Inferences from Mitochondrial DNA Patterns on the domestication history of alfalfa (*Medicago sativa*).

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Keywords : mtDNA variation, gene flow, domestication, phylogeography, crop-weed complexes, *Medicago sativa*

To clarify the evolutionary history of alfalfa (*Medicago sativa*) wild-cultivated complex, we adopted a phylogeographical approach based on a characterization for Mitochondrial DNA variation through restriction fragment length polymorphisms of a sample of natural and cultivated populations. Twenty-two mitotypes were identified in the whole data set (155 individuals, one by population) with five probe/restriction enzymes (4).

In the wild pool (*M.s. ssp sativa* 4x and *M.s. sp coerulea* 2x) from the presumed centre of origin (Near East to Central Asia), the diversity was high but the absence of geographic differentiation hinders a more precise location of the domestication.

Within the cultivated alfalfa, the genetic differentiation associated with a geographic structure strongly suggests the existence of at least two independent routes of dissemination of alfalfa (East and West) from its center of origin. Namely, one original mitotype was detected in the cultivated pool from western Europe and North Africa. Its absence from the wild pool suggests an other wild source for the domesticated form, particularly for European ones (Flemish, Provence). This source could be the subspecies *falcata* which has been used in alfalfa breeding in the North of Europe; but recurrent gene flow in both directions between cultivated alfalfa and natural populations of *ssp. falcata* prevents any definitive conclusion.

Finally, the Spanish wild populations (ref 1 to 4), located outside the presumed area of domestication, were shown to be highly original, with one abundant original mitotype. These wild populations could constitute an endemic wild pool present before alfalfa domestication and now partially introgressed by cultivated alfalfa.

References

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