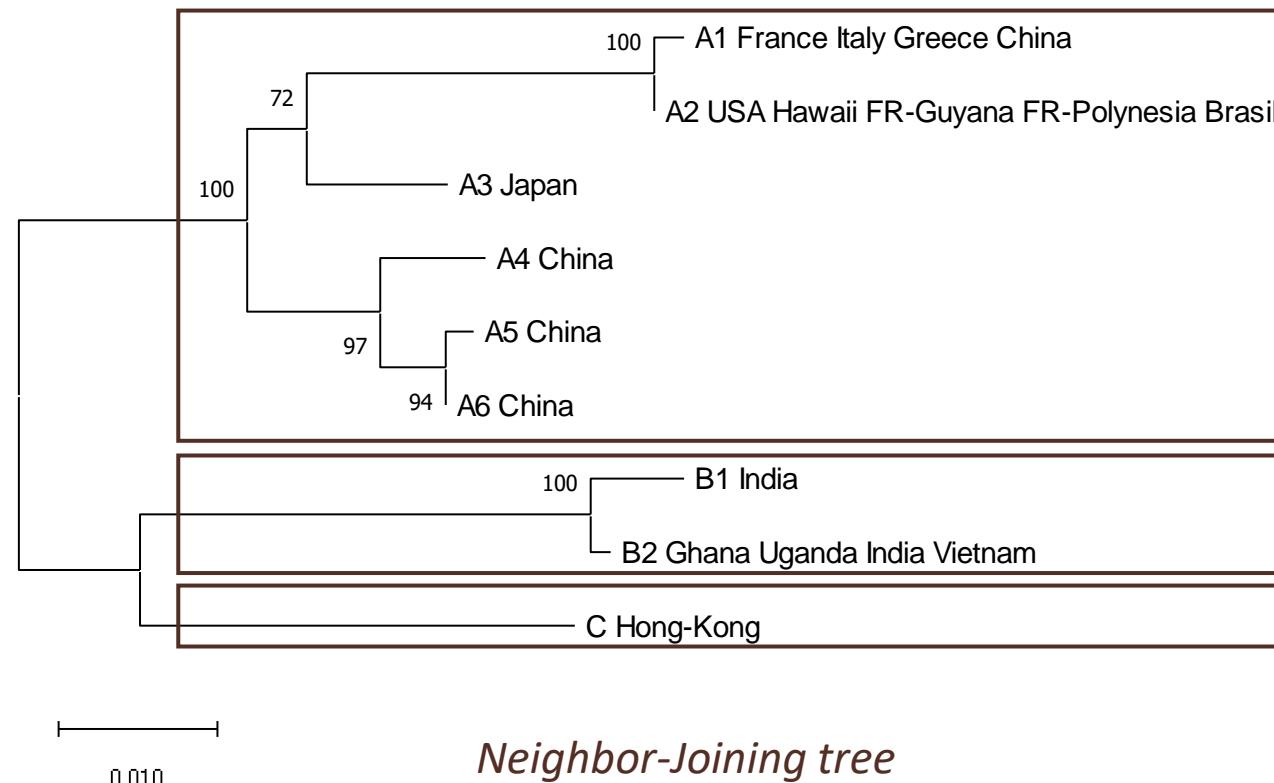
Urvois T., Perrier C., Roques A., Sauné L., Courtin C., Li Y., Johnson A. J., Hulcr J., Auger-Rozenberg M.-A., Kerdelhué C. (in press) A first inference of the phylogeography of the worldwide invader *Xylosandrus compactus*. *Journal of Pest Science*

# *X. compactus*' genetic structure

## Mitochondrial DNA analysis

- Genetic distances suggest 3 lineages
- Lineage A ⇒ Invasive in Europe, the Americas and Pacific Islands
- Lineage B ⇒ Invasive in Africa
- Lineage C ⇒ Only one specimen (Cognato et al. 2020)

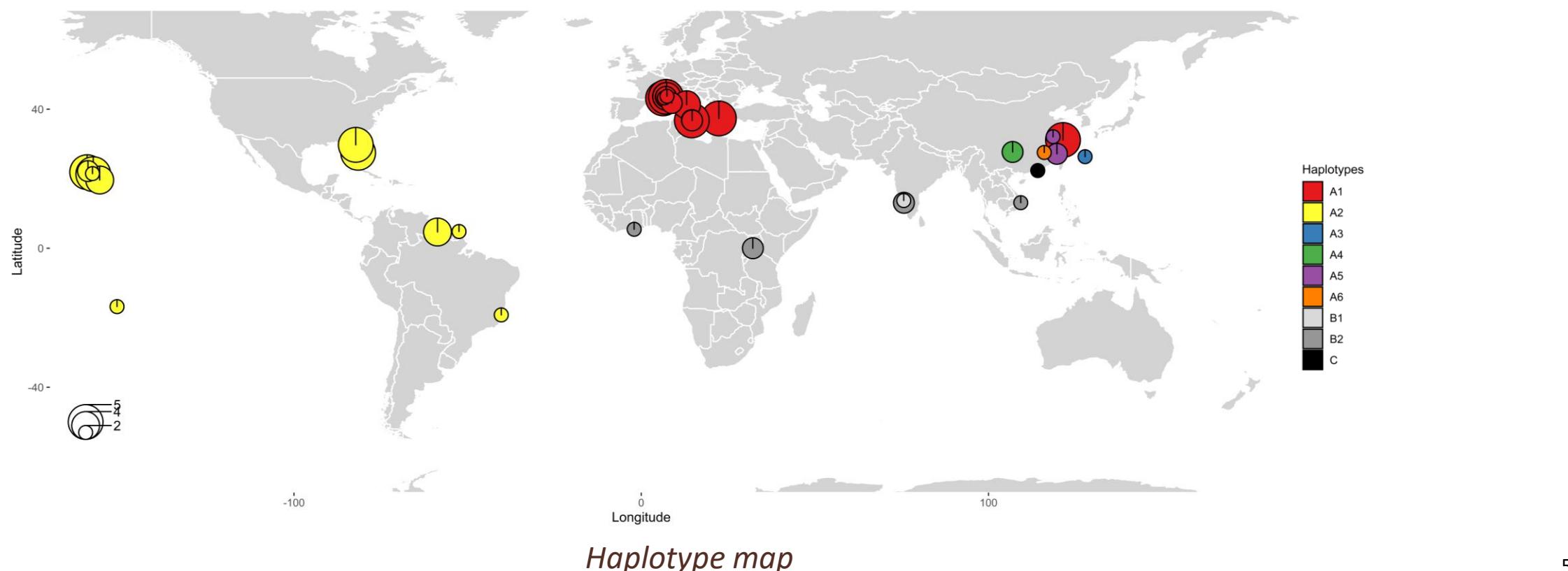
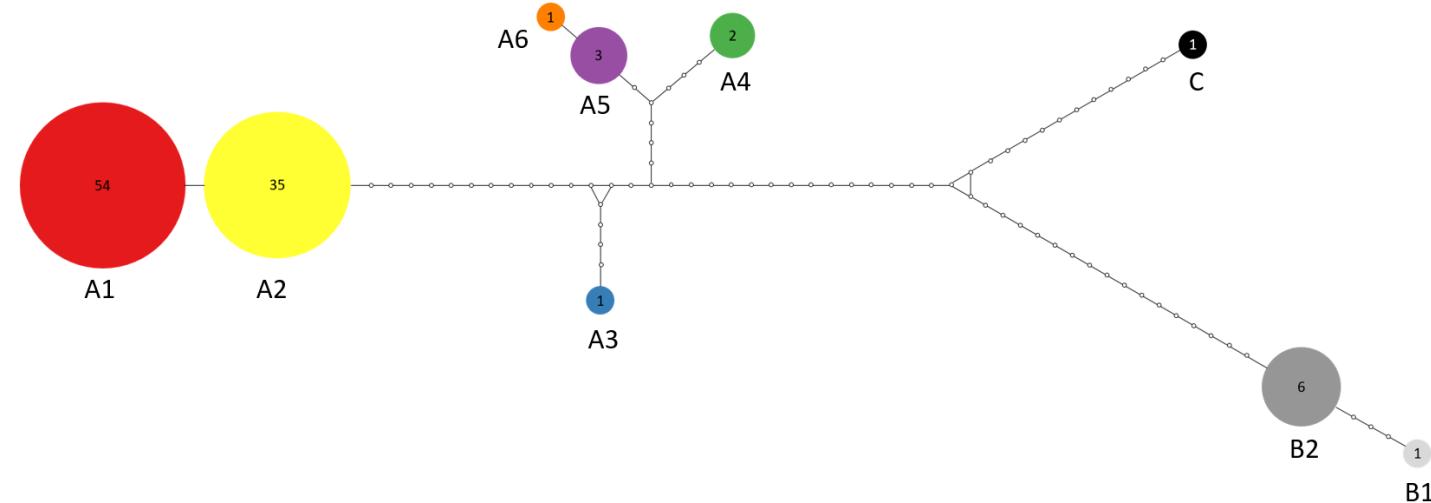
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# *X. compactus'* genetic structure

# Mitochondrial DNA analysis

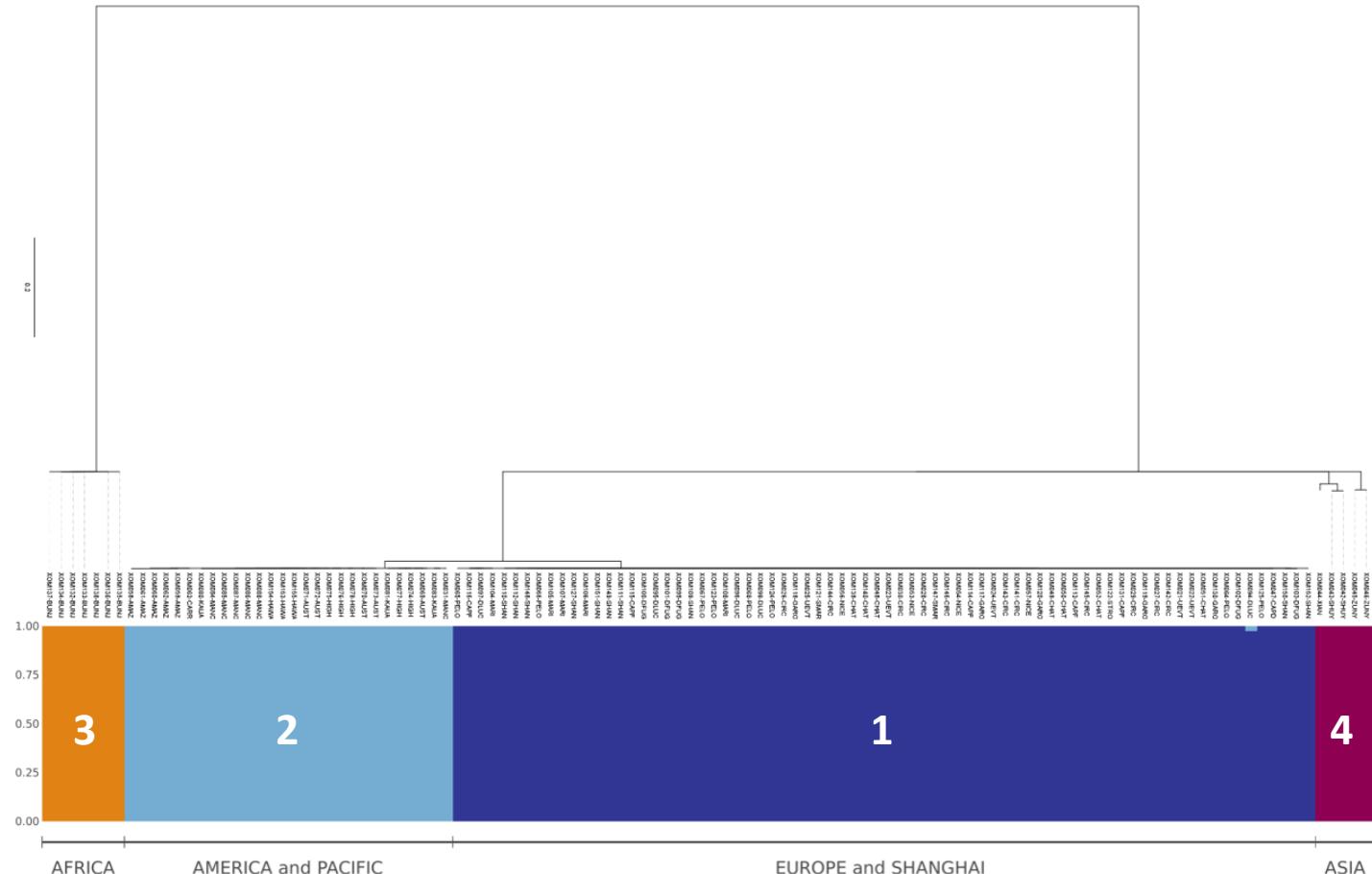
- A1 in Europe and Shanghai
  - A2 only in American-Pacific region
  - B2 in Africa, India and Vietnam
  - Higher genetic diversity in native are



# *X. compactus'* genetic structure

## RAD sequencing analysis

- 4 distinct groups
- Almost no genetic diversity in groups 1, 2 and 3

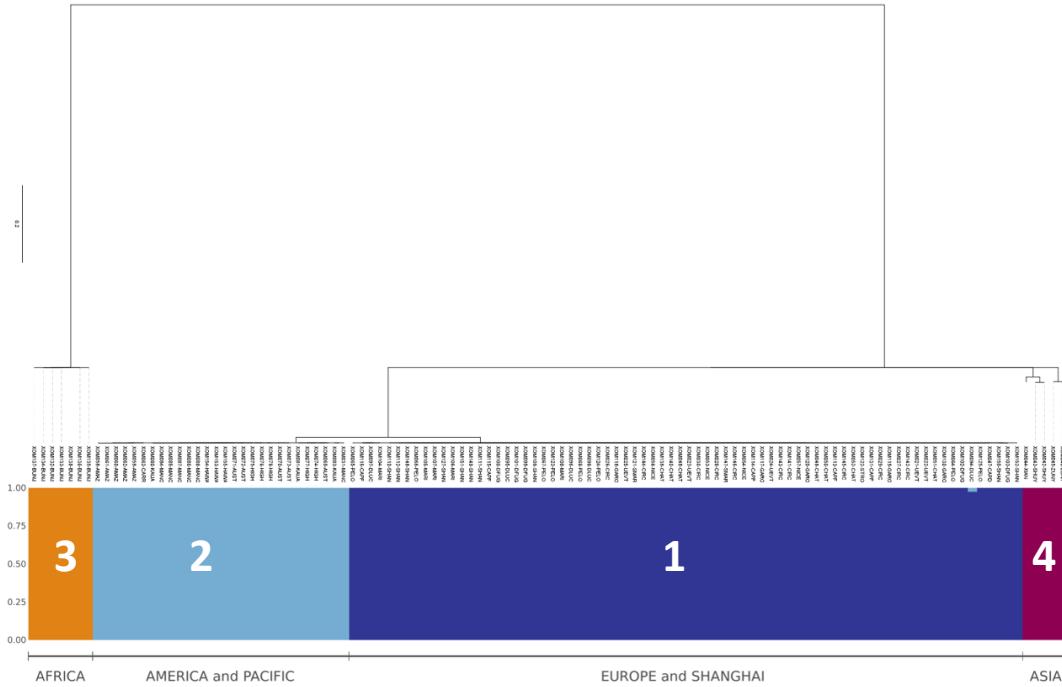
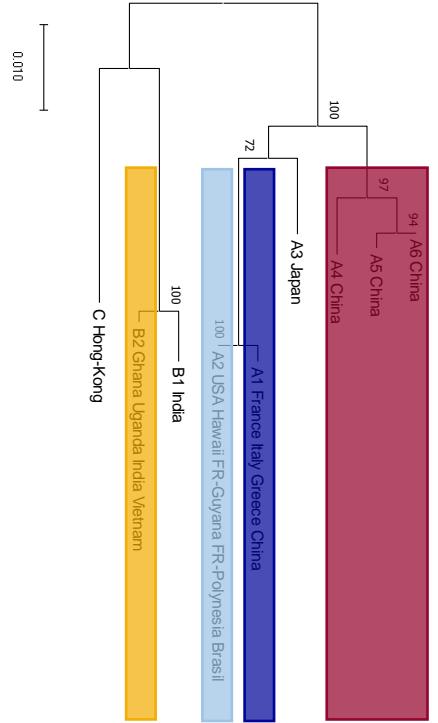


Maximum Likelihood tree and Admixture plot

# *X. compactus'* genetic structure

# RAD sequencing analysis

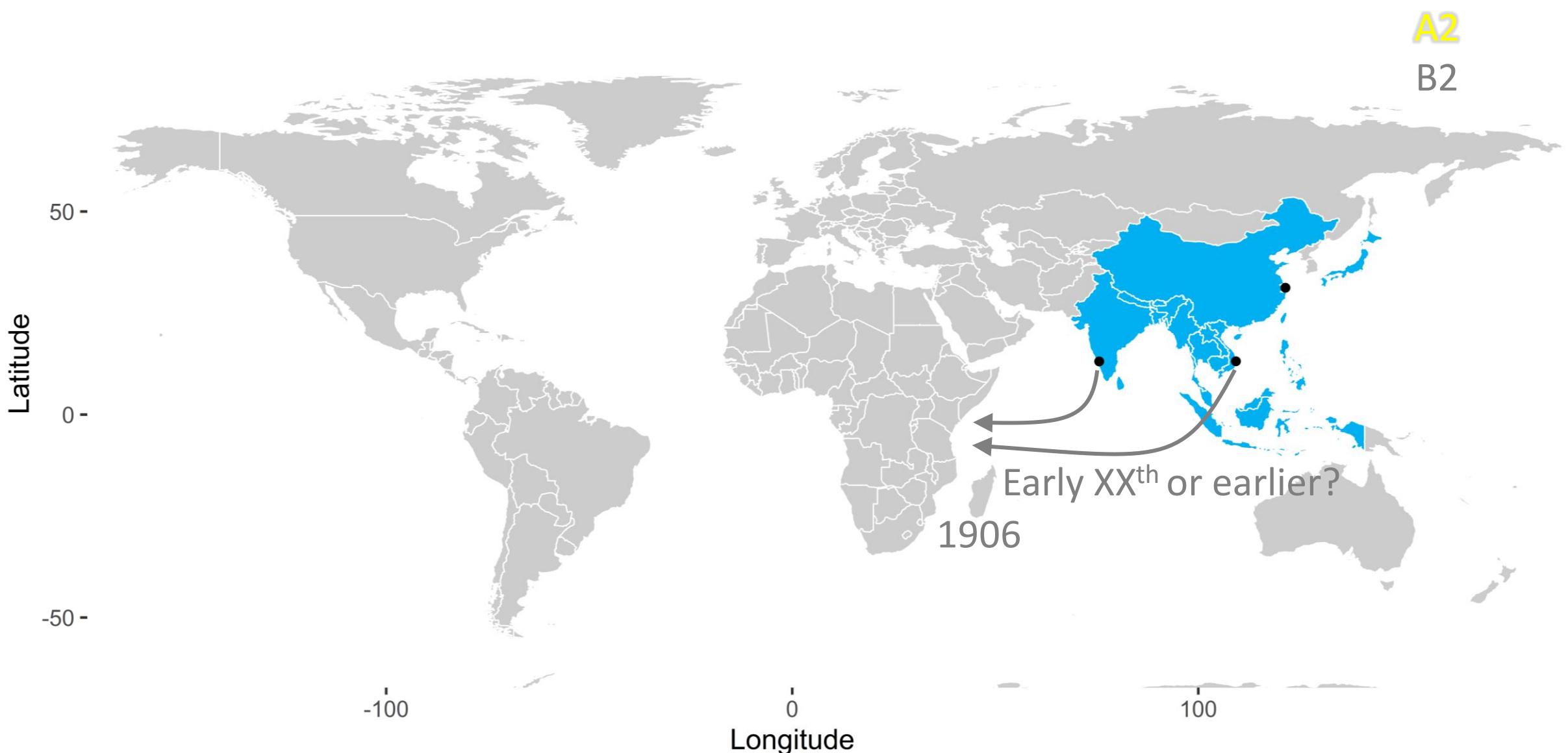
- 4 distinct groups
  - Almost no genetic diversity in groups 1, 2 and 3
  - Similar to mitochondrial DNA results
    - Europe grouped with Shanghai
    - Proximity between American-Pacific and Europe



## *Maximum Likelihood tree and Admixture plot*

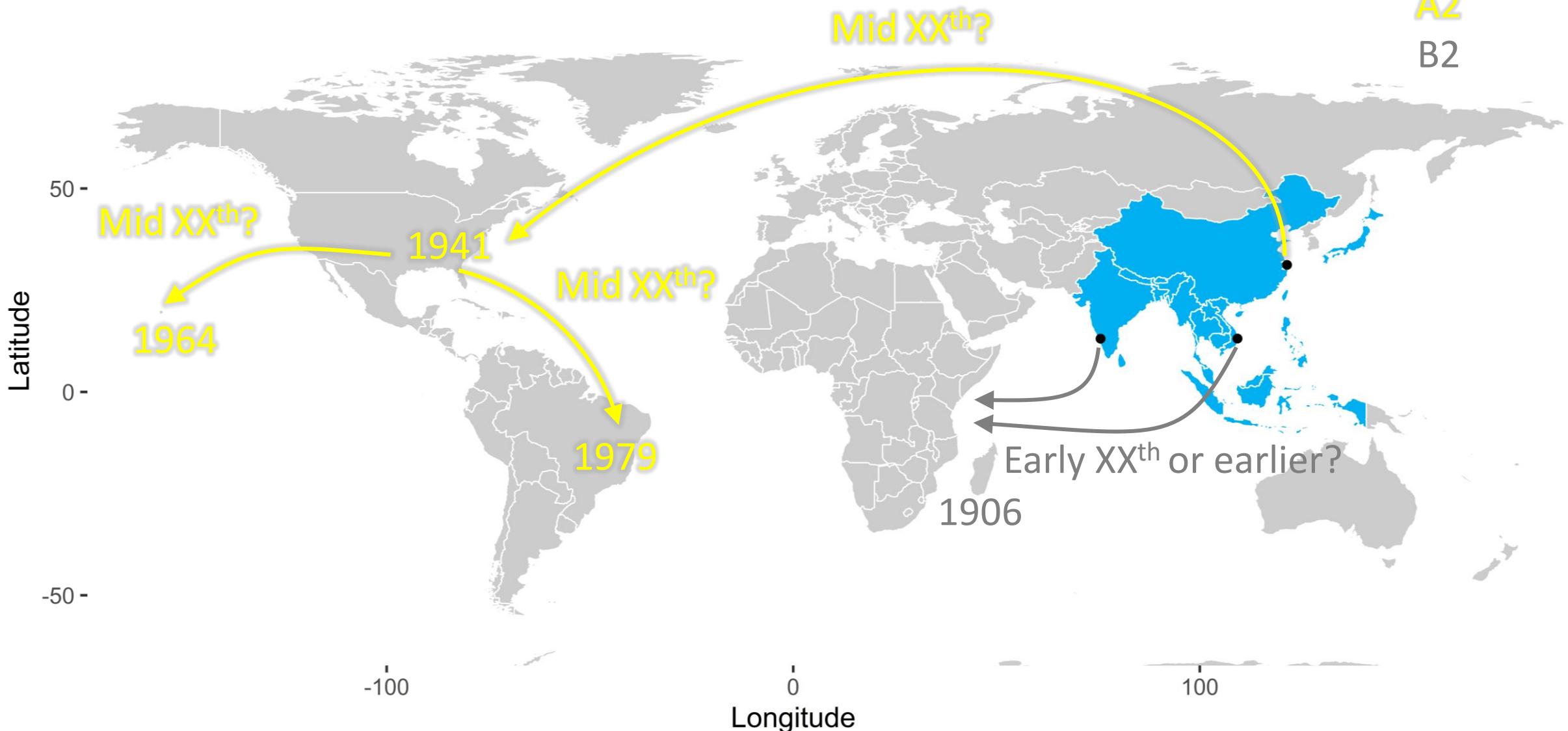
# *X. compactus*' genetic structure

## Invasion history



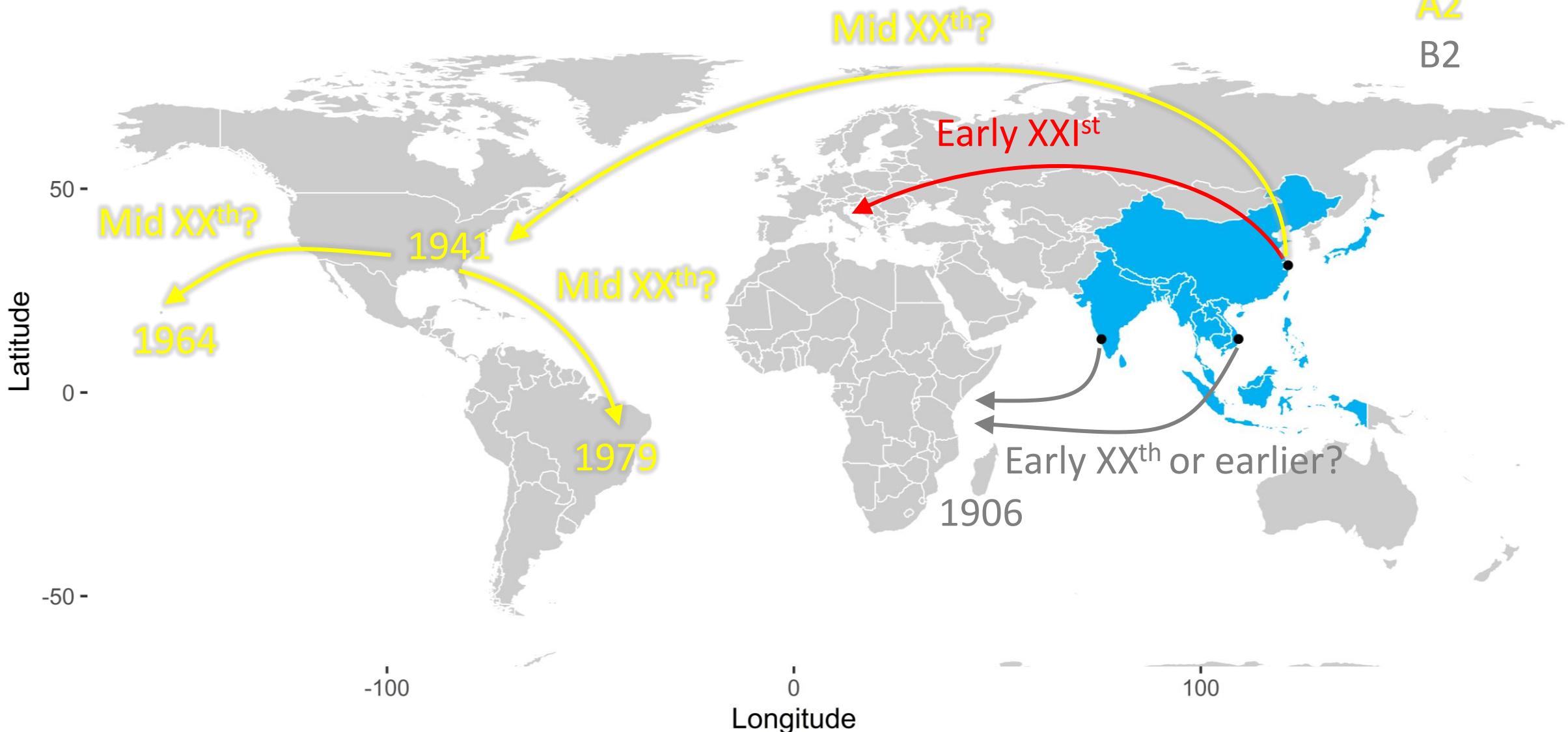
# *X. compactus*' genetic structure

## Invasion history



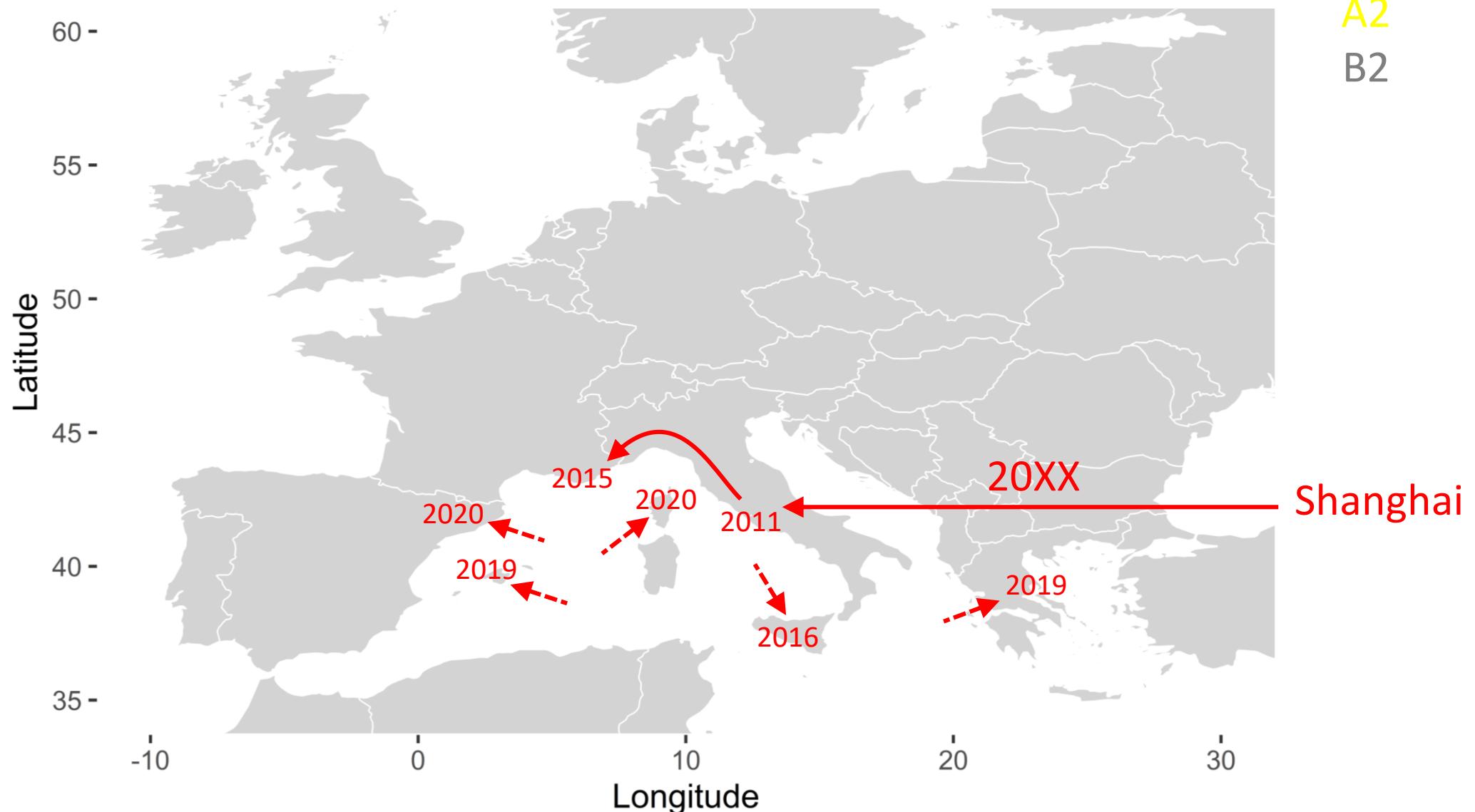
# *X. compactus*' genetic structure

## Invasion history



# *X. compactus'* genetic structure

## European invasion history



# *X. crassiusculus'* genetic structure

## Summary of the litterature

- 3 non-overlapping papers

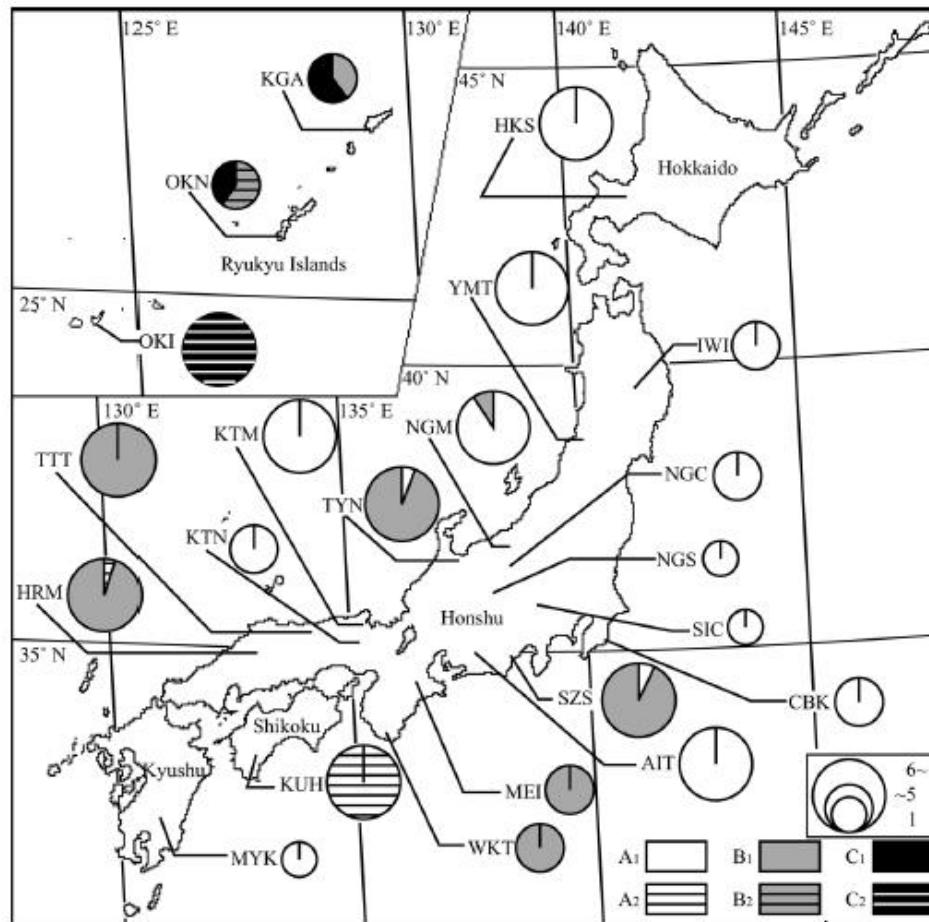
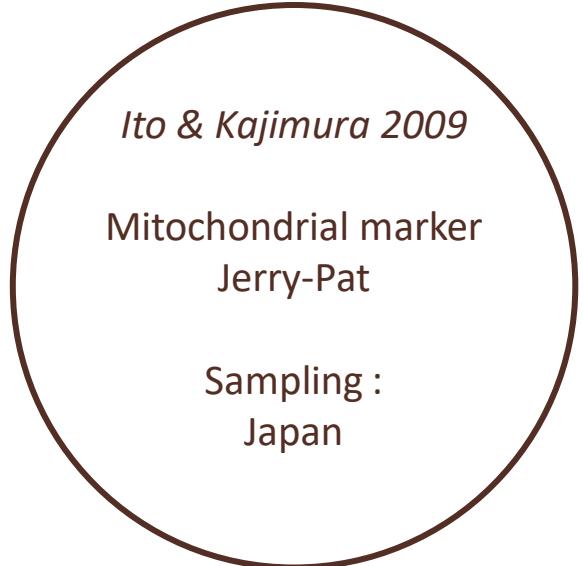


Fig. 2. Distribution of *COI* mitochondrial DNA haplotypes across 22 Japanese *Xylophagus crassiusculus* populations. Pie graphs represent the frequency of *COI* haplotypes belonging to subclades A<sub>1</sub>, A<sub>2</sub>, B<sub>1</sub>, B<sub>2</sub>, C<sub>1</sub> and C<sub>2</sub> in each population (Table 2). Circle size is proportional to sample size. Population names are defined in Table 1.

# *X. crassiusculus*' genetic structure

## Summary of the litterature

- 3 non-overlapping papers

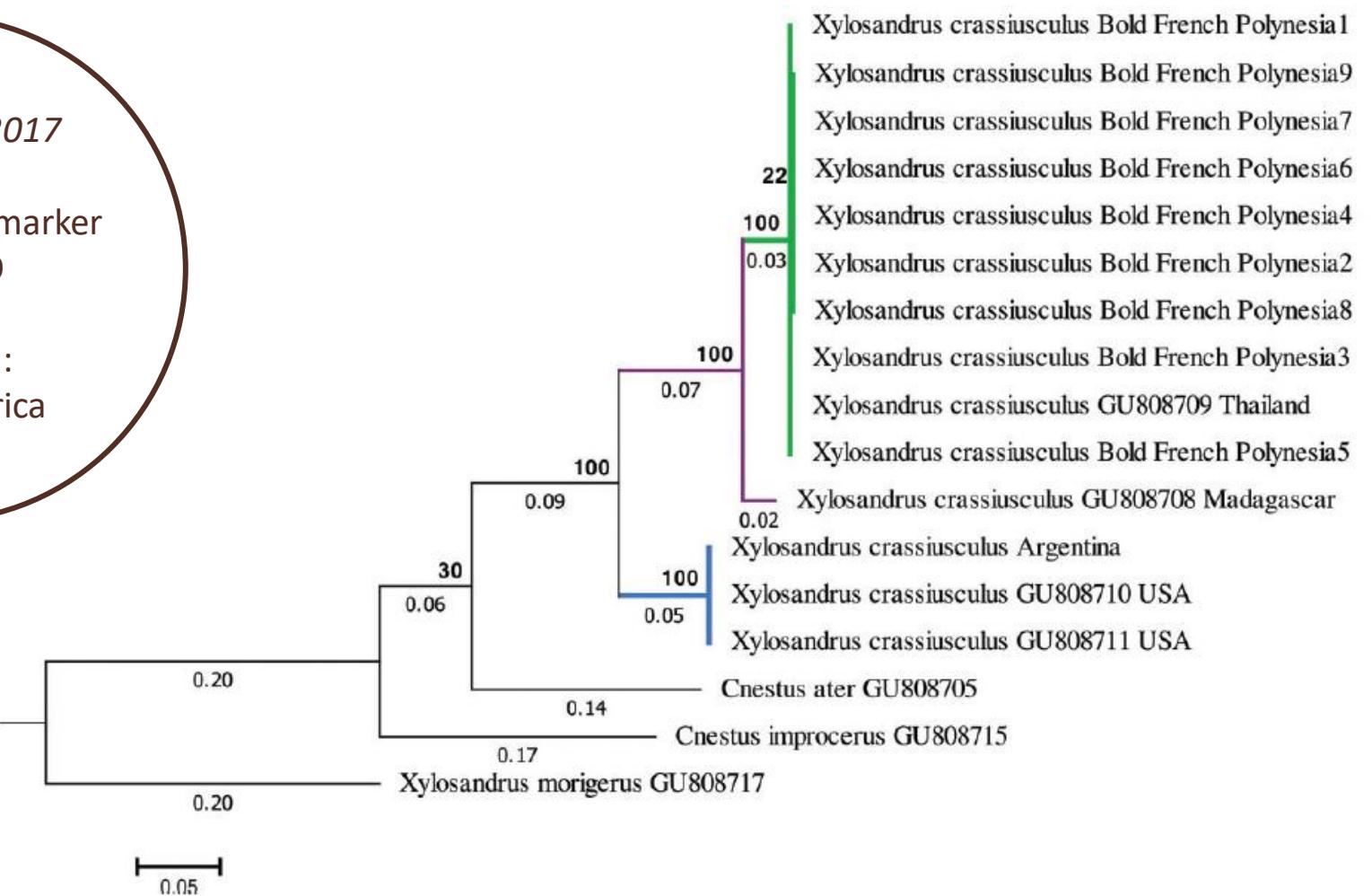
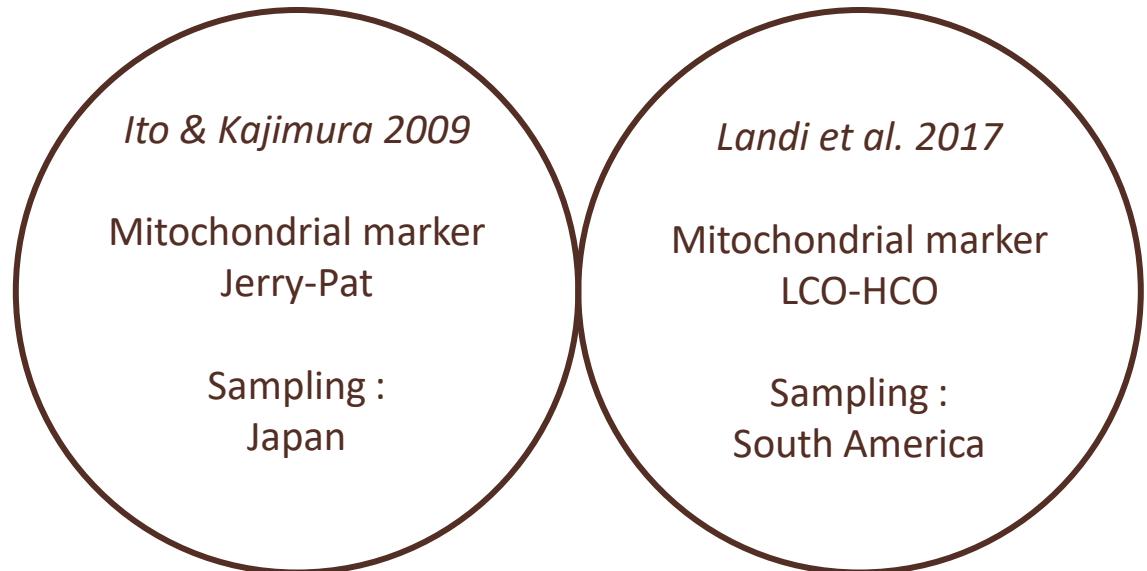


Fig. 3. ML tree, numbers above and below branches indicate bootstrap values and branch lengths, respectively. Sequences from GenBank are identified with their accession numbers on the right. Other sequences were obtained from BOLD public database.

# *X. crassiusculus*' genetic structure

## Summary of the litterature

- 3 non-overlapping papers

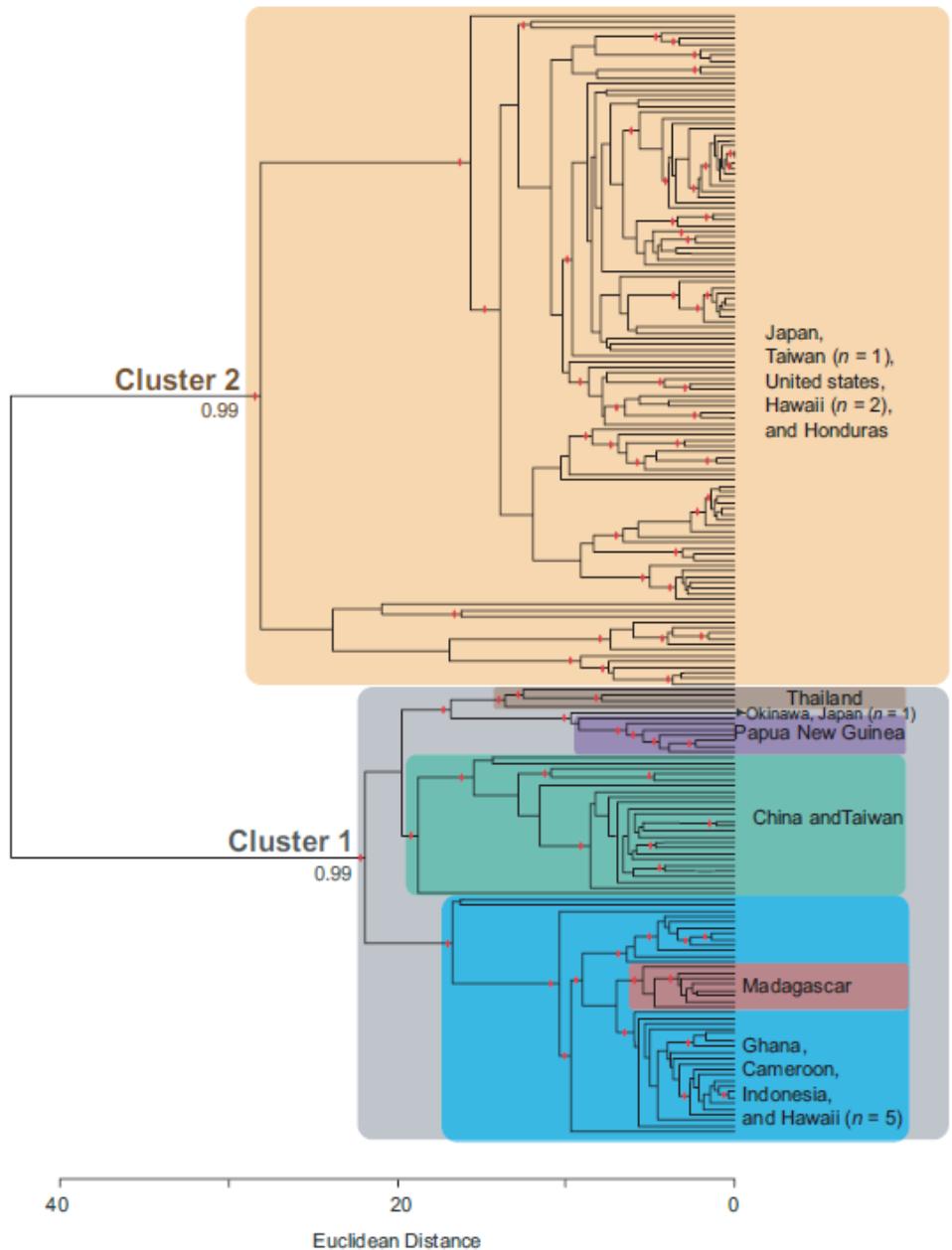
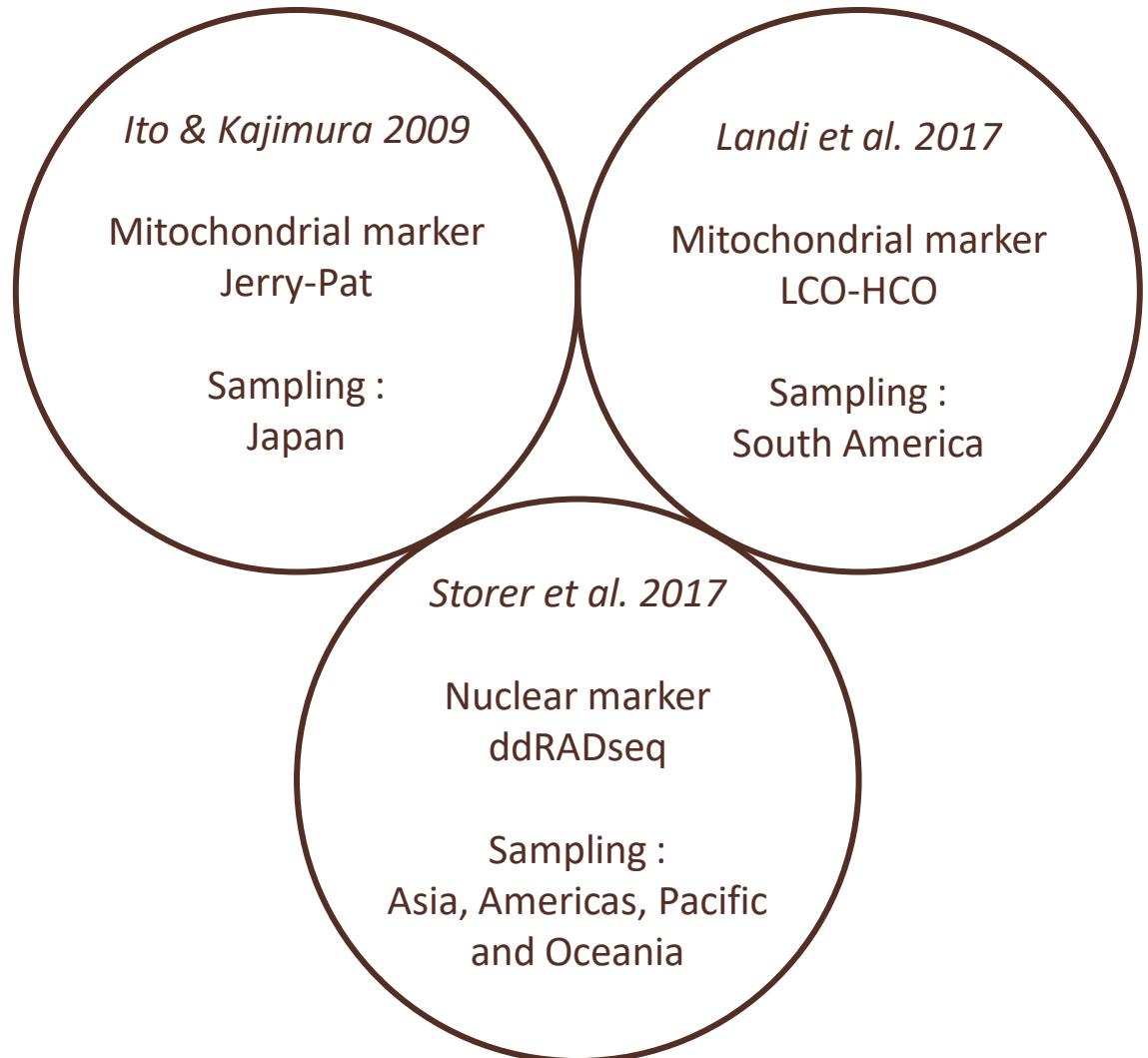


FIGURE 3 Ultrametric dendrogram of hierarchical clusters for all individuals. Statistically significant clusters ( $p < .05$ ) are indicated by red hatch marks at cluster nodes. Clusters containing all individuals from one location are highlighted with color and labeled

# *X. crassiusculus*' genetic structure

## Summary of the litterature

- 3 non-overlapping papers

## Main goal

- Bridge the gap between these studies
  - Sampling every continent
  - Common genetic markers

# *X. crassiusculus'* genetic structure

## Mitochondrial DNA analysis

- 50 haplotypes corresponding to 5 lineages
- 2 clusters as in *Storer et al. 2017*
  - Cluster 2: Lineages A-C
  - Cluster 1: Lineages D-E

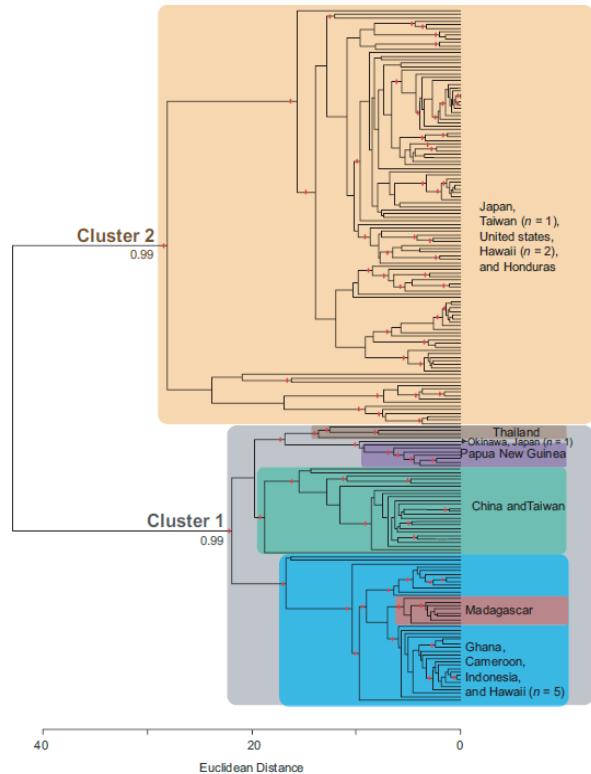
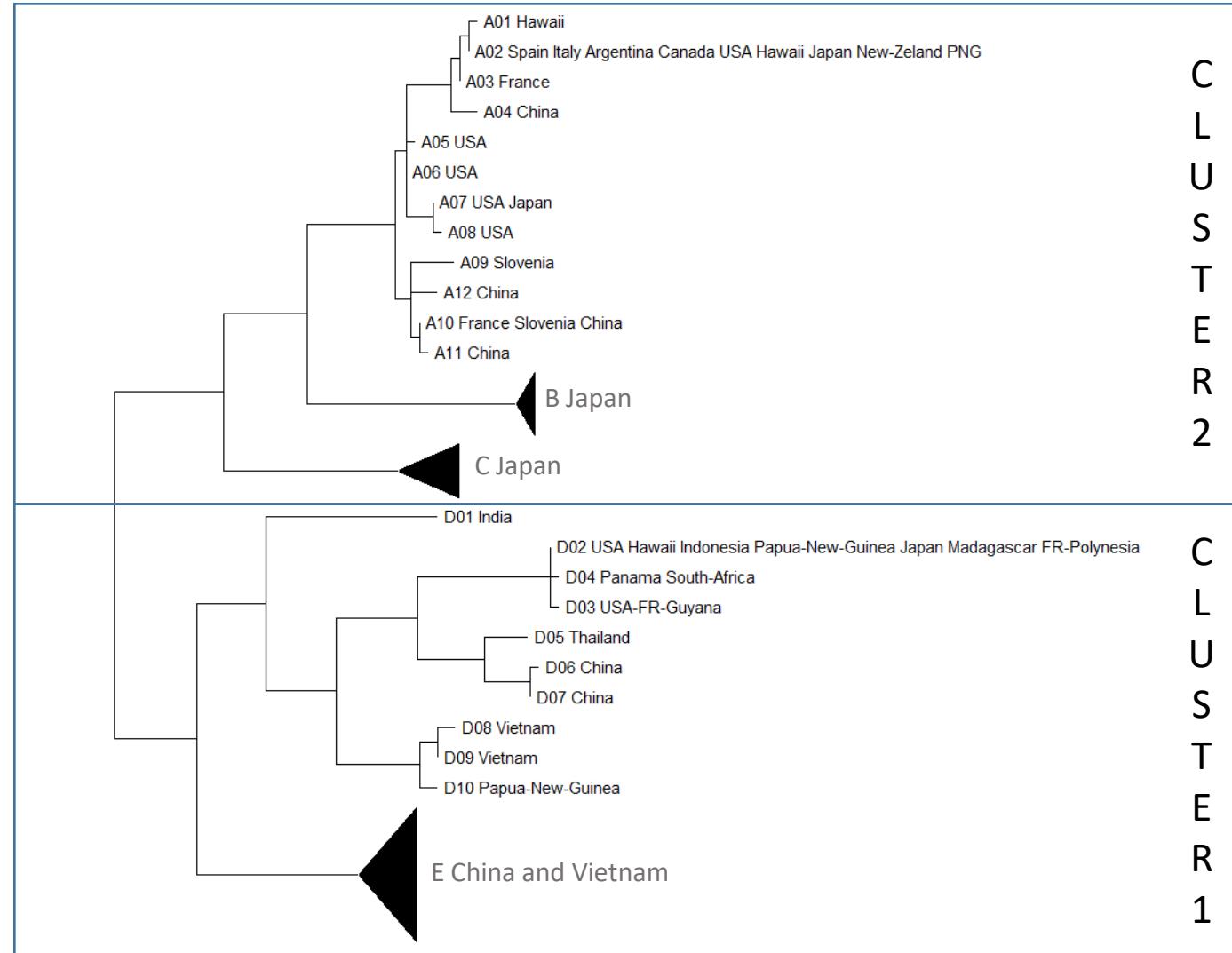


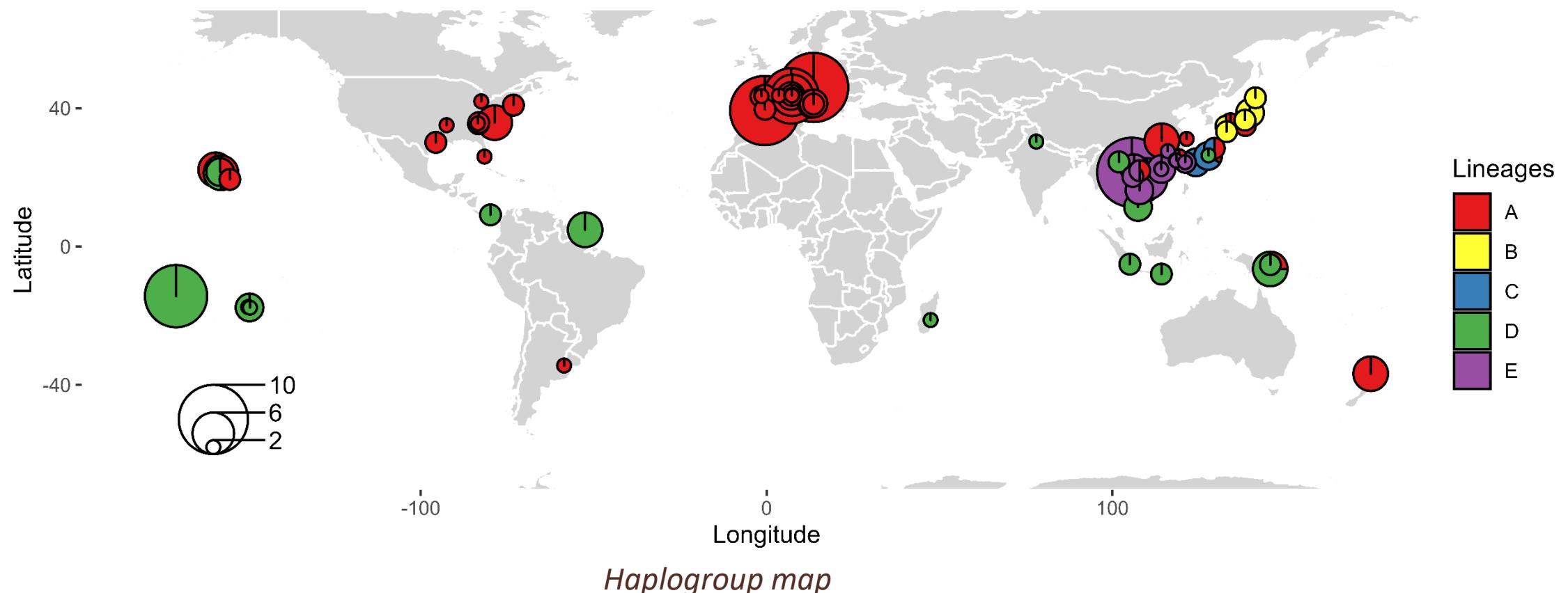
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# *X. crassiusculus*' genetic structure

## Mitochondrial DNA analysis

- 12 invasive haplotypes from lineages A or D
- 4 invasive haplotypes found in the native area
  - 3 in one or several Japanese Islands
  - 1 in China



# *X. crassiusculus*' genetic structure

## Invasion in Europe

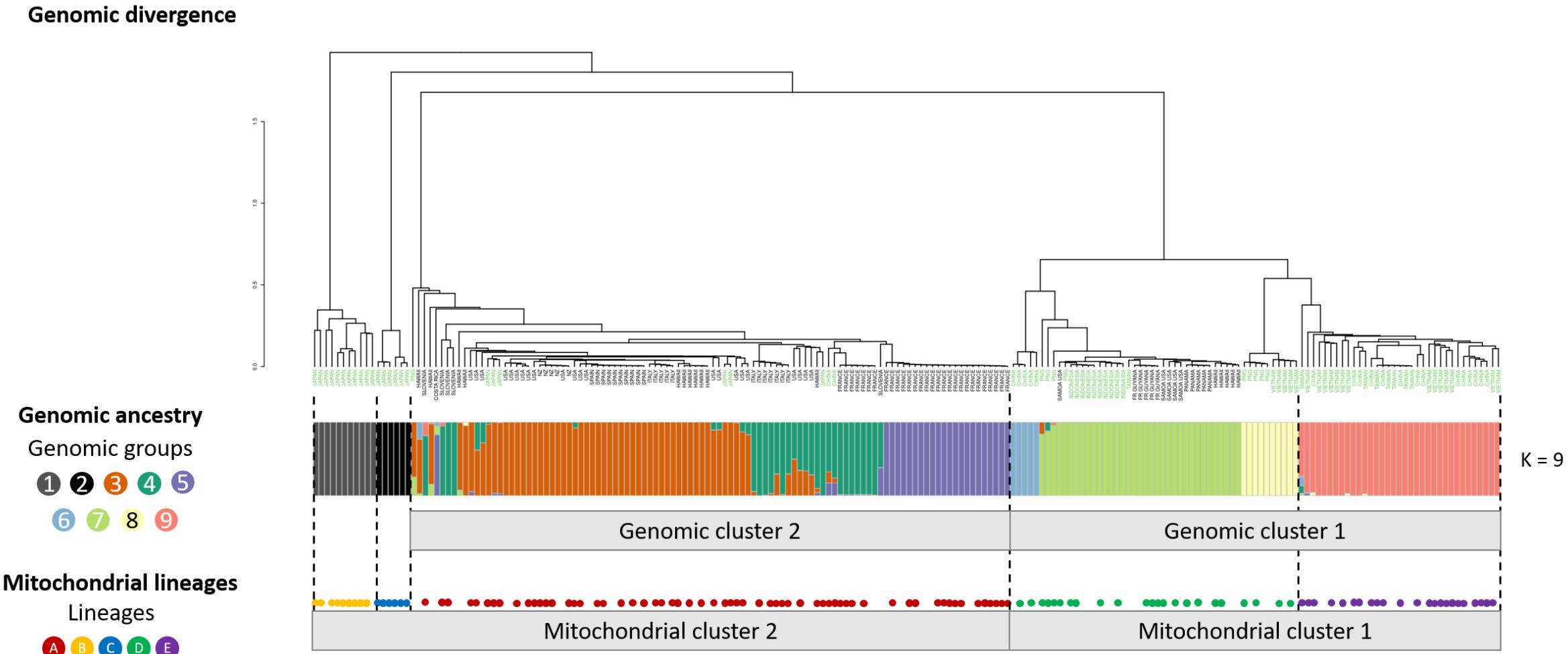
- A2 in Italy, Spain and Japan
  - A3 in Western France
  - A9 only in Slovenia
  - A10 in France, Slovenia and Shanghai
- Differ by only one substitution



# *X. crassiusculus*' genetic structure

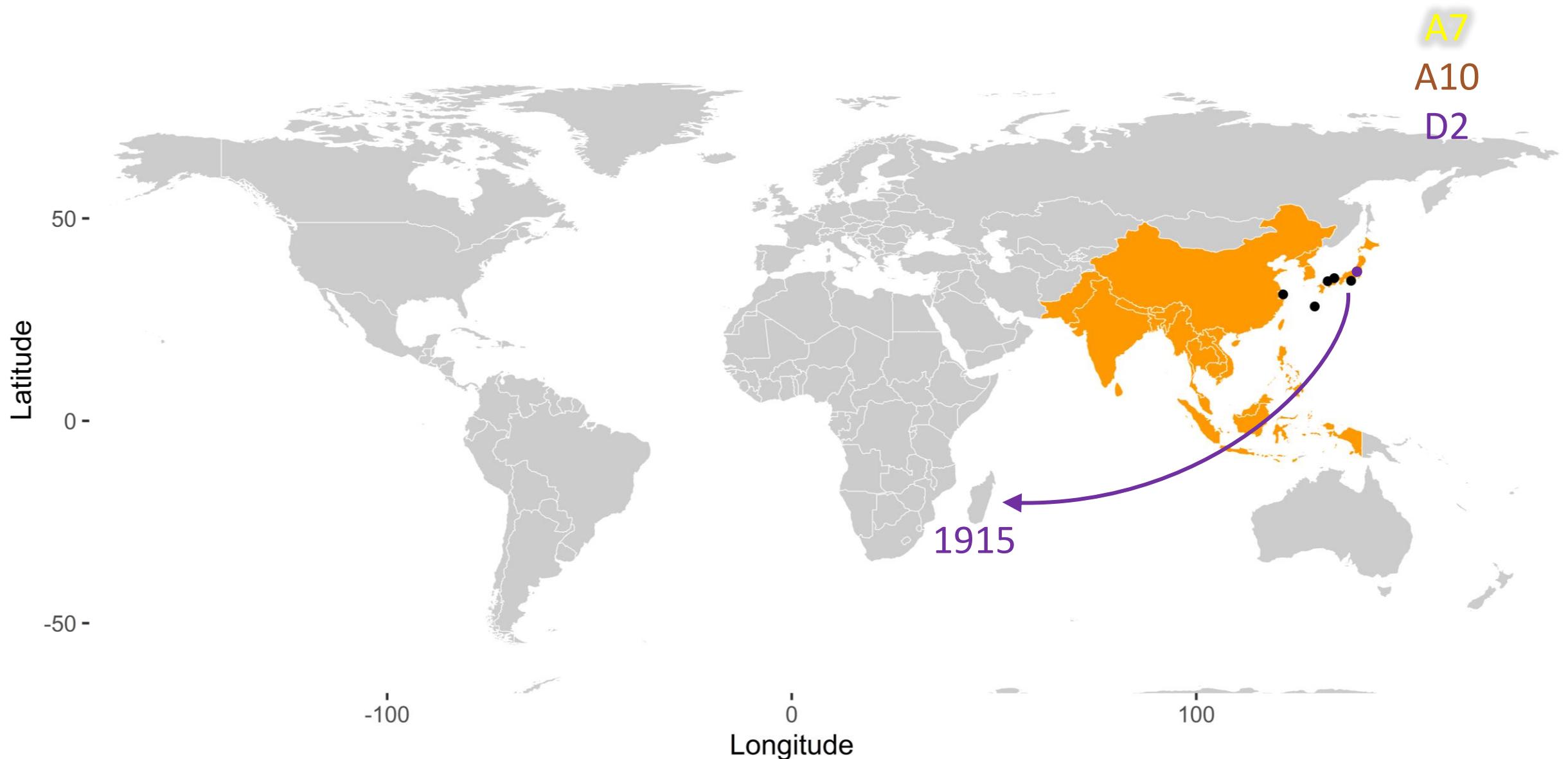
## RAD sequencing analysis

- Mostly coherent with mitochondrial DNA results



# *X. crassiusculus*' genetic structure

Hypotheses for invasion history (still in progress)

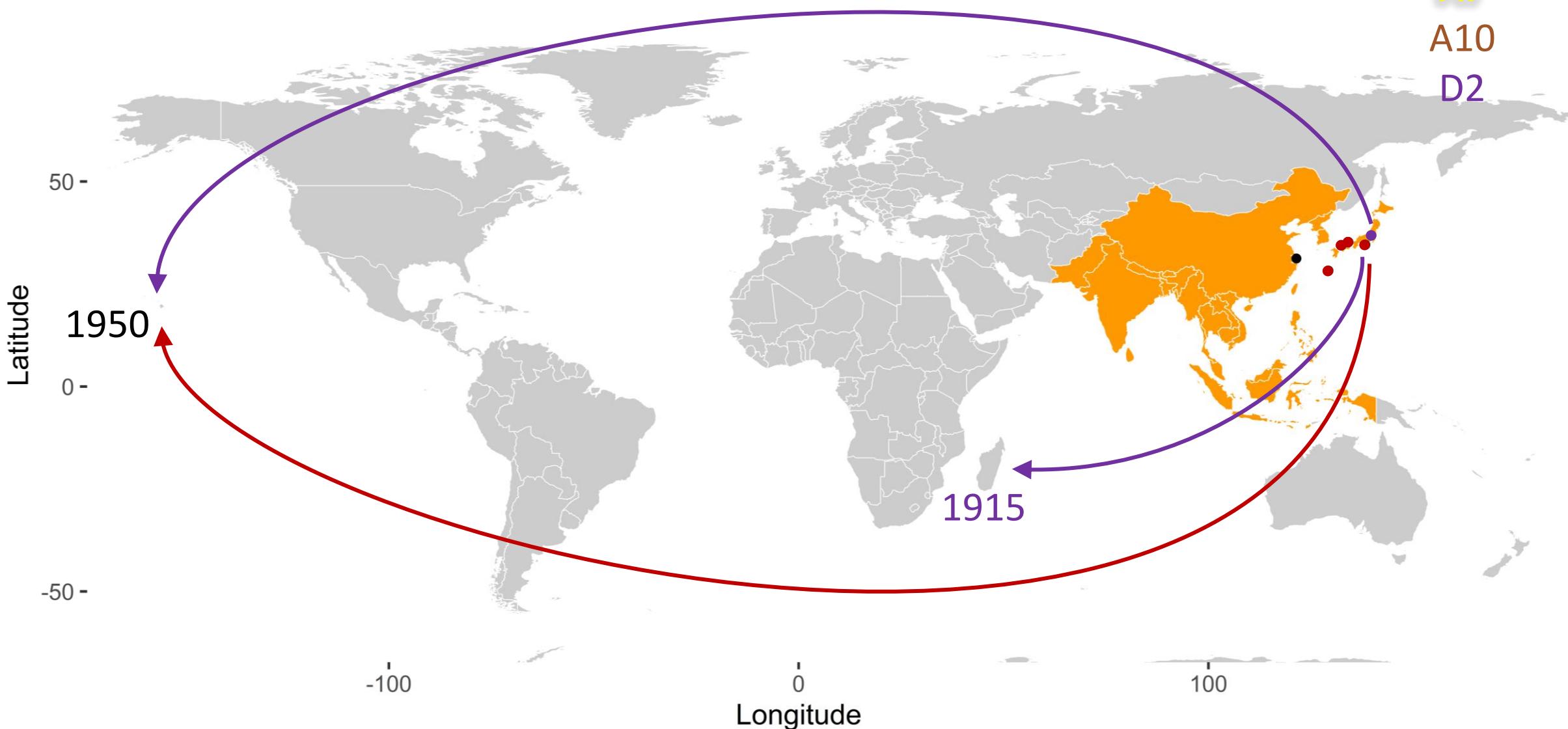


# *X. crassiusculus*' genetic structure

Hypotheses for invasion history (still in progress)

Haplotypes

- A2
- A7
- A10
- D2

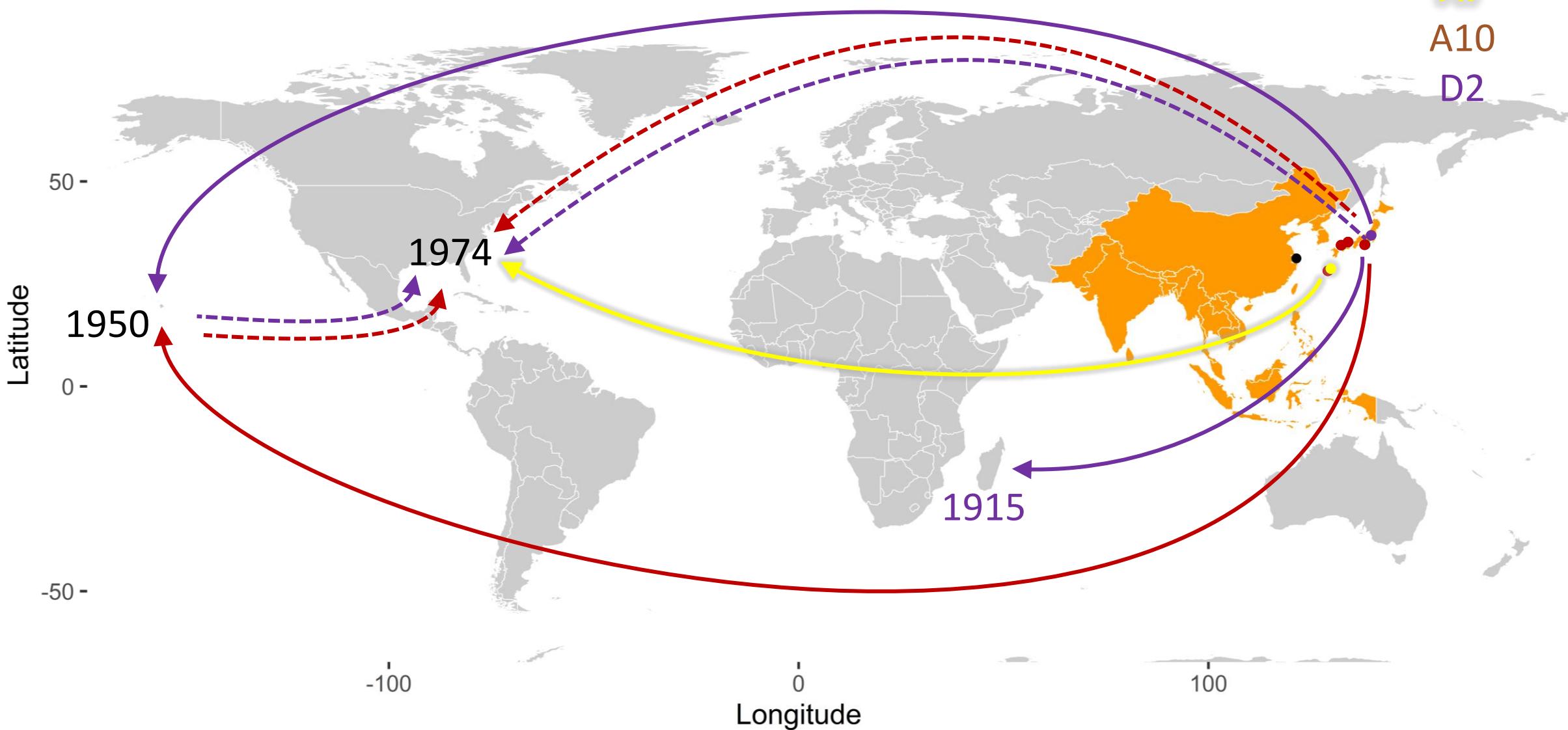


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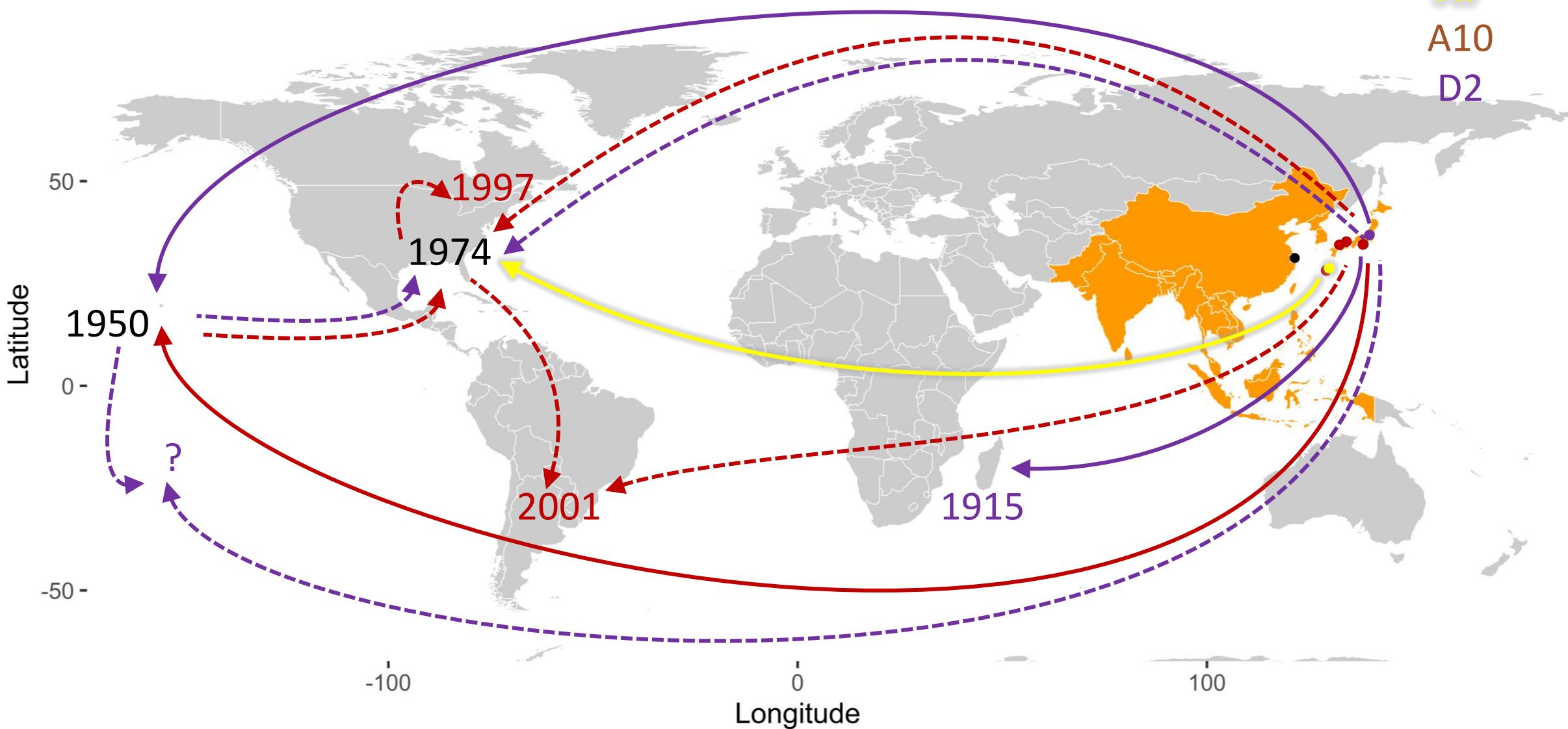
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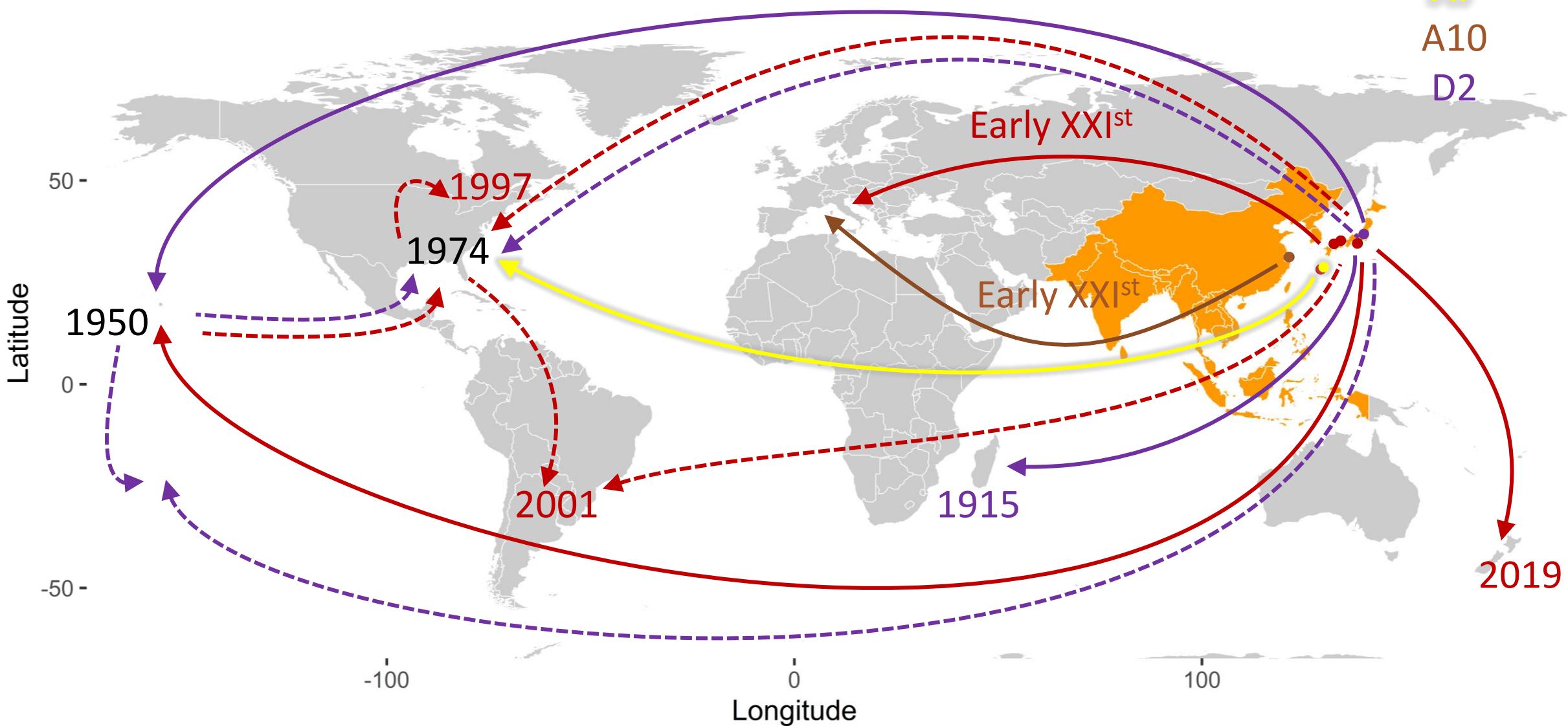
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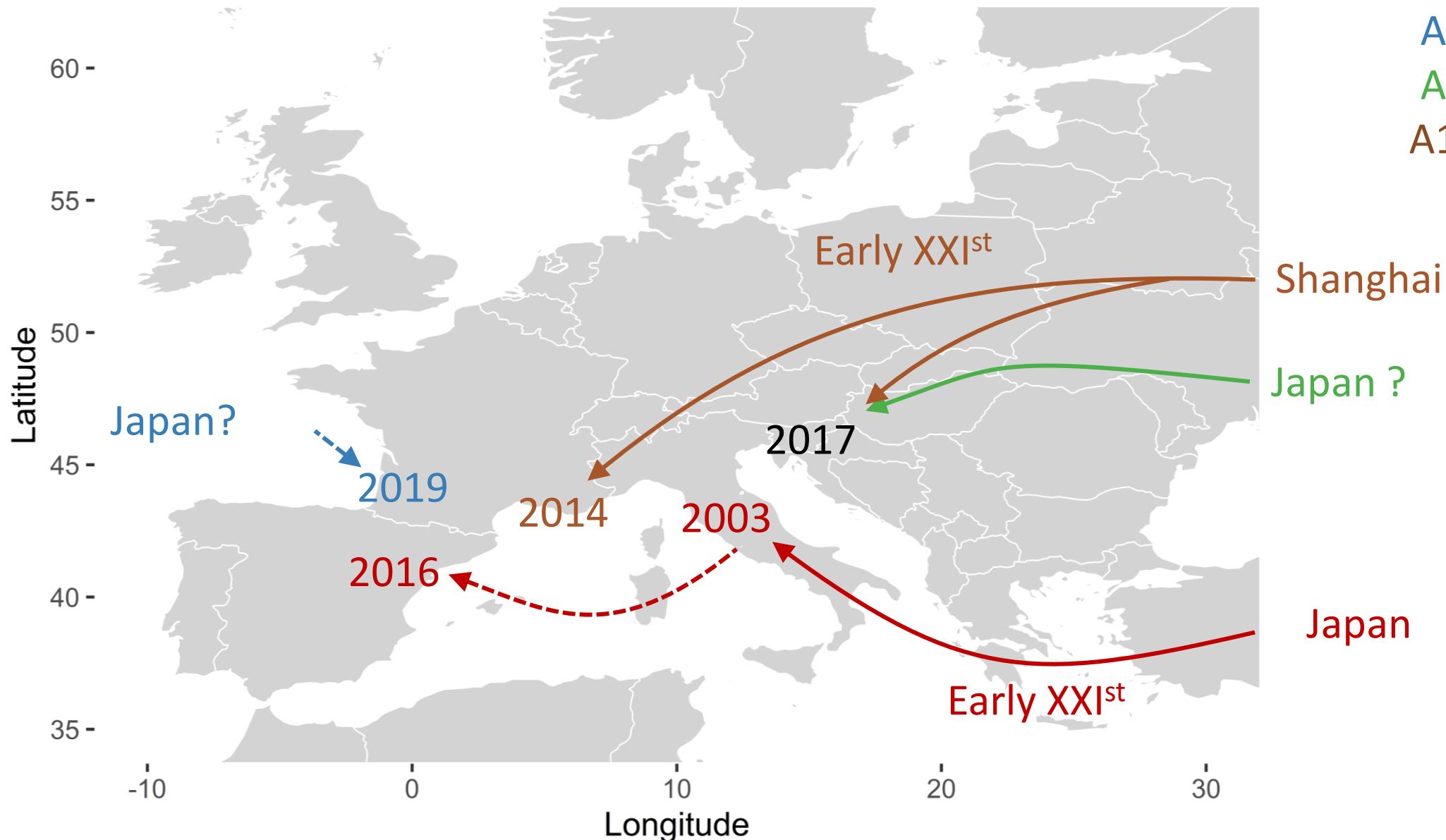
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# *X. crassiusculus*' genetic structure

Hypotheses for invasion in Europe (still in progress)

Haplotypes
A2
A3
A9
A10



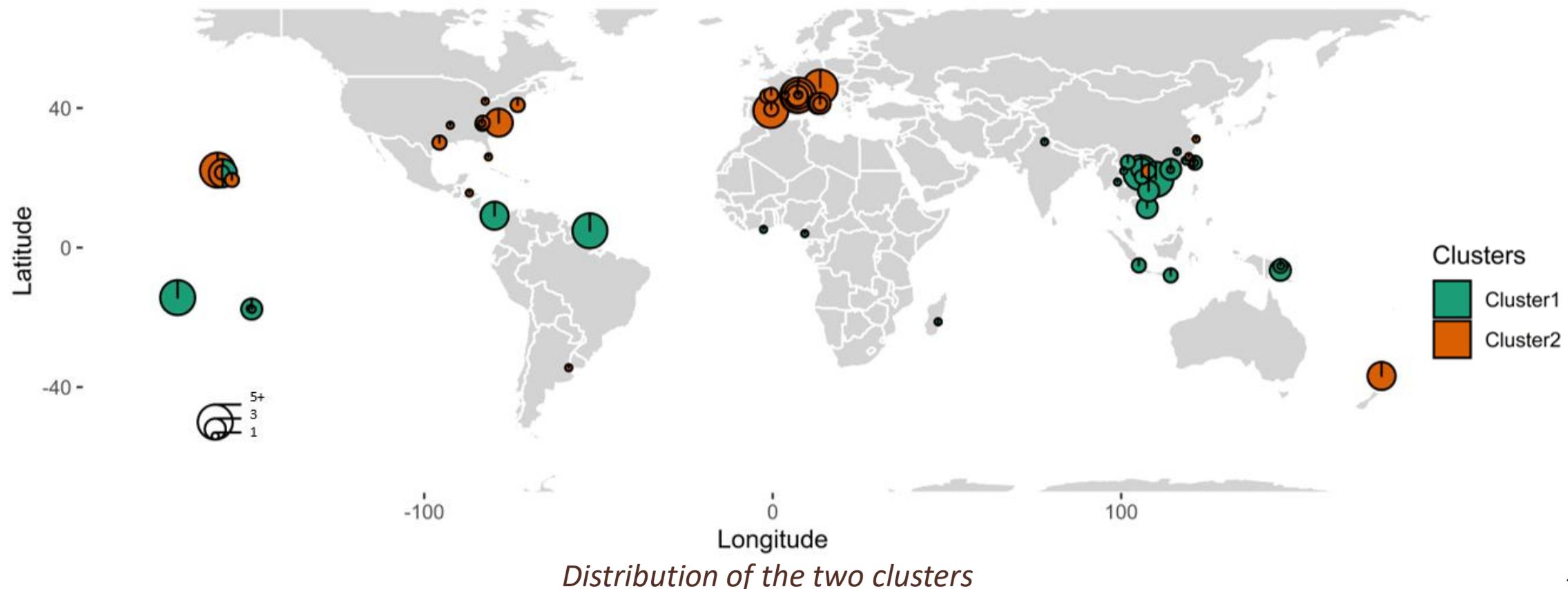
# *X. crassiusculus*' SDM failure

Major hypothesis: Clusters could have different ecological preferences

⇒ Geographical structuration

- Cluster 1: Circumtropical distribution
- Cluster 2: Peripheric distribution

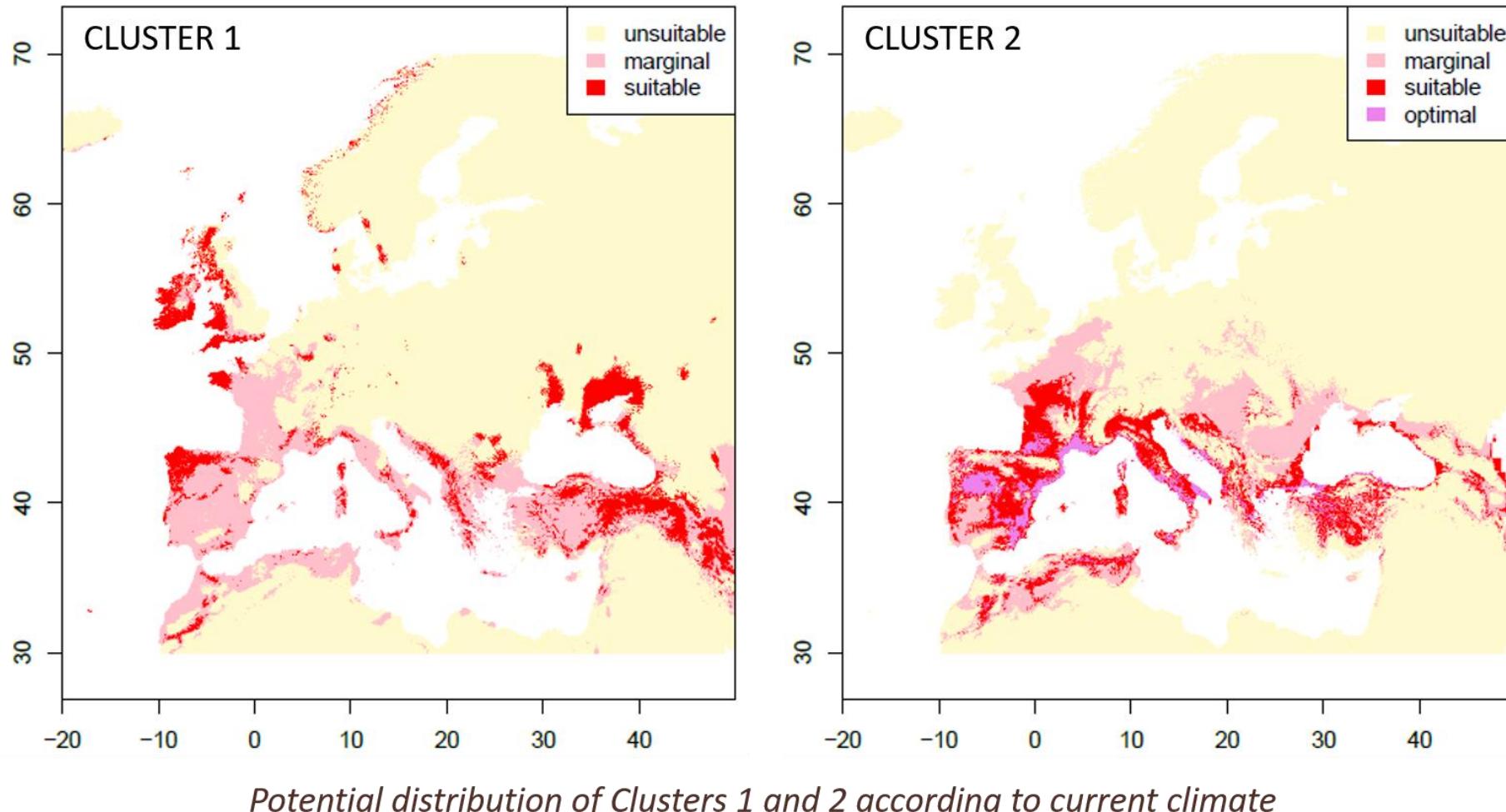
} Perform SDM on each cluster separately !



# *X. crassiusculus*' SDM failure

SDM by cluster (still in progress)

- Ecological niches significantly different
- Cluster 1 could potentially invade Europe



# Take Home Message

Two close species with different invasion history

*X. compactus*, low diversity and simple history

- Single introduction from Shanghai in Italy
- Stepping stone in Europe

*X. crassiusculus*, higher diversity and more complex history

- Several introductions from several origins
- Possibly Japan and China (Shanghai)
- Italy is not the source for all European invasions

**Thank you for your attention!  
Any questions?**

