

T54 Molecular passport of a new *Zea* weed emerged in European maize fields

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Maize is the cereal with the highest production worldwide for the last decade. This explains the considerable concern caused by the discovery of a new weed in European maize fields. Its focal points are mainly in the Northeast of Spain, and on a smaller scale, in the Southwest of France. Early identification of crop-related weeds becomes crucial to determine the success of their control. As the origin of this new weed is uncertain, our objective was to characterize it using microsatellite markers. Maize-like weeds, putative hybrids between commercial maize and the weed, teosinte (*Zea mays* ssp. *mexicana* and *Zea mays* ssp. *parviglumis*) and commercial maize varieties were genotyped with 17 microsatellites and the data used to: explore the genetic relationships among them by constructing a dendrogram; determine their associations by Principal Component Analysis; and study the population genetic structure. All samples were distinguished using only six microsatellites. All analyses showed that the samples mainly grouped according to the type they belonged to, though a close genetic relationship between the crop and the weeds became clear. In terms of genetic structure, the highest levels of admixture were observed in the weeds and the teosintes, and the lowest in the commercial varieties. The weeds shared most of their genetic background with the commercial varieties, what reveals their high degree of hybridization. Consistently, the genetic variation (F_{ST}), that is a measurement of the genetic differentiation among groups, was negligible in all cases except when the teosintes were compared to the commercial group. In agreement with this, most of the molecular variance occurred within populations (51.83%) and not among populations (10.09%). All the commercial varieties had a high membership in their own group and seem to have originated in a small portion of the huge genetic variability present in teosinte. This, together with the lower levels of gene diversity found in maize compared to teosinte, supports the occurrence of a bottleneck during maize domestication. The weeds genetically resemble most the commercial maize cultivars grown nowadays at the infested regions, though they still maintain some genetic similarity with maize putative wild ancestor (*Z. mays* ssp. *parviglumis*). Our findings also evidence the gene flow between weed and cultivated maize. Natural spontaneous hybridizations between the crop and the weeds have been found and the genetic proximity between the modern maize varieties and the hybrids has been verified. The most similar weed to the cultivated maize seems to be the closest to the original cross between them. On-going pollinations by the weeds (favoured crossing direction) explain the generation of more and more weedy plants.

Finally, the vague separation between the two teosinte subspecies could be due to misclassification and/or hybridization between them.