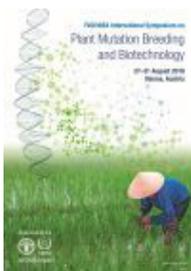


# FAO/IAEA International Symposium on Plant Mutation Breeding and Biotechnology



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## EXPLOITING MUTATIONS IN THE ERA OF GENOMICS AND GENOME ENGINEERING

**Background:** Plant breeding relies on exploiting genetic variation present in crops and their wild relatives. Much natural variation is complex in its genetics and inheritance while induced mutations are generally simpler in their genetics, but usually associated with multiple deleterious characters.

**Methodology:** Key steps to using mutations include identification of phenotype and the gene (or marker) involved, selection and stable expression of the character. Many crop species are polyploids or hybrids, and the presence of multiple genomes can give advantages and disadvantages. Chromosome engineering can introduce novel traits from mutants and wild relatives into breeding programmes to increase resistance to biotic and abiotic stresses. Our research with use a variety of crops, their wild relatives and hybrids uses high throughput DNA sequencing and repeat finding algorithm to identify tandem repeats and transposable elements. The genomic variation and chromosomal organisation of repeats provide useful markers for identifying alien chromosome segments and diversity linked to mutations and economically important traits.

**Results:** In wheat, we have identified terminal and intercalary translocations of rye, *Aegilops ventricosa*, *Secale cereale*, *Thinopyrum intermedium* and *Th. bessarabicum* involving different recipient wheat chromosomes and transferring resistance to wheat streak mosaic virus and other diseases. Our Brassica and oats programmes exploit the wild relatives, while the banana and Ensete programme use the variation in different accessions of the species and hybrids.

**Conclusion:** High throughput sequencing has changed genome analysis from mapping and identifying genes, finding new repeats and DNA variation that can be used as markers to GBS (genotyping by sequencing). Our aim is to understand genome restructuring during hybridization and mutation events and to developing super-domestication strategies to exploit biodiversity for sustainable agriculture.

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