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

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10 June 2021

Two ambrosia beetles

Xylosandrus crassiusculus: 2003 in Italy

Xylosandrus compactus: 2011 in Italy

Xylosandrus compactus

Xylosandrus crassiusculus

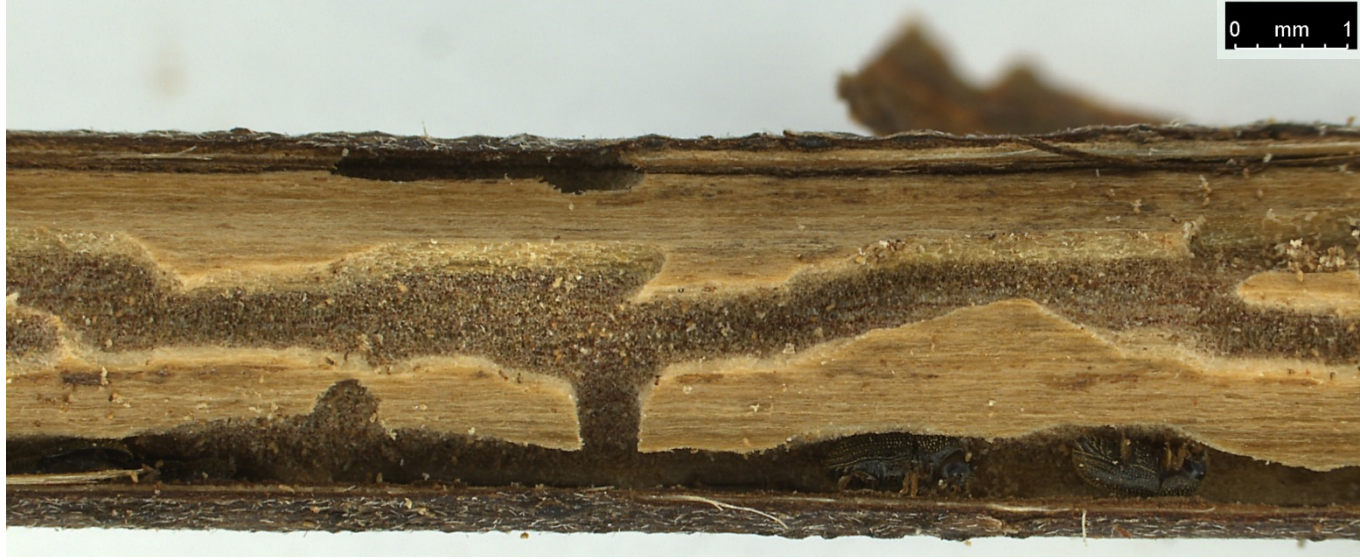
Two ambrosia beetles

Xylosandrus crassiusculus: 2003 in Italy

Xylosandrus compactus: 2011 in Italy

A biology favouring invasion

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



Two ambrosia beetles

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

X. crassiusculus' mycangium

Two ambrosia beetles

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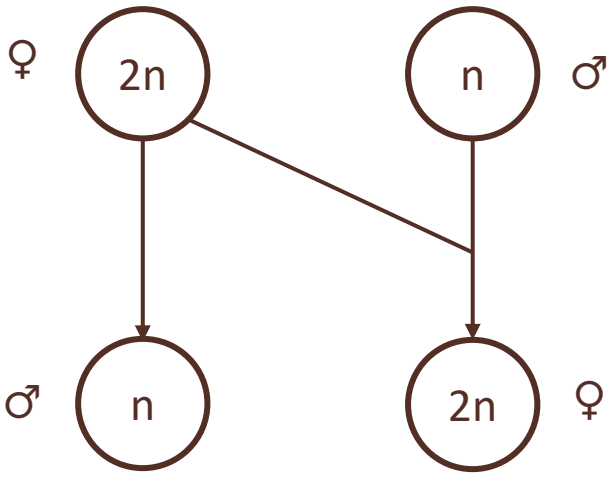

A biology favouring invasion

- 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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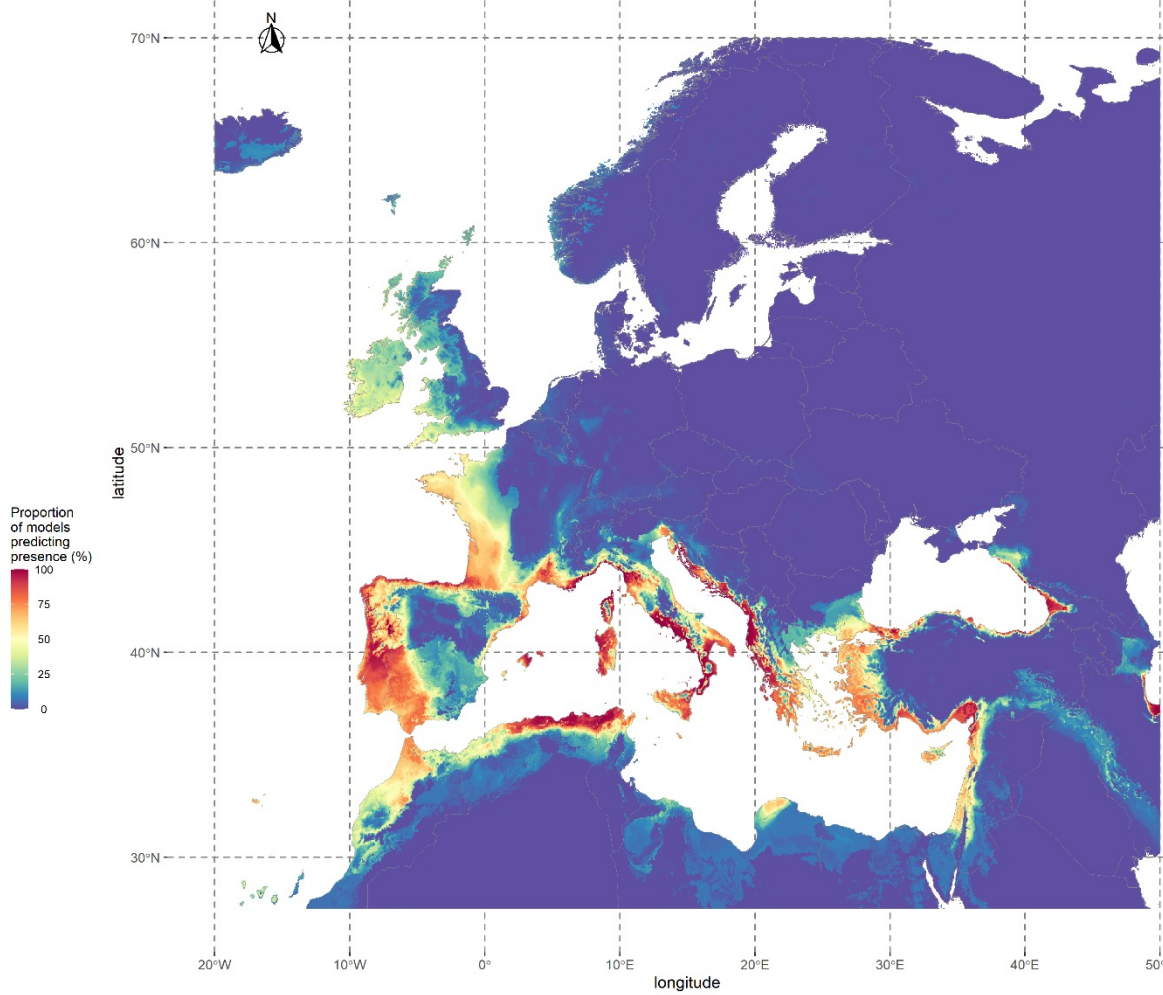

Predict suitable areas

- Species Distribution Modelling (SDM)
  - Published for *X. compactus* (Urvois et al. 2021)
  - Failed for *X. crassisculus* ⇨ **Could be solved wi**

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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

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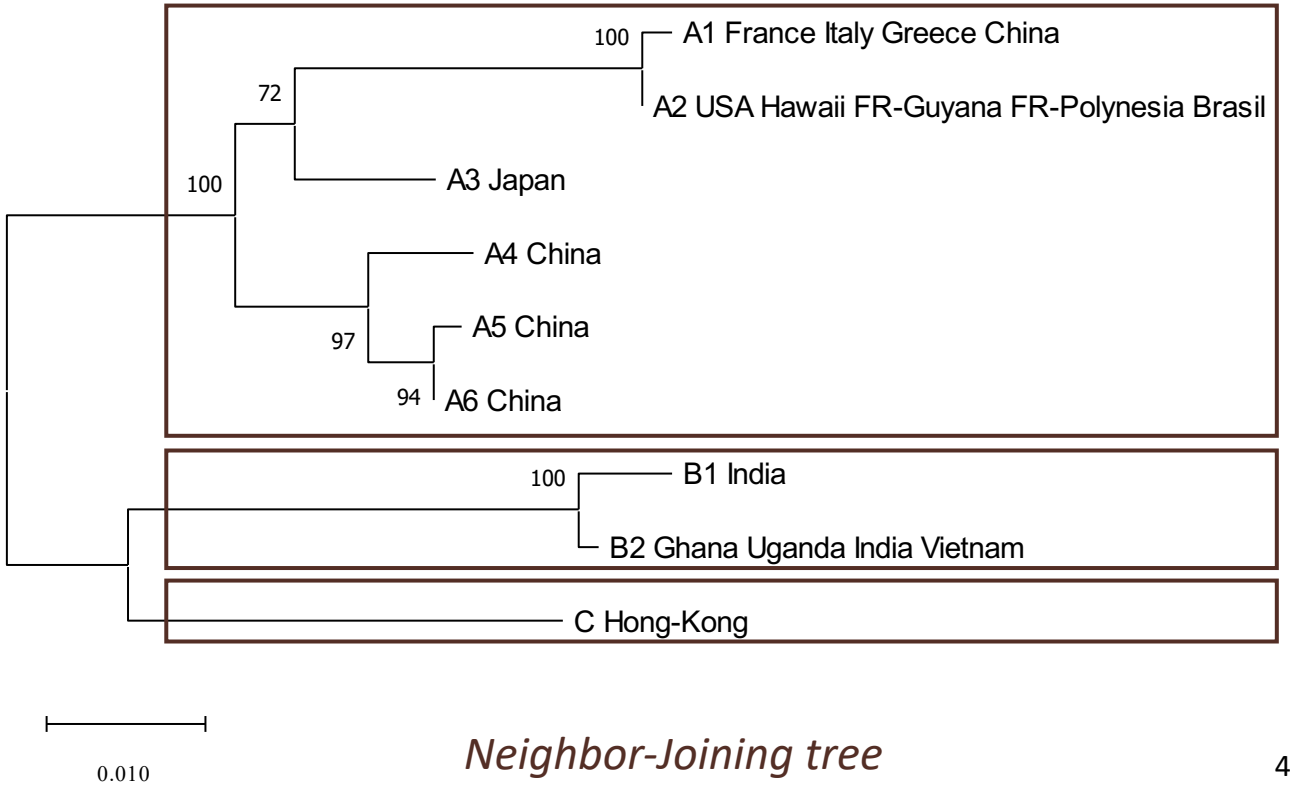
681 Accesses | **2** Citations | **1** Altmetric | Metrics

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)

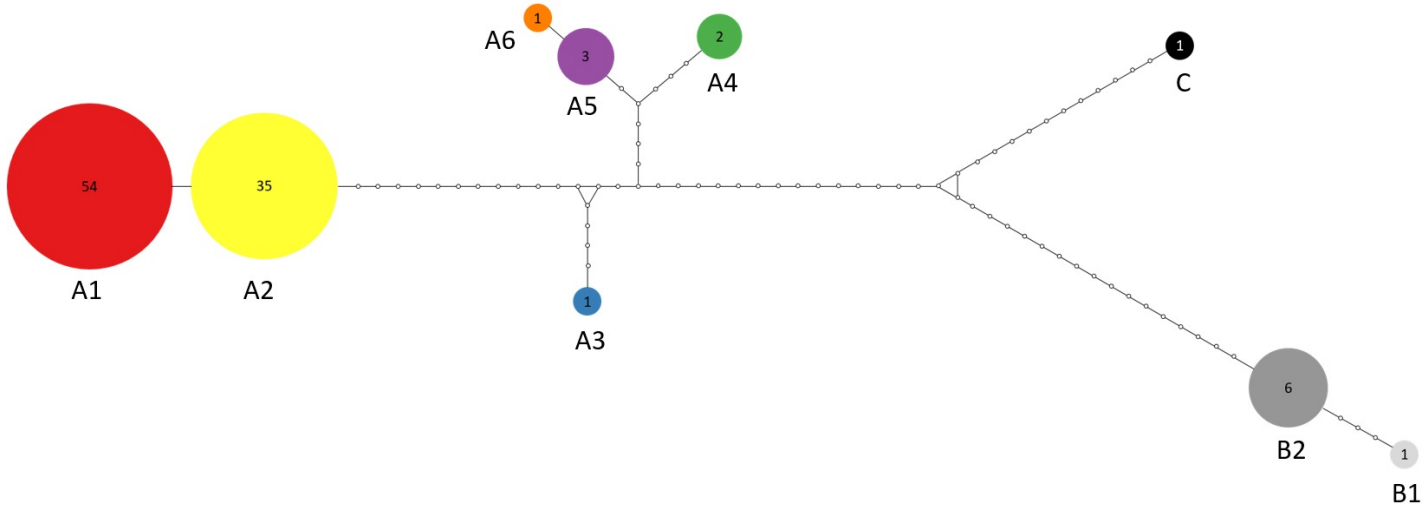


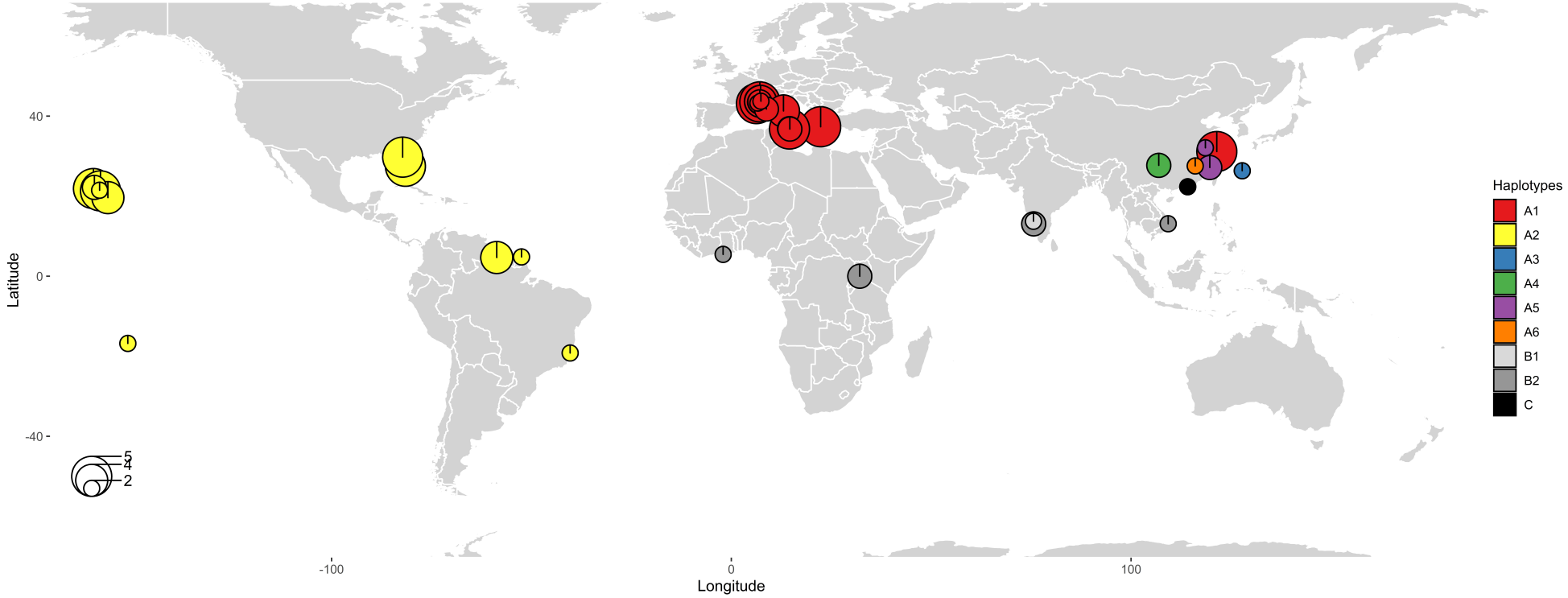
Neighbor-Joining tree

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 area



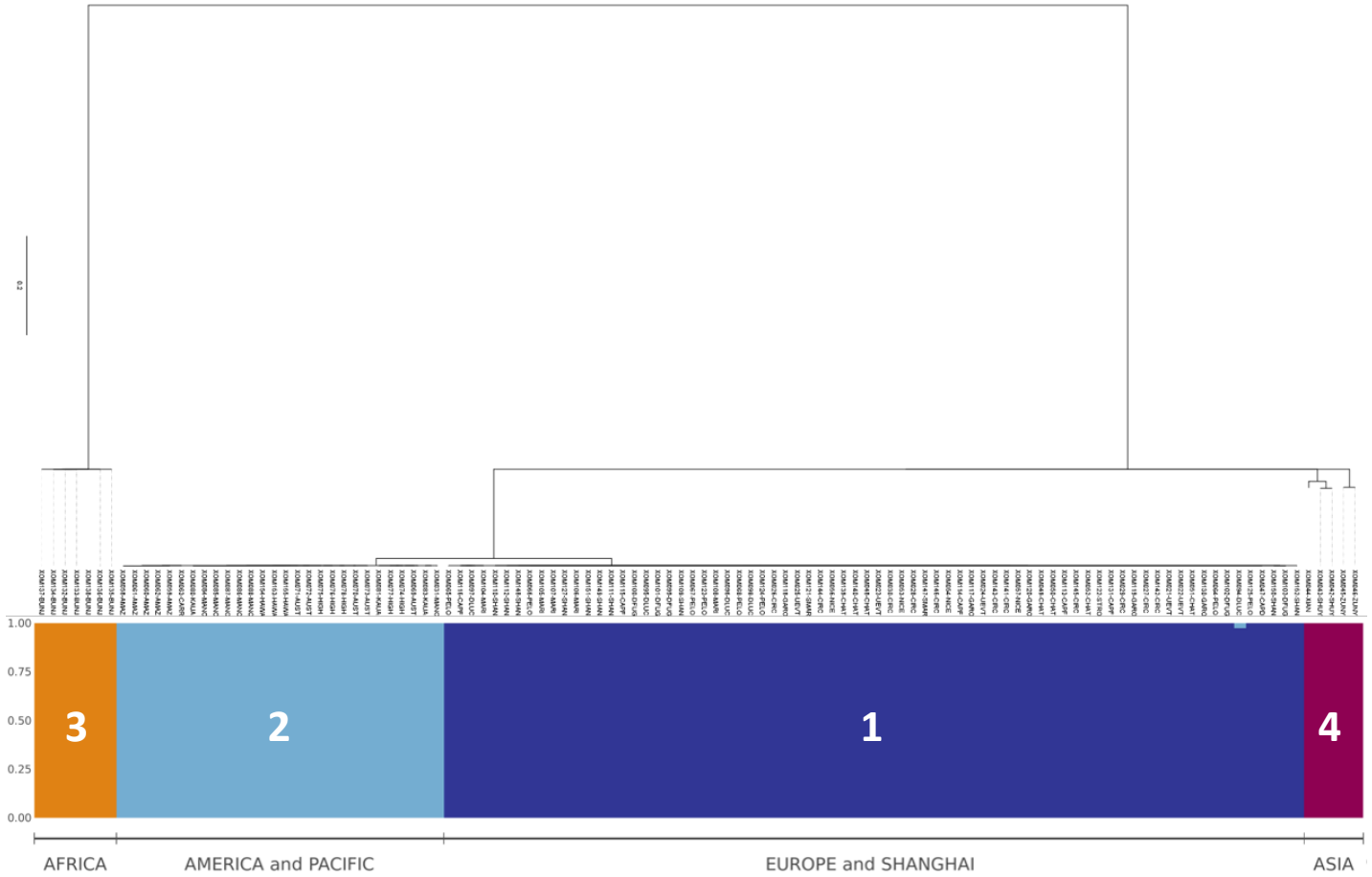


Haplotype map

X. compactus' genetic structure

RAD sequencing analysis

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

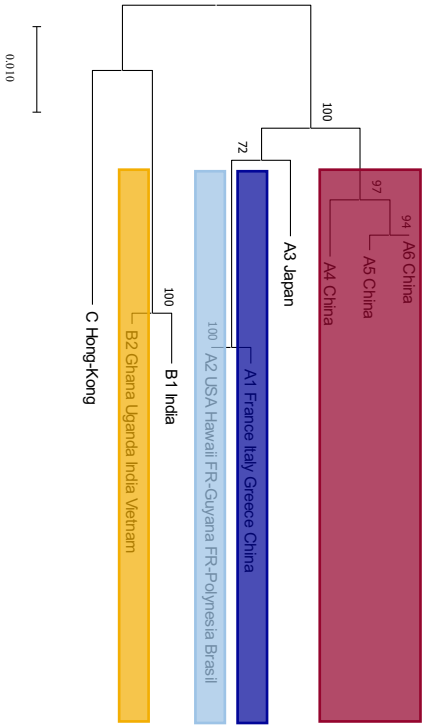


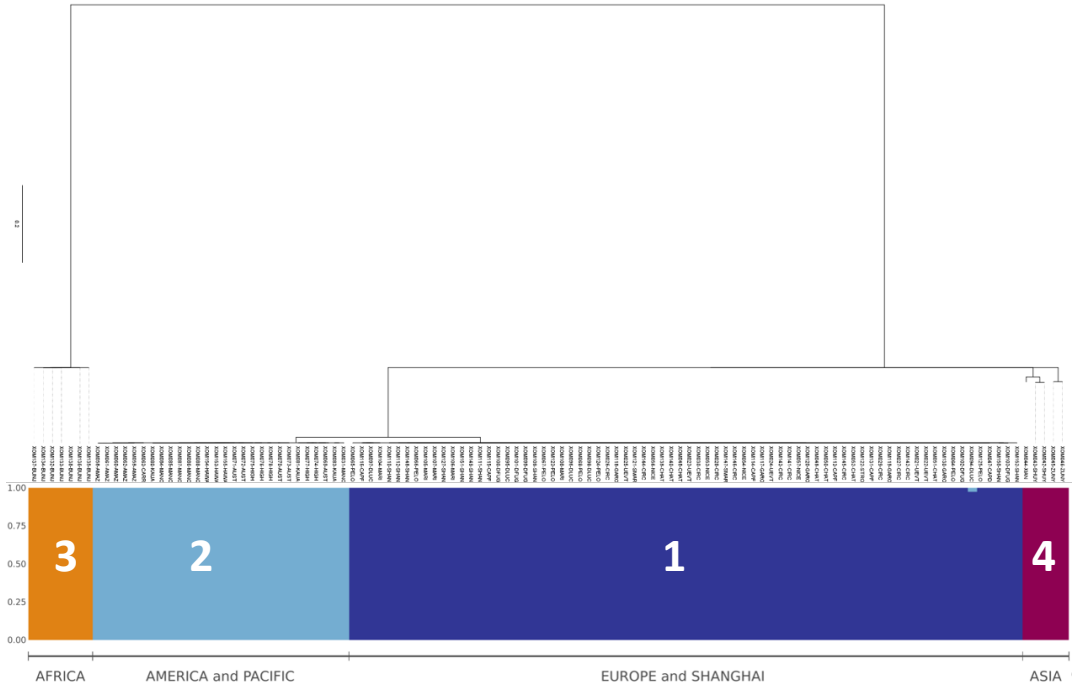
Maximum Likelihood tree and Admixture plot

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

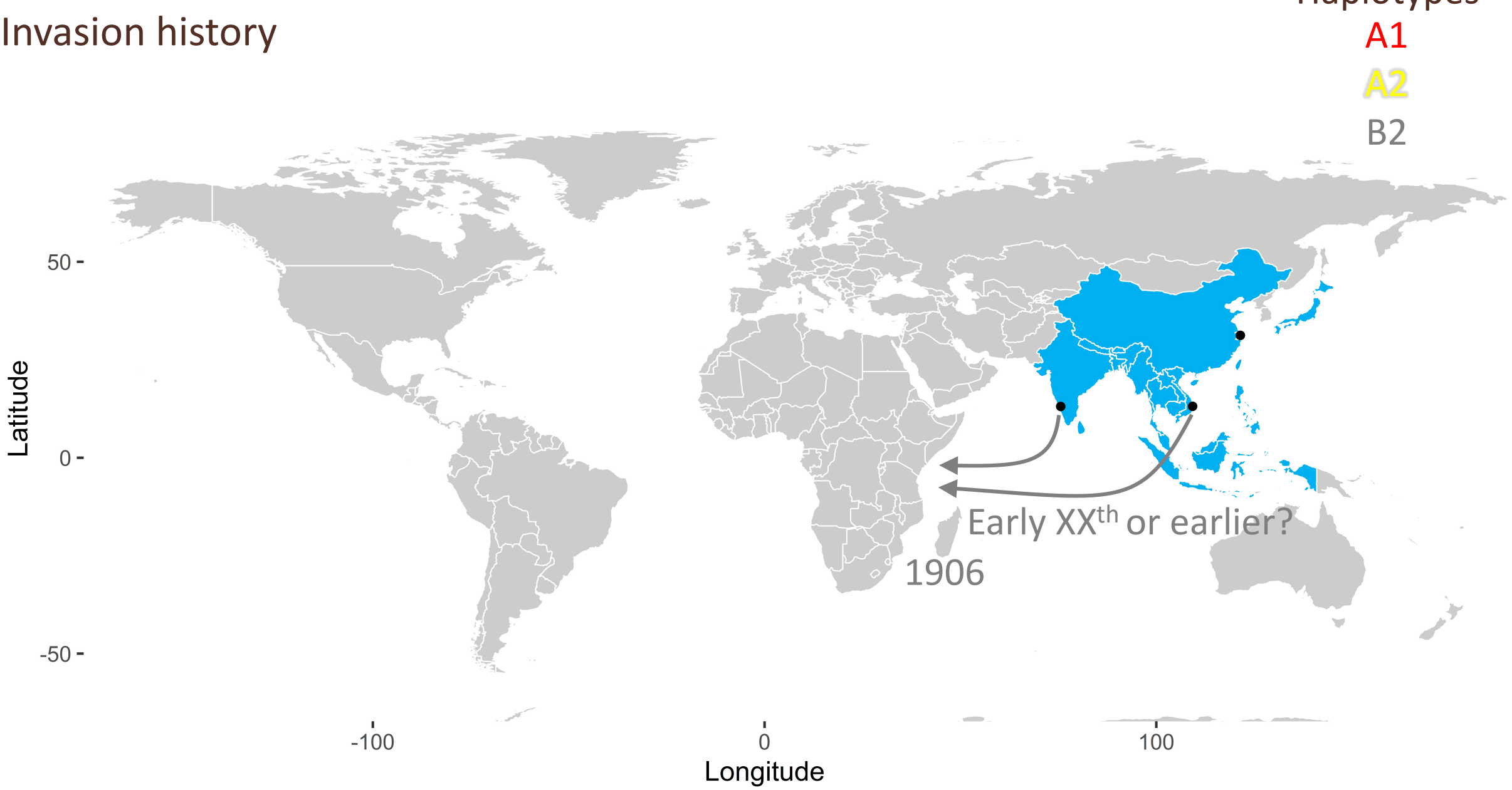




Maximum Likelihood tree and Admixture plot

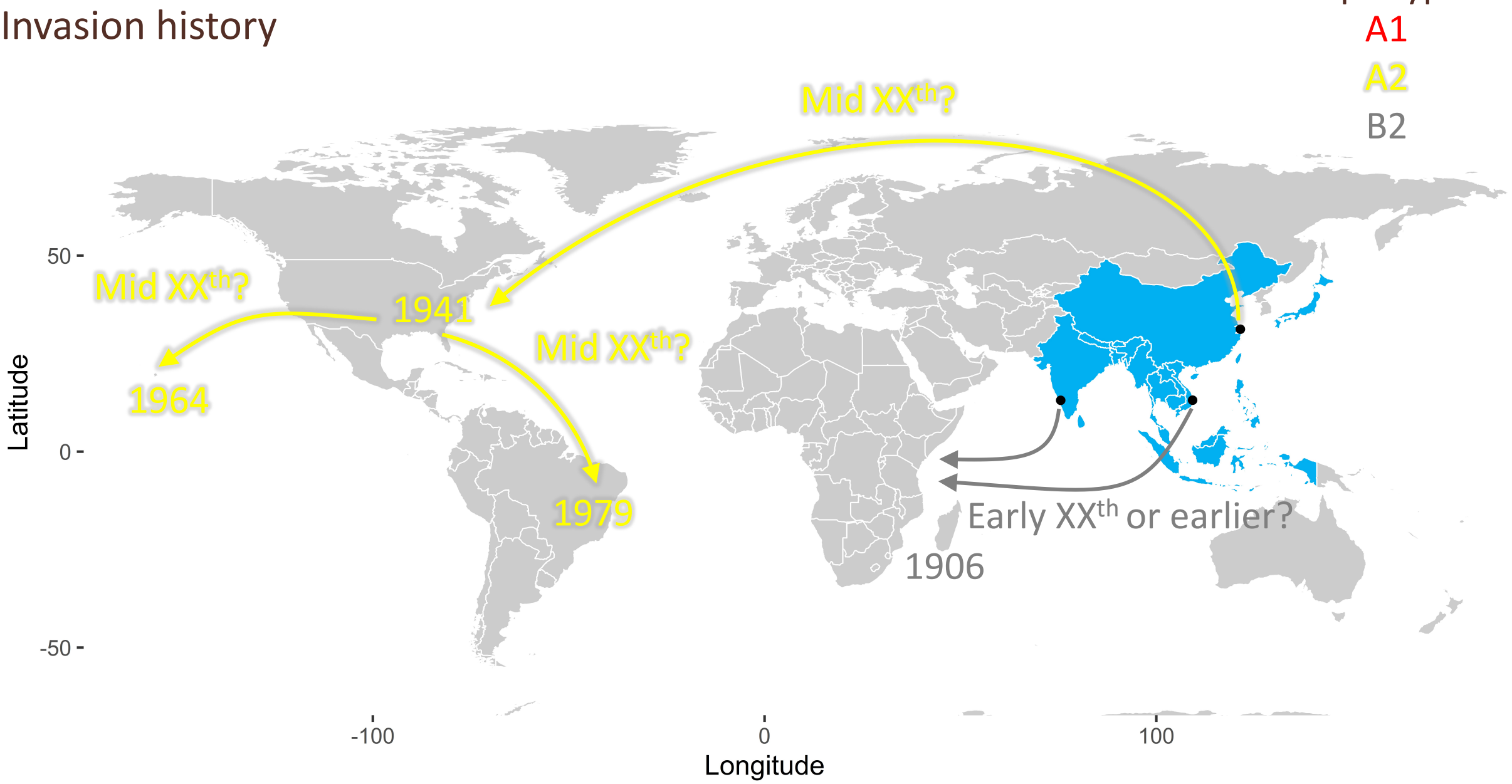
X. compactus' genetic structure

Invasion history



X. compactus' genetic structure

Invasion history



X. compactus' genetic structure

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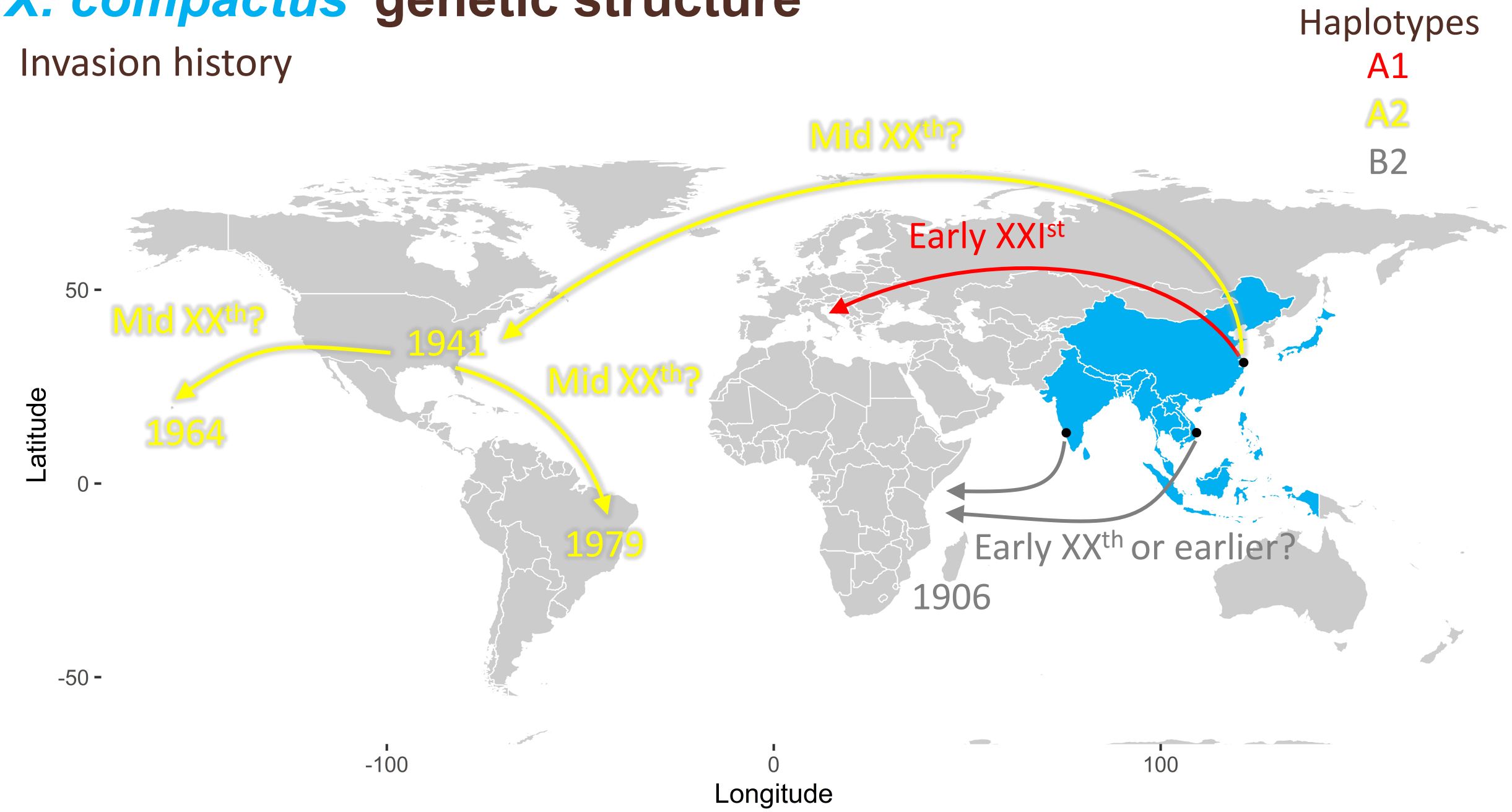
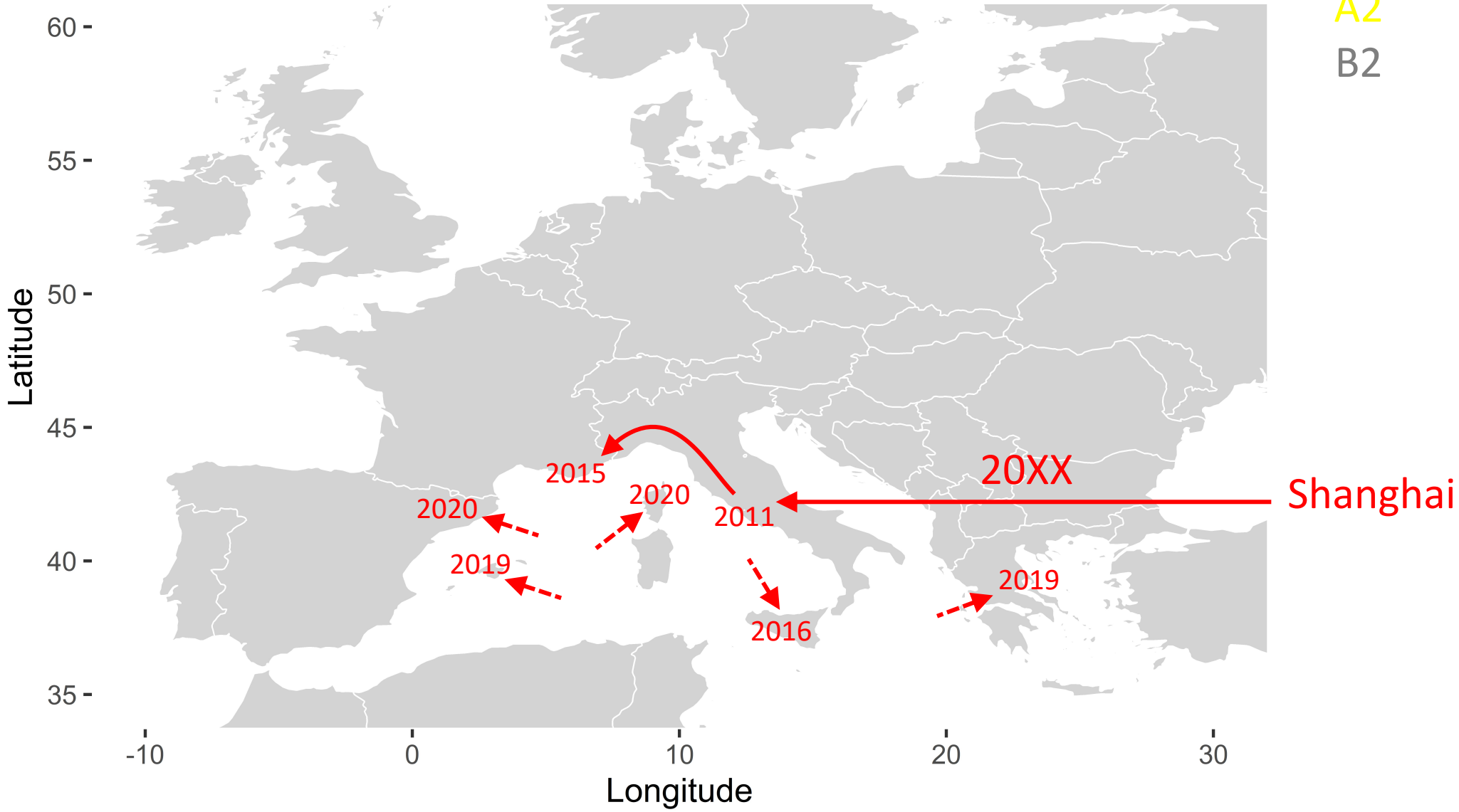


X. compactus' genetic structure

European invasion history



X. crassiusculus' genetic structure

Summary of the litterature

- 3 non-overlapping papers

Ito & Kajimura 2009

Mitochondrial marker
Jerry-Pat

Sampling :
Japan

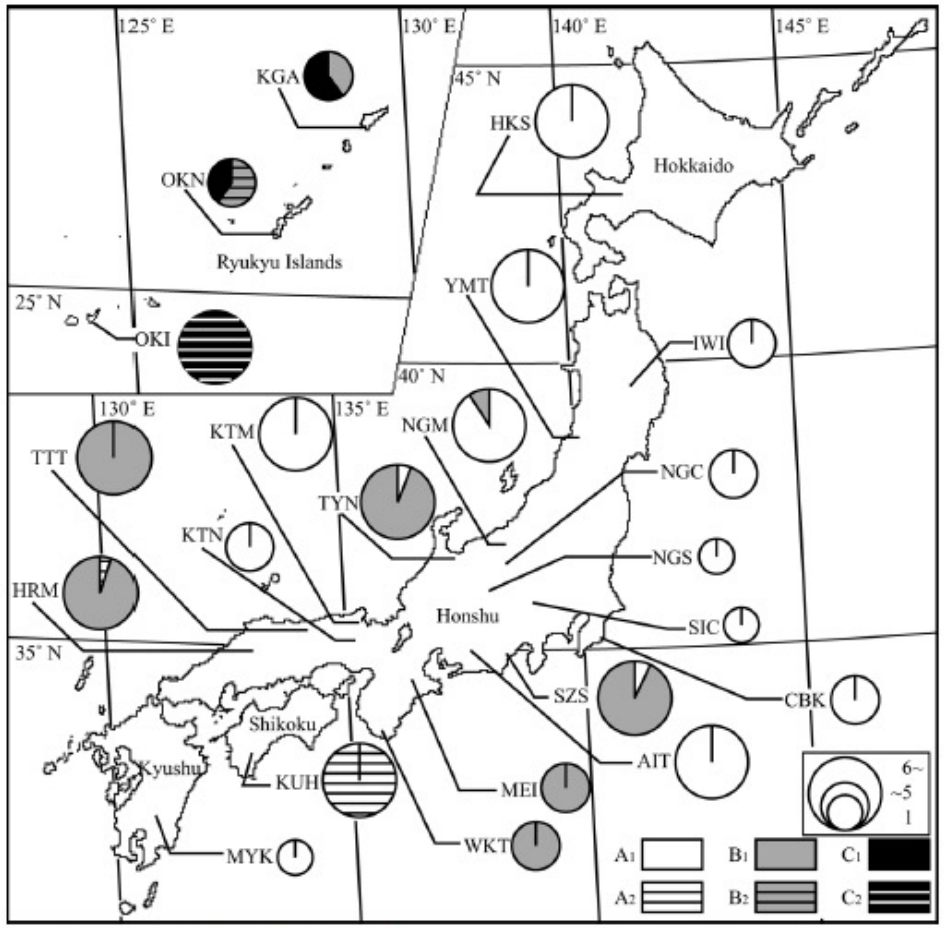


Fig. 2. Distribution of *COI* mitochondrial DNA haplotypes across 22 Japanese *Xylosandrus crassiusculus* populations. Pie graphs represent the frequency of *COI* haplotypes belonging to subclades A_1, A_2, B_1, B_2, C_1 and C_2 in each population (Table 2). Circle size is proportional to sample size. Population names are defined in Table 1.

X. crassiusculus' genetic structure

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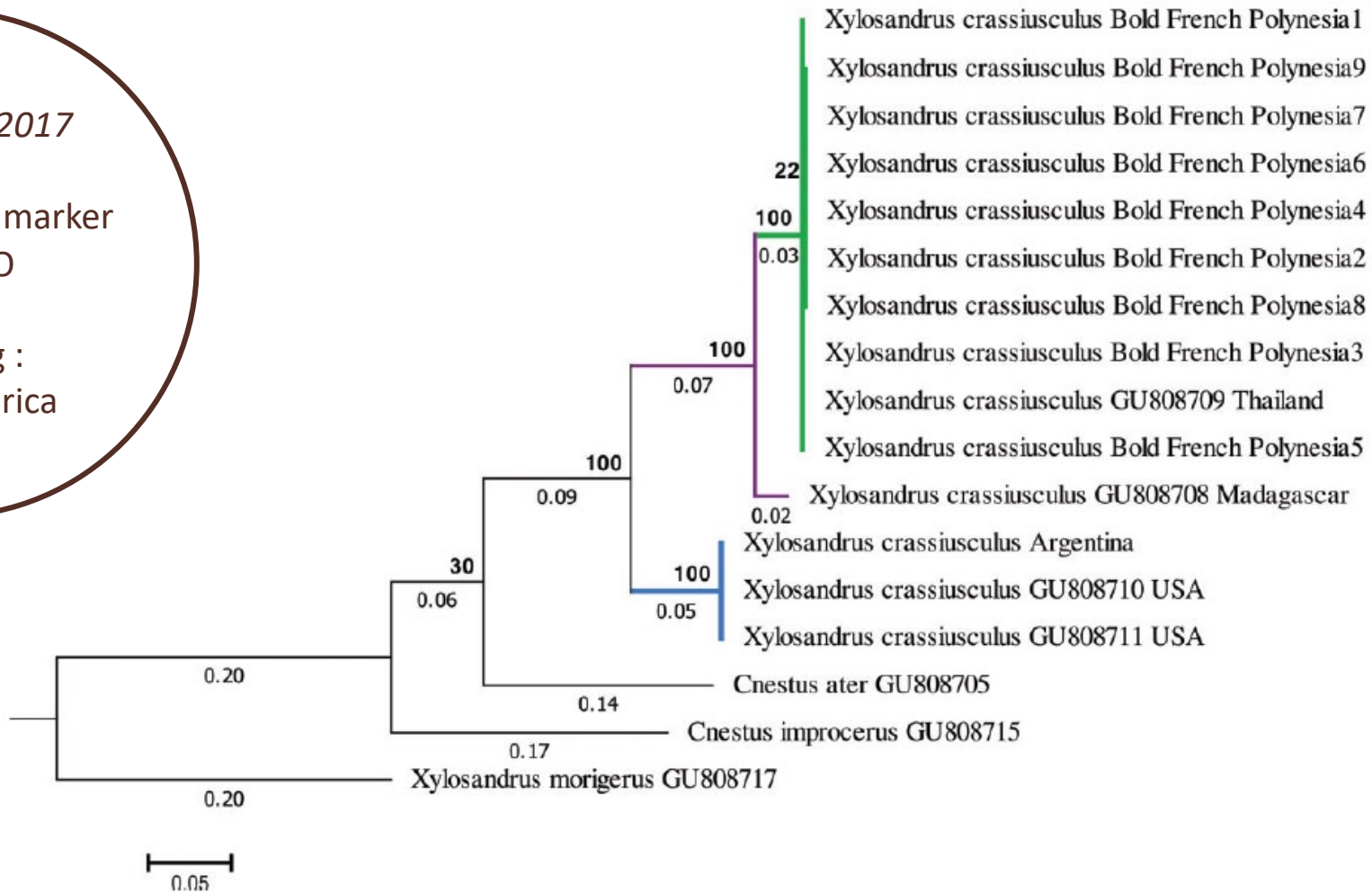

Fig. 3. ML tree, numbers above and below branches indicate bootstrap values and branch lengths, respectively. Sequences from GenBank are identified with their accession numbers on the right. Other sequences were obtained from BOLD public database.

X. crassiusculus' genetic structure

Summary of the litterature

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Ito & Kajimura 2009

Mitochondrial marker
Jerry-Pat

Sampling :
Japan

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Mitochondrial marker
LCO-HCO

Sampling :
South America

Storer et al. 2017

Nuclear marker
ddRADseq

Sampling :
Asia, Americas, Pacific
and Oceania

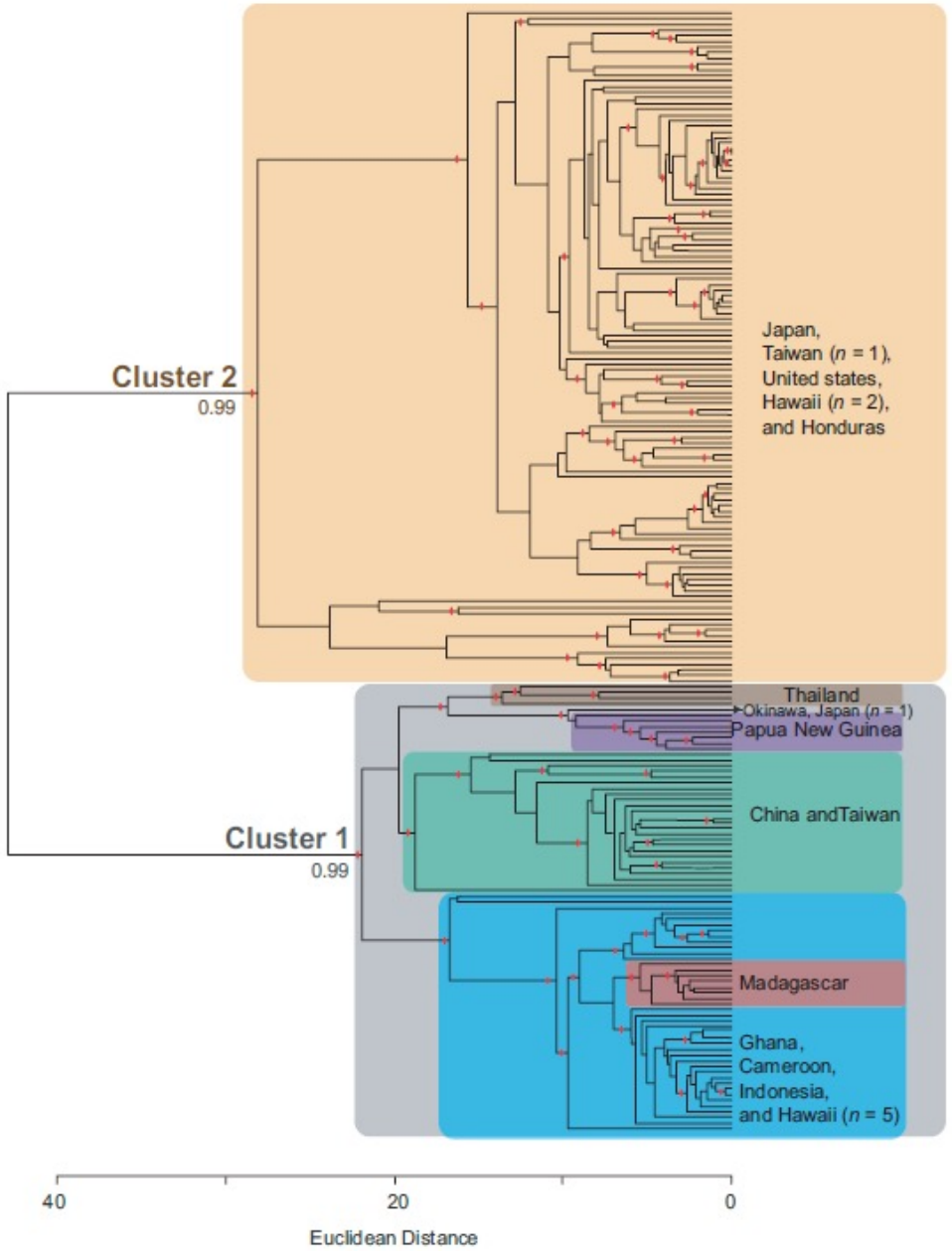


FIGURE 3 Ultrametric dendrogram of hierarchical clusters for all individuals. Statistically significant clusters ($p < .05$) are indicated by read hatch marks at cluster nodes. Clusters containing all individuals from one location are highlighted with color and labeled

X. crassiusculus' genetic structure

Summary of the litterature

- 3 non-overlapping papers

Main goal

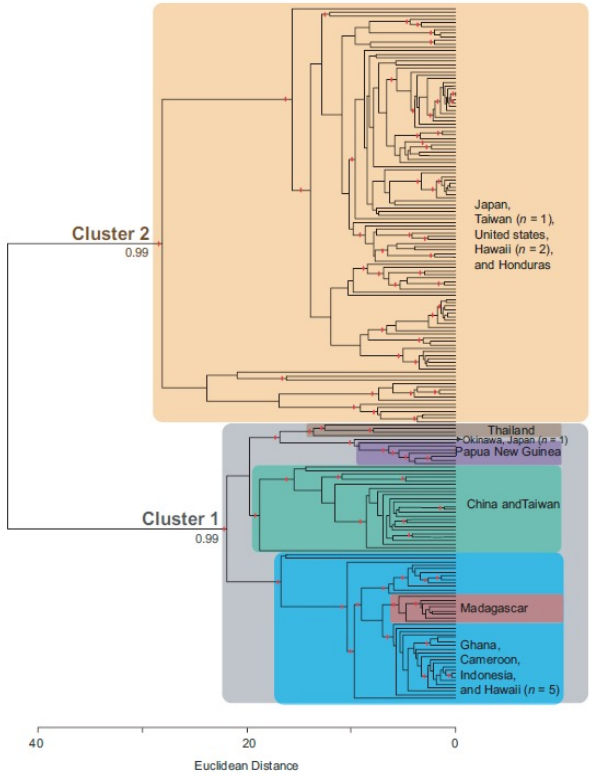
- Bridge the gap between these studies
  - Sampling every continent
  - Common genetic markers

RAD sequencing analysis in progress...

X. crassiusculus' genetic structure

Mitochondrial DNA analysis

- 49 haplotypes corresponding to 8 haplogroups
- 2 clusters as in *Storer et al. 2017*
  - Cluster 2: Haplogroups A-C
  - Cluster 1: Haplogroups D-F



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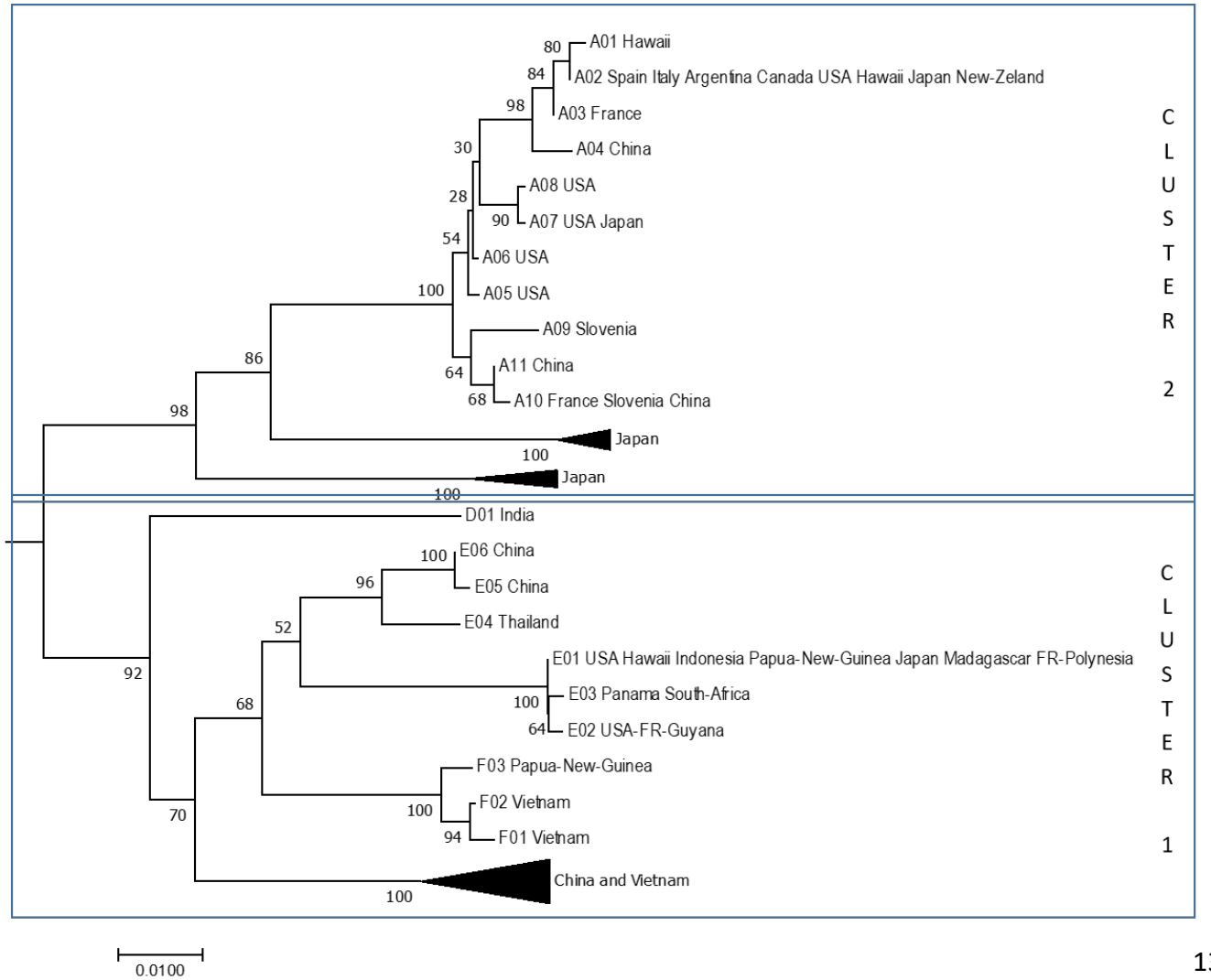
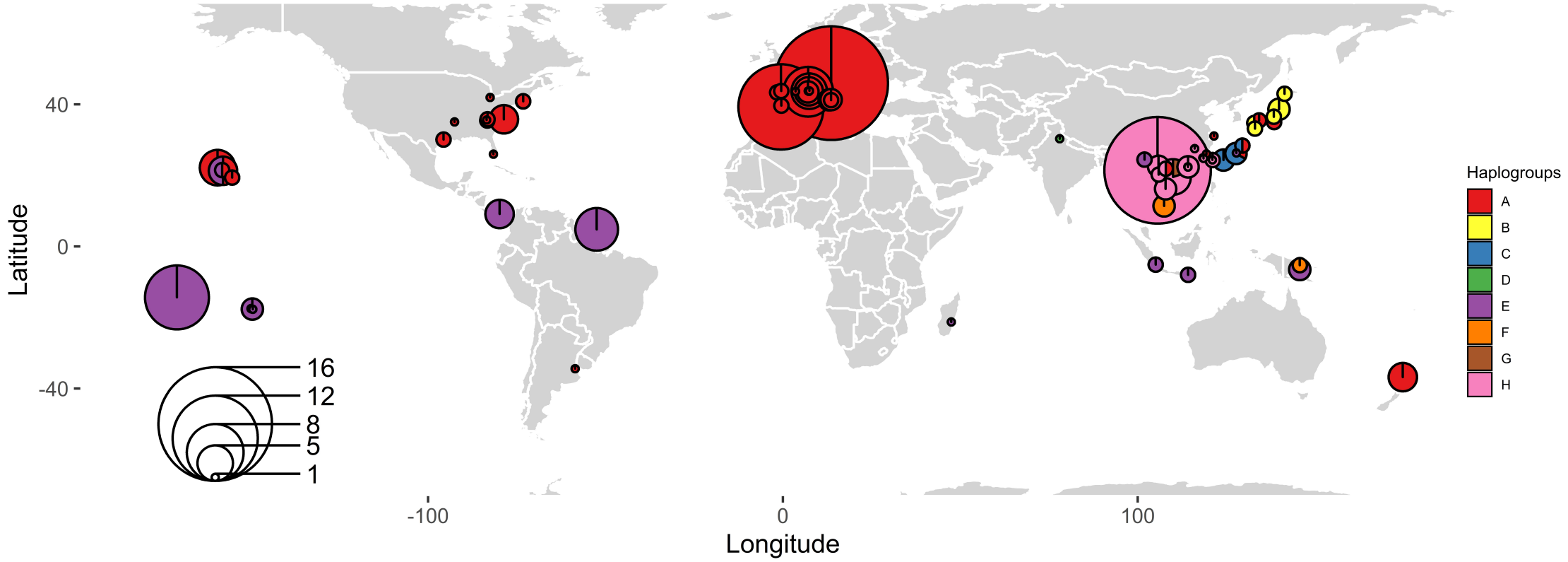


X. crassiusculus' genetic structure

Mitochondrial DNA analysis

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



Haplogroup map

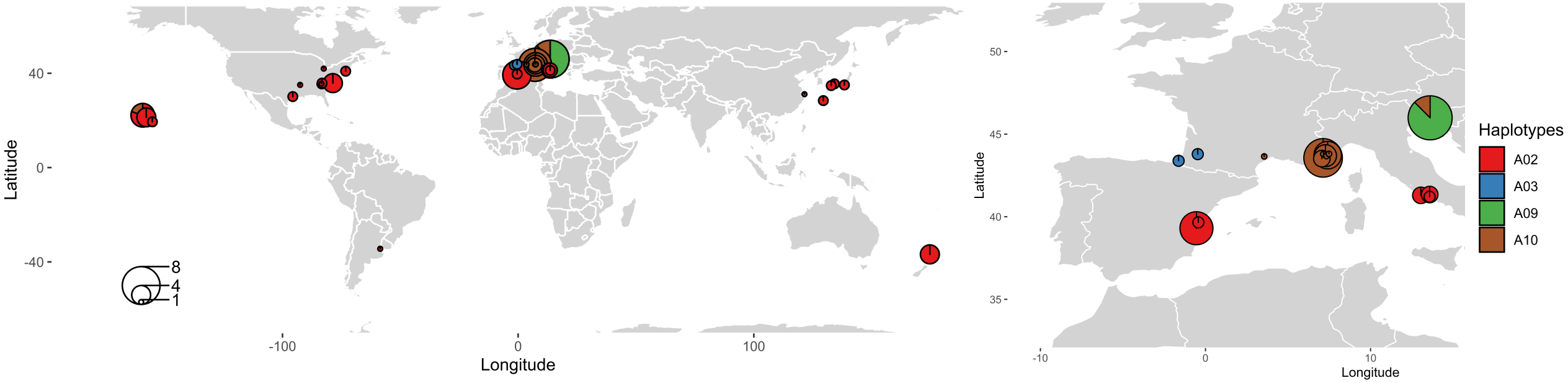
X. crassiusculus' genetic structure

Invasion in Europe

- A2 in Italy, Spain and Japan
- A3 in Western France

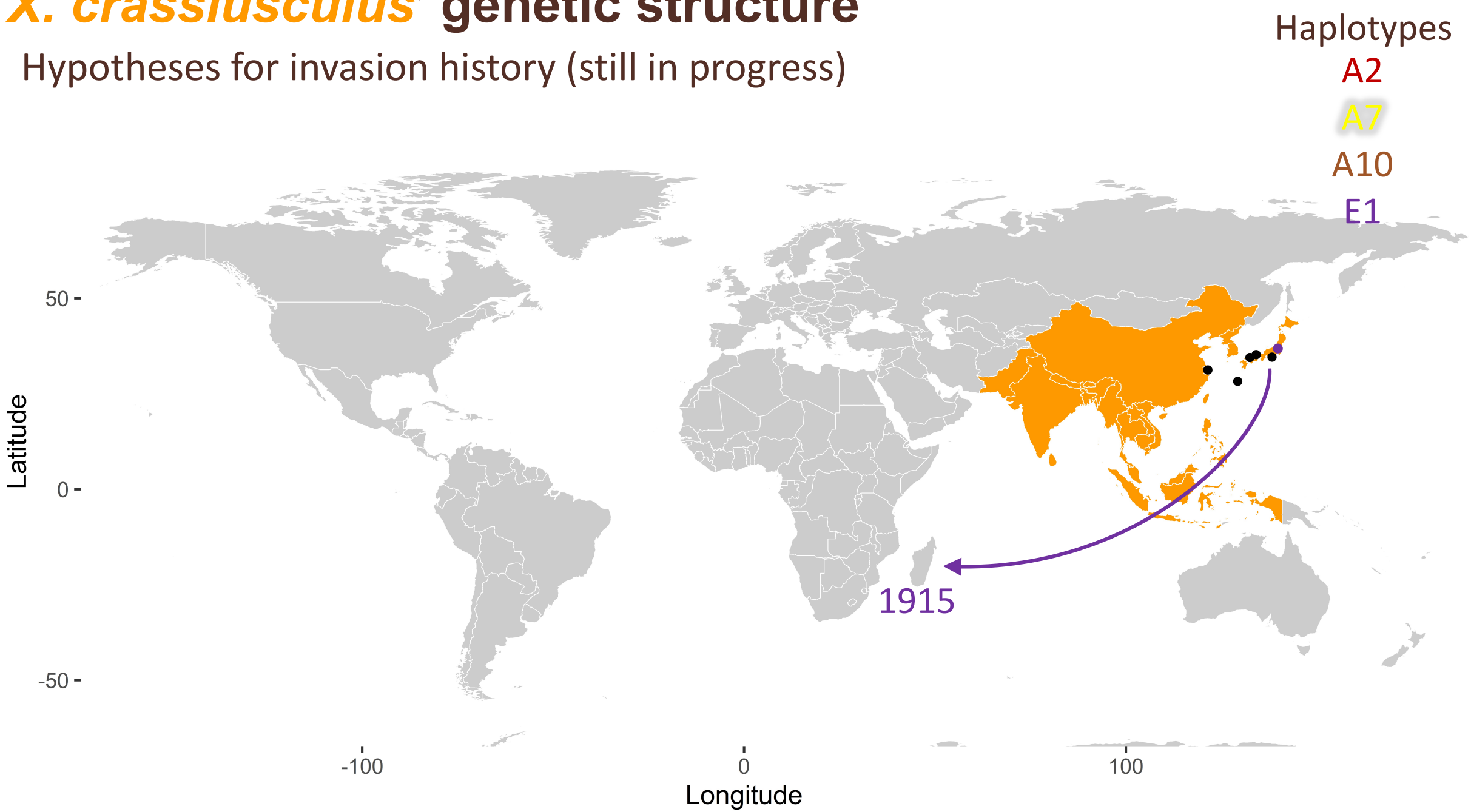
} Differ by only one substitution

- A9 only in Slovenia
- A10 in France, Slovenia and Shanghai



X. crassiusculus' genetic structure

Hypotheses for invasion history (still in progress)



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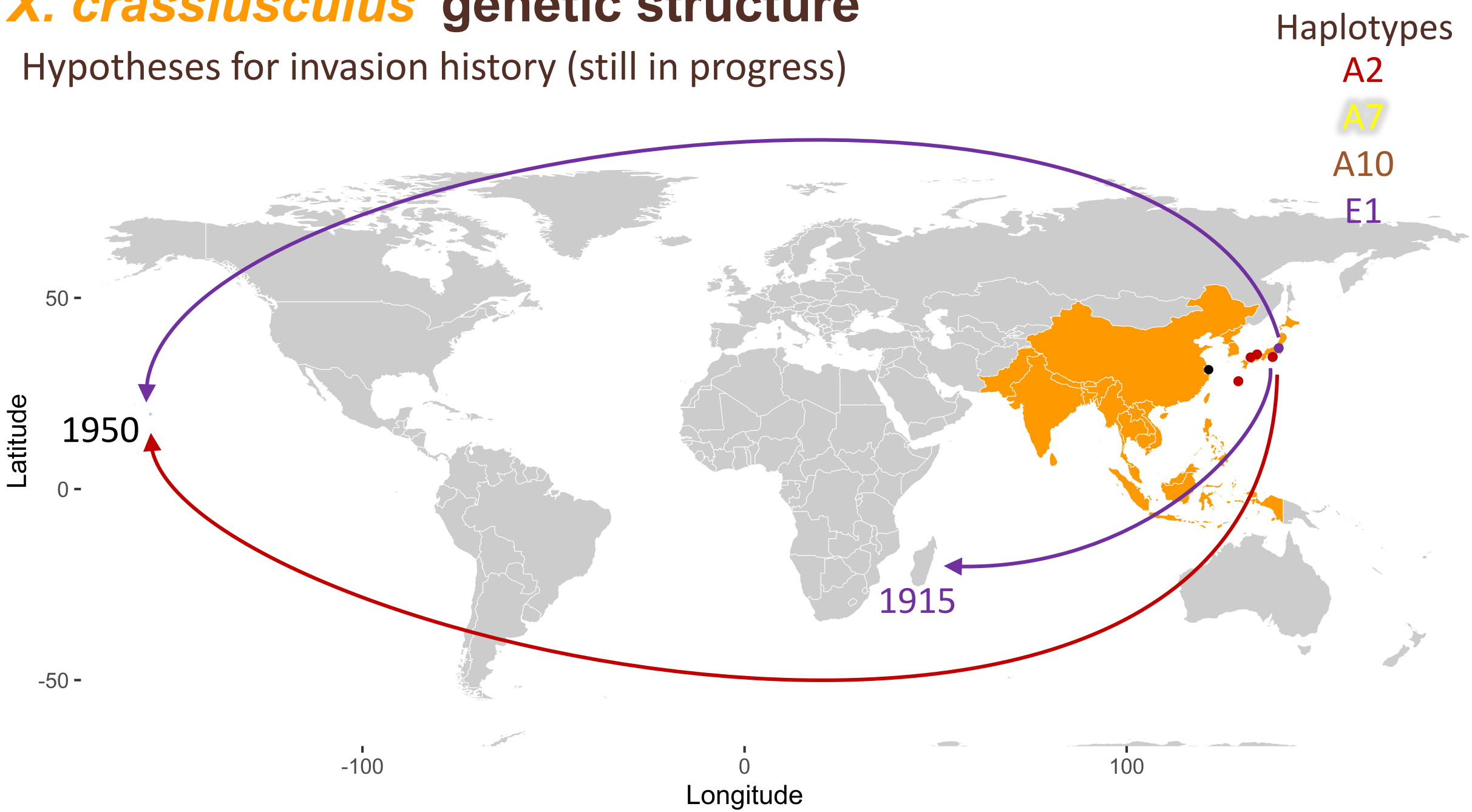

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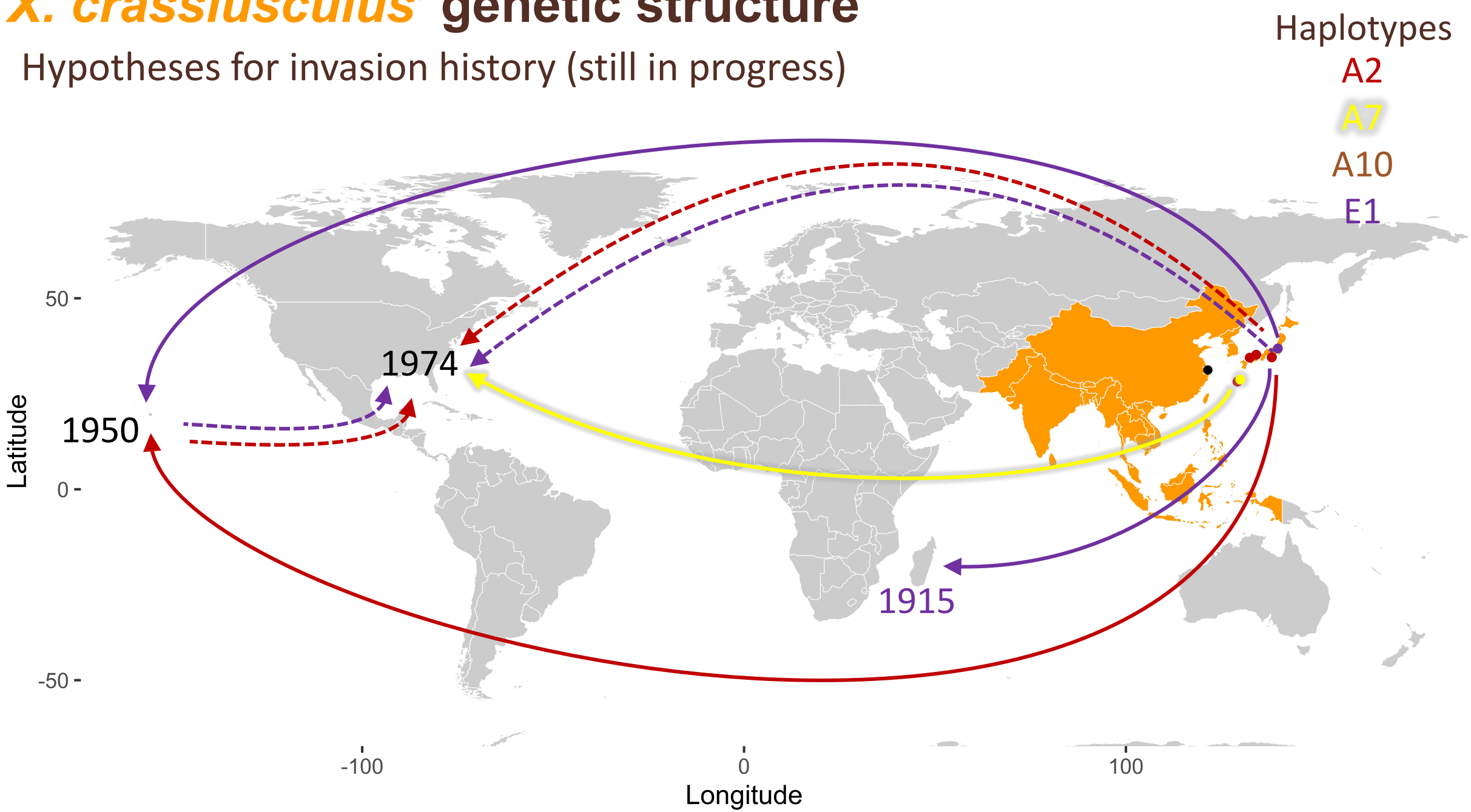

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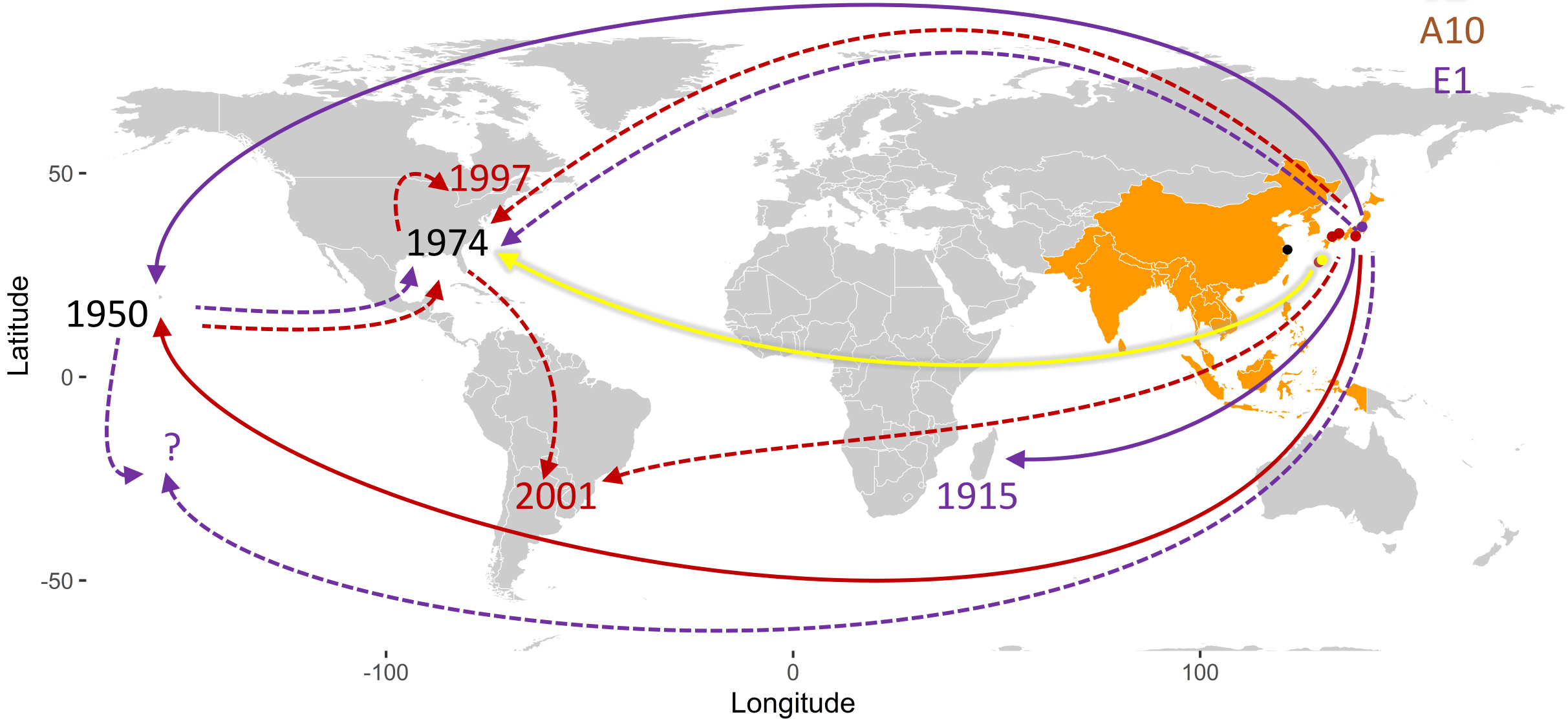

X. crassiusculus' genetic structure

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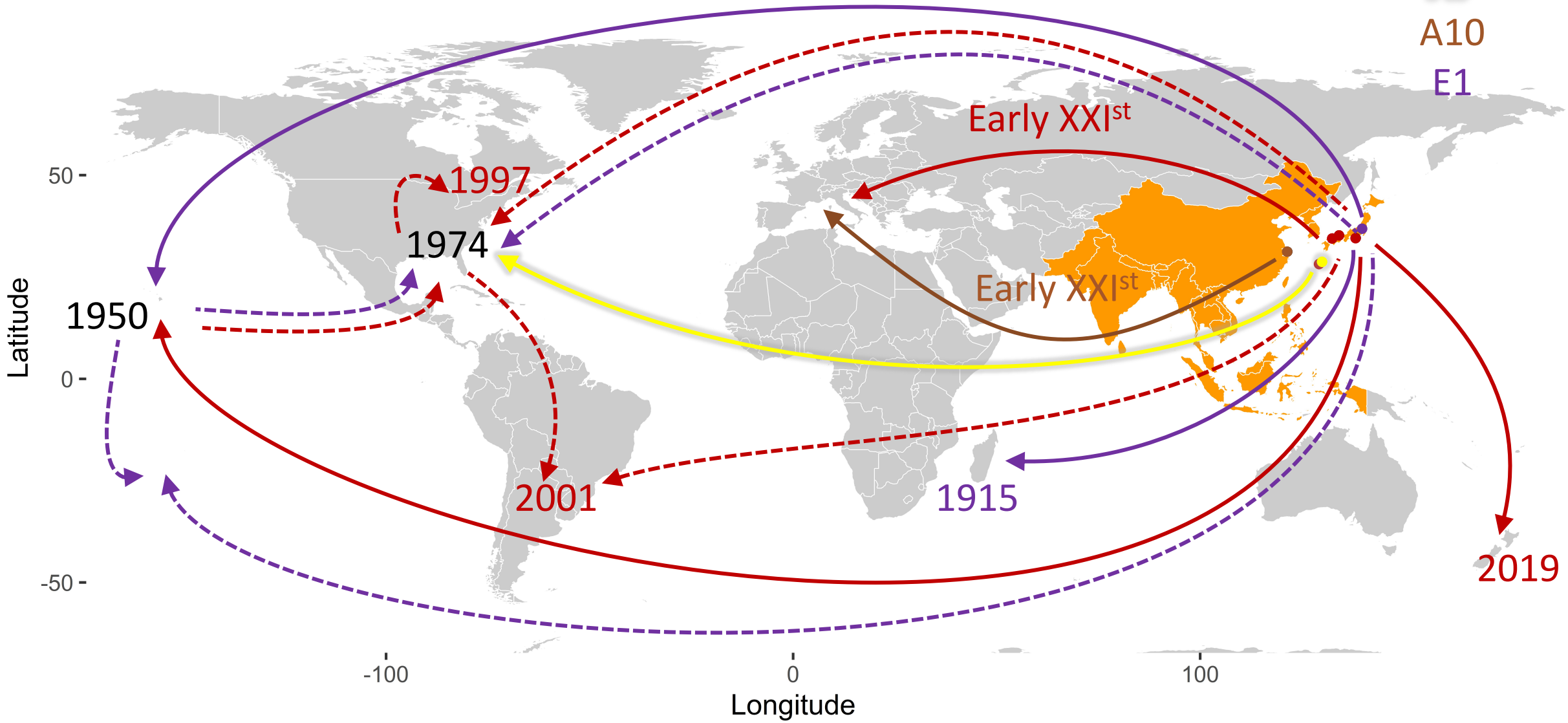
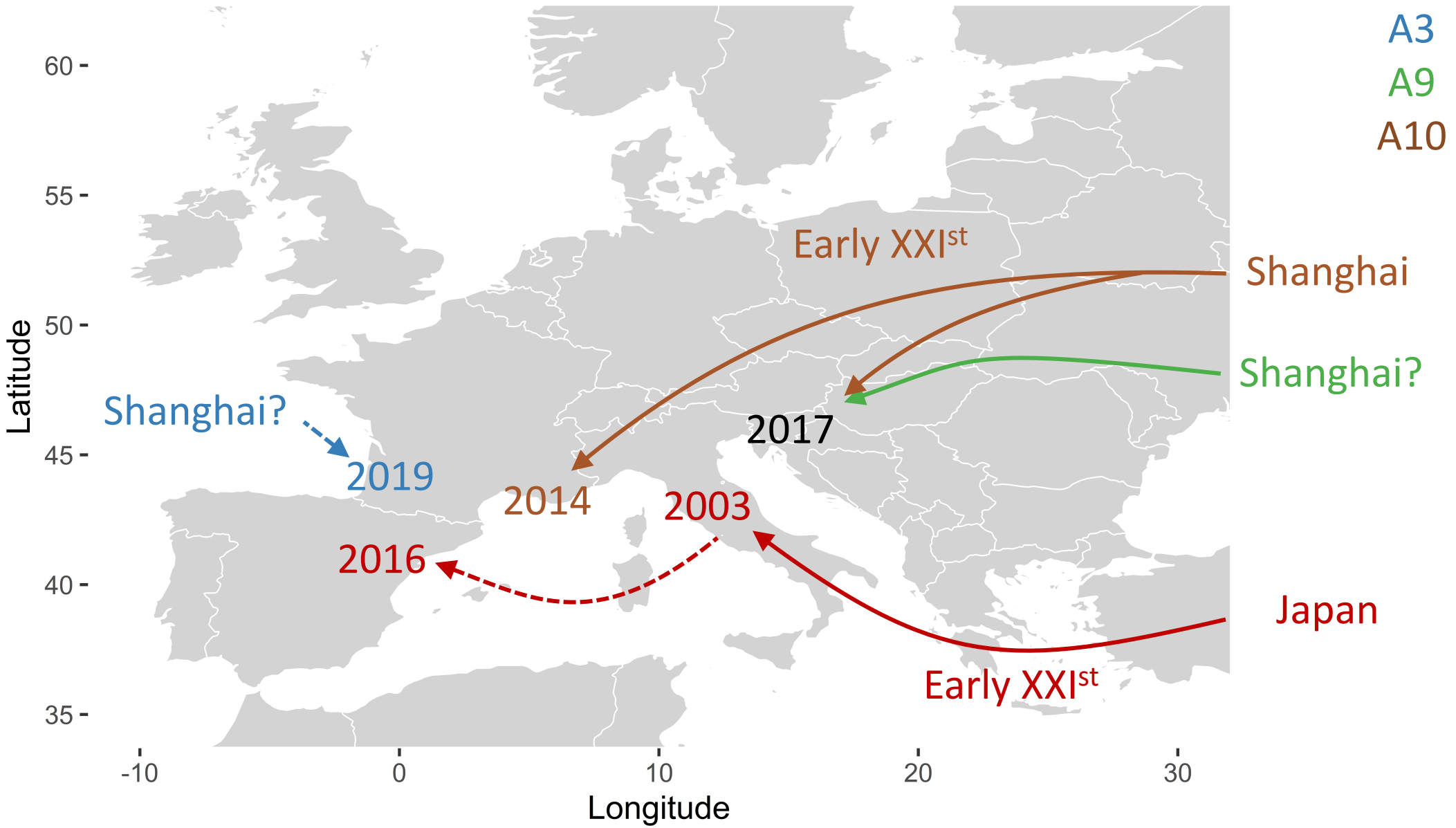


X. crassiusculus' genetic structure

Hypotheses for invasion in Europe (still in progress)



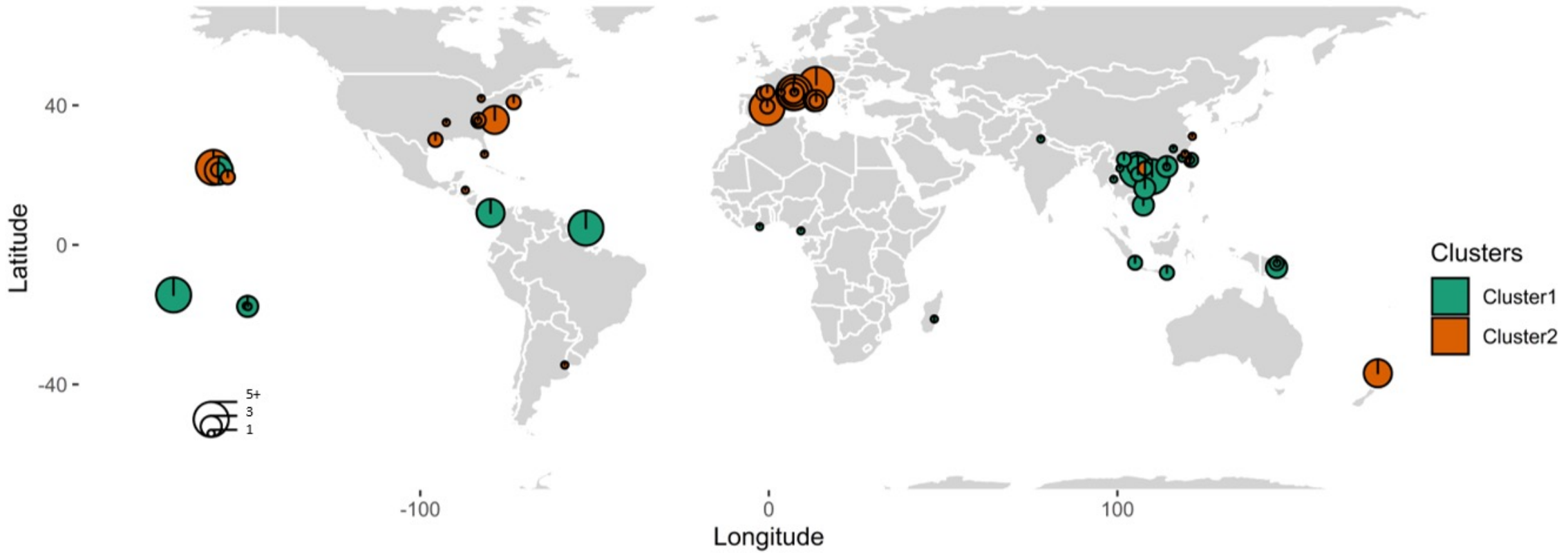
X. crassiusculus' SDM failure

Major hypothesis: Clusters could have different ecological preferences

⇨ Geographical structuration

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

} Perform SDM on each cluster separately !



Distribution of the two clusters

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

SAMFIX
SAving Mediterranean Forests from Invasions of Xylosandrus beetles and associated pathogenic fungi

CNiE 2021 TORINO

THANKS

for your attention

Bark and ambrosia beetles invasive of Mediterranean forest ecosystems

LIFE SAMFIX, co-funded by the European LIFE Programme Grant Agreement LIFE17 NAT/IT/000609

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