

Multiple origins of introductions of *Cryphonectria parasitica* in North America and Europe



Cyril Dutech¹, Benoit Barrès¹, Julien Bridier¹, Cécile Robin¹, Olivier Fabreguettes¹, Martine Martin¹, Michael Milgroom², Virginie Ravigné³
 1 INRA, UMR 1202 BIOGECO, Laboratoire de pathologie forestière, Domaine de Pierroton, F-33612, Cestas Cedex, France
 2 Department of Plant Pathology & Plant-Microbe Biology, Cornell University, Ithaca, NY, 14853 USA
 3 CIRAD, UMR BGPI, Campus International de Baillarguet, TA A 54/K, 34398 Montpellier cedex 5, France

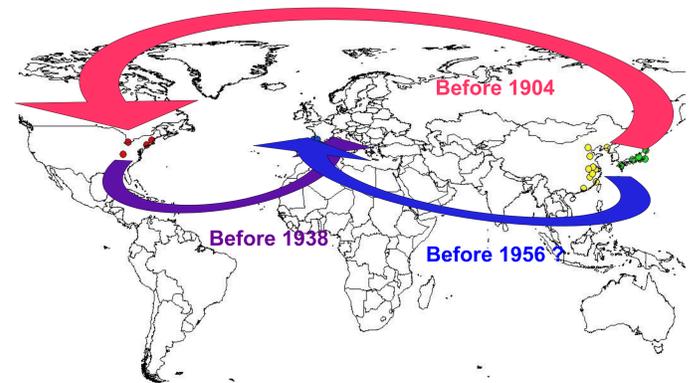
❖ Introduction of *C. parasitica*: dramatic effects on chestnut stands in America and Europe



American chestnut (*Castanea dentata*) before and after the introduction of *C. parasitica* in North America

The chestnut blight fungus (*Cryphonectria parasitica*), an Ascomycete infecting bark and cambial tissues of its host, is a prominent example of an invasive plant fungal pathogen that has had a dramatic impact in its introduced range: North America and Europe.

Meanwhile, the history of its spread has not been completely retraced in the areas of introduction since the first report of the pathogen in North America in 1904, Northern Italy in 1938 and, in France in 1956. Multiple introductions are assumed in Europe (Dutech et al. 2010) and North-America (Milgroom et al. 1996)



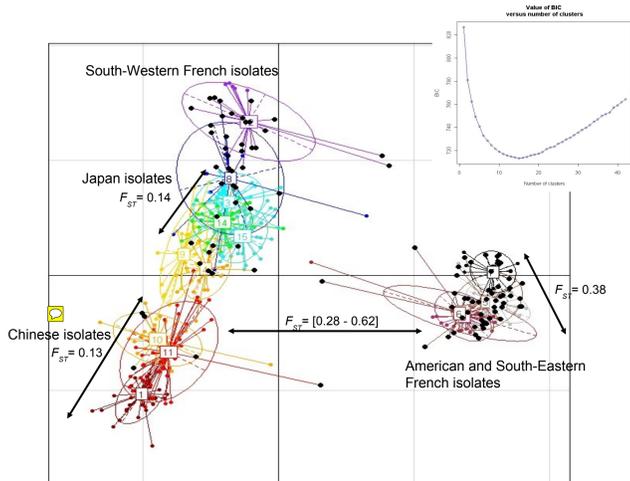
Geographic origins of the *C. parasitica* samples analyzed in this study

Native areas of the species :China (yellow circles) and Japan (green circles). Areas of introduction: North America (red circles) and France (blue circles). Dates are the first reports of the disease in the areas of introduction, and the arrows represent the assumed routes of introduction.

❖ Genetic analyses to infer routes of colonization

- 382 isolates from the native area and the North-American area of introduction (from Milgroom et al. 1996) + 105 different French genotypes from Dutech et al. (2010) - 10 microsatellite loci
- The world genetic structure was investigated using a discriminant analysis of principal components (DAPC, Jombart et al. 2010)
- Different scenarios of introduction in North-America from different Asian populations (China, Japanese islands, not sampled population) were tested using an approximate Bayesian computations (ABC) method, implemented in Do It Yourself ABC program (DIYABC; Cornuet et al. 2010)

➤ Multiple differentiated genetic pools observed in North America and France



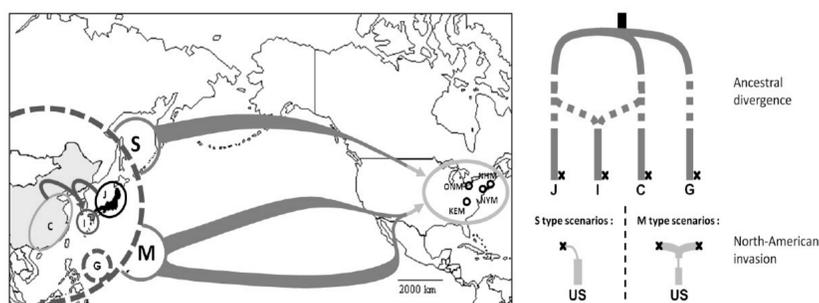
Scatterplots of the DAPC of the world genetic data of *C. parasitica*. The two first principal components of the DAPC are represented. Above, the Bayesian information criterion relative to the assumed number of clusters is represented. Number and colors represent the 15 genetic groups found by the k-means method. Black points are French genotypes.

1 - Strong genetic differentiation (F_{ST}) between Asian and North-American/ South-eastern French genotypes, and high decrease of allelic richness in areas of introduction (4.41 and 2.10 alleles per locus in Asia and North-America respectively)

2 - Multiple origins of French genotypes (Asia and North-America) with low admixture events between these genetic pools in France (see also Dutech et al. 2010)

3 - One genetic lineage (cluster 13) observed in North America, Europe and Chinese populations. These genotypes found in China have a higher probability of assignment to Japanese than Chinese populations (probabilities of assignment inferred from Piry et al. (2004)).

➤ Reconstructing routes of introductions in North-America using DIYABC



Scenarios of *Cryphonectria parasitica* colonization in North-America.

S: introduction from one Asian population among the fourth putative sources - M: admixture among a pair of Asian populations (C: Chinese populations, J: Japanese populations, G: Ghost or unsampled populations from unknown origin, I: intermediate population from an ancestral admixture between Japanese and Chinese populations)

Each scenario was independently tested on the four American populations, and using different priors, with all or clone-corrected data.

Assessment of the posterior probabilities of scenarios of North-American introductions

Population	Simple Introduction Japan	Admixture Japan+China	Admixture Japan+Intermediate	Admixture Japan+Ghost
NYM	0.34 [0.31-0.38]	0.30 [0.26-0.33]	0.14 [0.12-0.17]	0.19 [0.17-0.22]
KEM	0.10 [0.08-0.12]	0.09 [0.08-0.10]	0.25 [0.22-0.28]	0.41 [0.38-0.45]
NHM	0.21 [0.18-0.23]	0.15 [0.13-0.17]	0.24 [0.21-0.26]	0.34 [0.31-0.38]
ONM	0.18 [0.15-0.20]	0.08 [0.07-0.09]	0.26 [0.23-0.29]	0.34 [0.31-0.38]

Only scenarios with a posterior probability higher than 10 %, and only one set of simulations are given. All simulations give the same trend

➤ Conclusions

High decrease in allelic richness and high genetic differentiation between North-America and Asia suggest strong bottleneck and/or genetic admixture among genetically differentiated sources in the areas of introduction.

Occurrence of one genetic lineage on the three continents assuming successive events of introductions, probably due to regular intercontinental exchanges of infected chestnuts. This lineage could have emerged in North-America, and could be a genetic lineages well-adapted to new areas of introductions (Bridgehead effect, Lombaert et al. 2010).

ABC simulations confirmed the importance of introductions from Japan in North-America (Milgroom et al. 1996), but suggested at least one admixture event with another Asian source populations which was not accurately determined. This conclusion is in agreement with the hypothesis of the advantageous effect of admixture between genetically differentiated sources during invasion (Novak 2007).