

Rapporteur's report

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This was the first of 3 sessions on host resistances, in which speakers from different parts of the world exchanged experiences in breeding for resistance to late blight. Topics included summaries of 5 different applied breeding/selection programs, with attention to strategies for developing durable resistance, the different sources used, and entry points for new technologies. Measures of success for the applied breeding programs presented included the increasing area covered by improved varieties, entry into existing and new markets, long-lasting resistance and the identification of superior progenitors for sustained genetic advance. Needs were recognized in the areas of uniform evaluation methods for population testing, networking for multi-locational testing schemes and broadening the genetic base of resistance. The use of only AUDPC for field evaluations was questioned since clones may differ in the rate of disease increase.

The problem of the poor correlation between tuber and foliage resistance was raised by the participants. Concern was expressed about the lack of knowledge of whether the genetic systems for resistance are different. At present investigators evaluate tuber and foliage resistances separately.

Collective lessons seem to include a preference for broad based resistance, and strategies of recurrent selection to develop varieties that meet stringent market or consumer demands. The need for communication among partners in distance-targeted breeding programs (e.g. CIP-Peru to sub-Saharan Africa), and between breeders, farmers and end users was recognized by all. Partial resistance confers a higher degree of predictability in the performance of materials under selection, and is generally preferred over extreme resistance.

R genes were a controversial subject for discussion. Some felt that any combination of R genes will be overcome because of pathogen race complexity. Others cited recent investigations indicating that not all R genes depend on recognition.. It was noted that Pampeana has shown stable resistance, yet it traces back to *S. demissum*, the well-known source of all described R genes. Most participants agreed that this topic needs to be further explored and more knowledge is needed.