Origin and evolution of domesticated plants. (C08-gepts174615-Oral)

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Abstract:

Molecular analyses with a wide variety of markers and DNA sequences have shed additional light on the process of domestication of crops. Using molecular markers, patterns of domestication and location of domestication have been clarified in several crops, including common bean, maize, cassava, einkorn and durum wheat, and barley. The availability of this information can lead to more precise comparisons of wild progenitors and their domesticated descendants. Molecular data consistently document one or more genetic bottlenecks during and after domestication, which strongly suggest that wild relatives of crops can be important sources of genetic diversity. Both inheritance experiments and sequencing information suggest that domestication may have proceeded fairly quickly in at most a few centuries although the archaeological record suggests a slower process. Finally, molecular markers provide more powerful tools to assess the direction and intensity of gene flow between crops and their wild progenitors. Results show that gene flow is a significant factor in the distribution of genetic diversity across populations and genomes not only in outcrossing species but also in selfing species.

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Presentation Information:

Presentation Date: Wednesday, November 13, 2002
Presentation Time: 8:25 am

Keywords:

biodiversity, domestication , molecular markers, inheritance