First insights into the genetic diversity of the pinewood nematode in its native area and around the world

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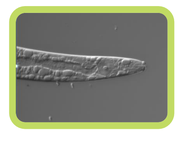
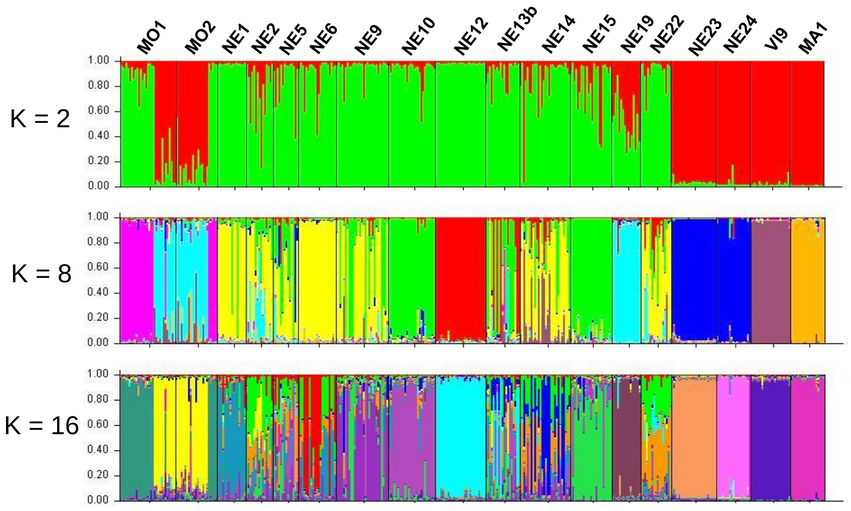


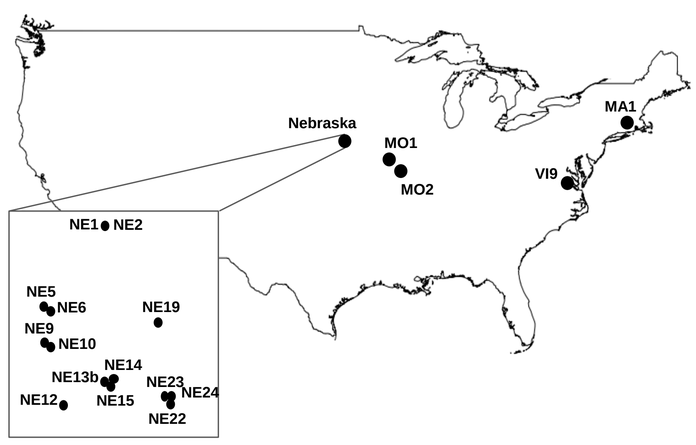
The pinewood nematode (PWN), *Bursaphelenchus xylophilus* is the causal agent of the pine wilt disease and is currently considered as one of the most important pests and pathogens in forest ecosystems. Native to North America, it has been introduced and it has spread in pine forests in Asia and more recently in Europe where it has now considerable economic and environmental impacts (annual loss of millions of pine trees worldwide). Anticipating the possibility of expansion of the PWN in European forests is essential. It is therefore important to decipher the invasion routes and better understand the invasion process of this species. To do this, 16 microsatellite markers have been developed and the study of genetic variability of the PWN was undertaken.

NATIVE AREA : NORTH AMERICA

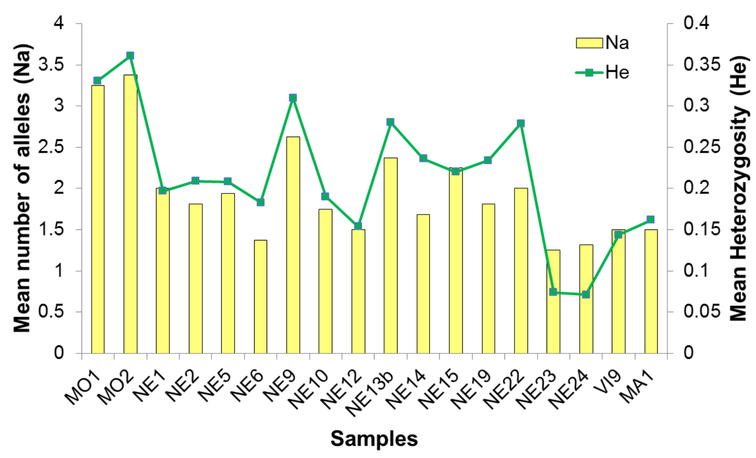
18 samples = 18 trees - 391 individuals

Genetic Structure





Genetic Diversity



➡ Fst from 0,067 to 0,78 between samples - Mean = 0,37

➡ No IBD pattern detected in Nebraska (Mantel test)

Very strong genetic structuration from tree to larger scales

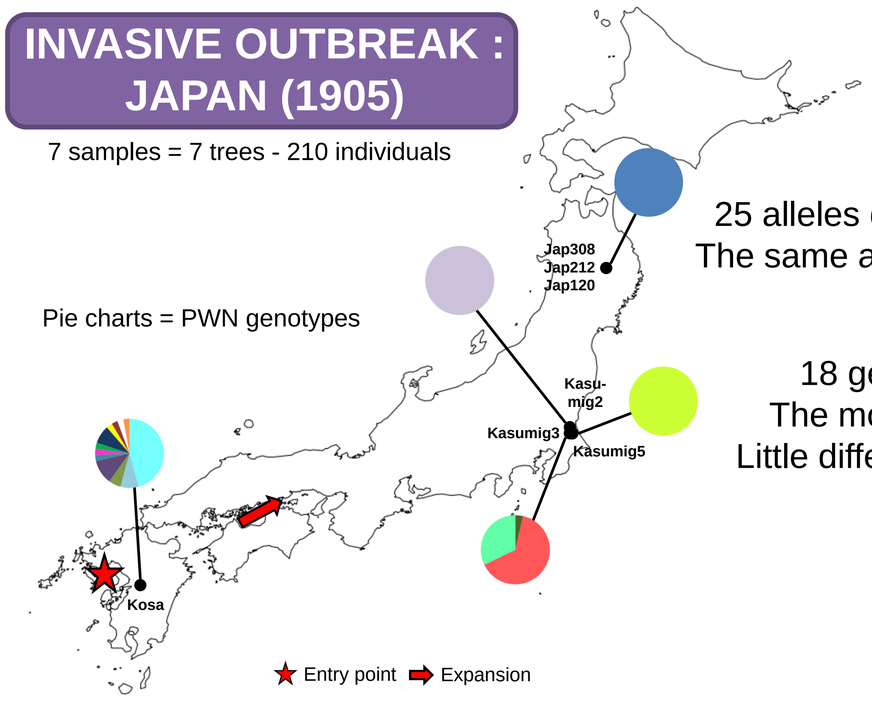
➡ Low level of polymorphism

➡ 19% of private alleles

➡ Diversity found at a global scale

INVASIVE OUTBREAK : JAPAN (1905)

7 samples = 7 trees - 210 individuals



25 alleles detected for 16 markers
The same allele fixed for 10 markers

⬇

18 genotypes detected
The most at the entry point
Little differences between them

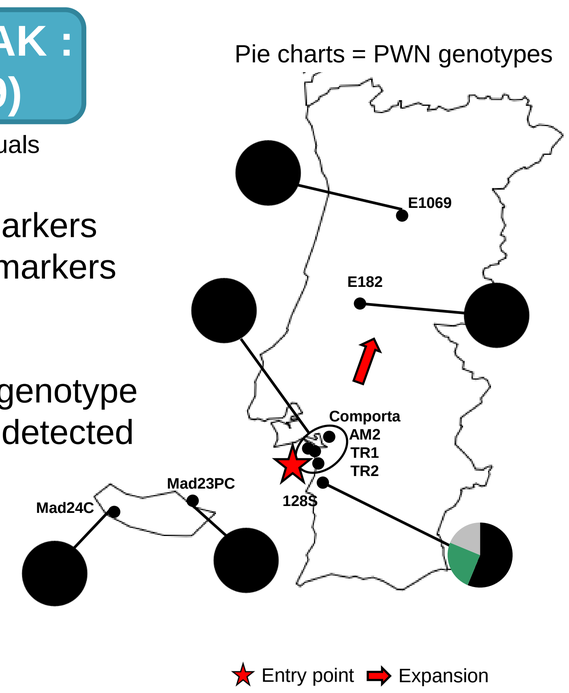
INVASIVE OUTBREAK : PORTUGAL (1999)

9 samples = 9 trees - 169 individuals

17 alleles detected for 16 markers
The same allele fixed for 15 markers

⬇

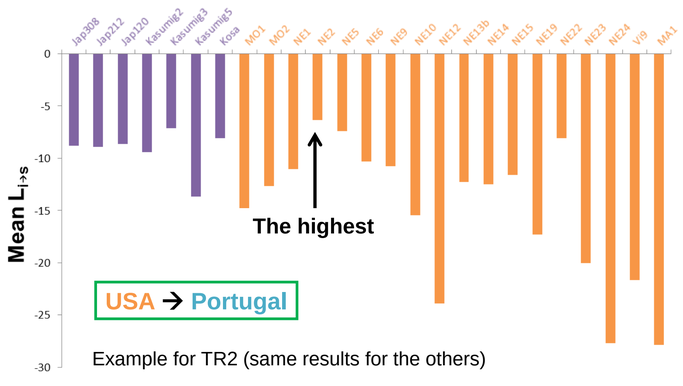
162 individuals with the same genotype
Only 3 very similar genotypes detected



Loss of diversity during introduction and expansion

ORIGIN OF THE PORTUGUESE POPULATIONS ?

- **Individual assignment likelihood**



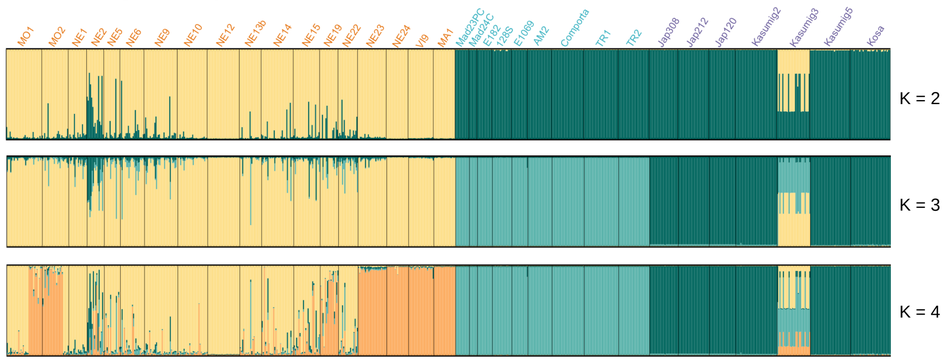
Example for TR2 (same results for the others)

- **Measure of population differentiation**

	Range		Mean	
	Fst	D's Jost	Fst	D's Jost
USA vs Portugal	**0.342 - 0.947**	0.019 - 0.237	**0.635**	0.096
Japan vs Portugal	0.701 - 1	**0.015 - 0.033**	0.925	**0.020**

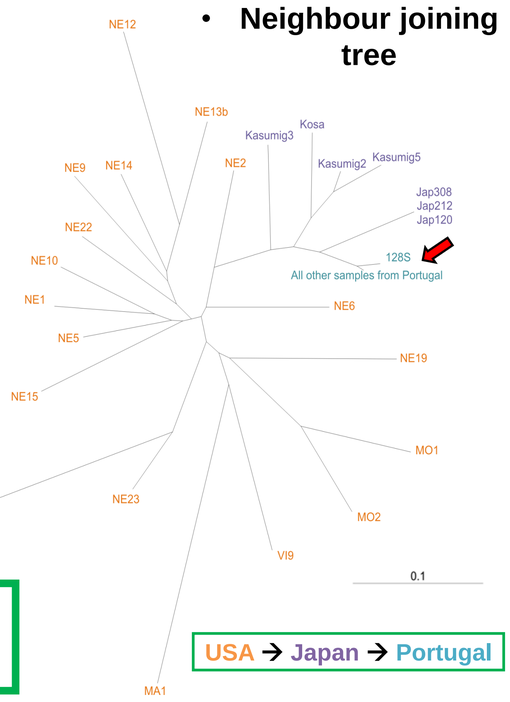
USA → Portugal **or** USA → Japan → Portugal **?**

- **Clustering analysis**



USA → Japan → Portugal

- **Neighbour joining tree**



USA → Japan → Portugal

Difficulties to identify the origin with classical methods
Need to use Approximate Bayesian Computation (ABC)

The PWN populations display a spatial genetic structure in their native area. This spatial genetic structure probably accounts for the existence of long distance human-induced dispersal and an important role of the genetic drift at shorter scales (i.e. neighboring trees of Nebraska significantly differentiated). Compared to the native area, the invasive ones are much less polymorphic, reflecting the intensity of the founder effect during the introduction and even the expansion, especially for the Japanese outbreak. The invasion routes and particularly, the origin of the Portuguese populations, are not clearly determinated yet. Indeed, the lack of polymorphism likely precludes the use of classical inference methods. More extensive sampling in native and invasive areas and ABC analyses are now in progress to improve our understanding of this invasive case.

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