

Proceedings of the Colloquium

Genome Mapping of Horticultural Crops

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Presiding: Ralph Scorza

Genome Mapping of Horticultural Crops: Introduction to the Colloquium

Ralph Scorza

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Genome Mapping of Horticultural Crops: Introduction to the Colloquium

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There is a tremendous interest in genome mapping of crop species. A great part of this interest is focused on the use of maps for cultivar development. Genome mapping offers the possibility of selection at the DNA level, eliminating the uncertainty of environmental effects. In practical terms, a genome map would, among other uses, allow breeders to select for characters in young seedlings without the need for evaluation in the field for traits that are only expressed in mature plants, such as flower or fruit quality. An ideal map would preclude the need for inoculation and insect feeding trials when selecting potentially resistant seedlings. But can this map ever be realized considering the vast size of most plant genomes and the many important traits that must be field-evaluated in mapping populations in order to place them on a map? If the ideal map cannot be realized in the near future, what will a less-than-ideal map offer the breeder?

With the goals of answering these questions and improving our understanding of genome mapping in horticultural crops, our distinguished participants have presented theoretical and practical information on genome mapping on a diverse group of horticultural crops,

including *Prunus* [mainly peach [*Prunus persica* (L.) Batsch], a self-fertile woody perennial with a small genome and a limited germplasm base], apple (*Malus ×domestica* Borkh.) (a highly heterozygous outcrossing woody perennial), onion (*Allium cepa* L.) (an outcrossing species with high levels of inbreeding depression and heterosis), and pea (*Pisum sativum* L.) (a widely studied species with a large genome, some well-characterized mutants, a linkage map, and well-defined genetics, but many chromosomal rearrangements). These species were selected to cover a wide range of considerations that would be applicable to most crops. A concise overview of the utility of some of the latest approaches in mapping is also presented, along with an update on the progress of some of the European mapping projects.

This is the best of times and the worst of times. We are on the verge of an exciting new technology that holds great promise to improve our effectiveness as breeders. But it is also a time of insecurity and uncertainty due to shrinking budgets. Difficult decisions must be made on the allocation of scarce resources between molecular technologies and field-based research, both of which are vital to breeding programs. For the breeder, a molecular map is not a goal but a tool to reach a goal—the improved cultivar. We, as breeders, now have the opportunity to work with molecular biologists in developing the tool. By taking part in this development we will more fully understand how best to use it.

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