

Enhancing crop genetic resources to meet the post-genomics era

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The use of various mutagens to generate genetic variation in crop plants has a history almost as long as that of conventional breeding. Induction of variability by irradiation of barley seeds with X-rays was already demonstrated in 1928 by Stadler. The application of this phenomenon has come a long way to become a real tool in crop breeding but also in basic research on plant genome, its structure and function. Breeders were the first to recognize the potential of induced mutations through analogy with spontaneous mutants, often selected as new plant types in many crops, from cereals to apples, not to mention ornamental and decorative plants. Many mutants with desired traits were selected in the second or third generation after mutagenic treatment and subsequently released as new cultivars after agronomic evaluation in the regional and national trials. Recent advances in plant genomics, especially large scale genome sequencing, have opened new possibilities for application of mutation techniques in crop improvement. Using the reverse genetic strategy called TILLING (Targeting Induced Local Lesions In Genomes), it is possible to induce a series of alleles in a targeted locus, providing that its sequence is known. The TILLING strategy has been initially developed for model plant and animal species as a discovery platform for functional genomics but soon it has become a valuable tool in crop breeding, alternative to the transgenic approach. The TILLING technology relies on a high frequency of mutations induced by chemical mutagenesis, combined with the high throughput screening method for single nucleotide polymorphisms (SNPs) in the targeted sequence. The feasibility of this technology for generation a series of new alleles in a gene of interest has been already demonstrated in barley, maize and wheat, not to mention the model organisms such as *Arabidopsis*. [not attending the symposium]