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Genomics Tools to Facilitate Plant Mutation Breeding

Continual genetic improvement of crops is necessary for global food security and climate change adaptation. The use of induced mutations has for more than 80 years been a powerful approach for generating novel genetic variation for breeding. Genomics tools, especially next generation sequencing, have advanced sufficiently in the past decade to consider their routine use in plant mutation breeding. While new technologies hold great promise, the challenge is adapting and applying them in a global context to maximize impact in the field. In terms of induced variation using chemical or physical methods, the density and spectrum of mutant alleles, and mode of propagation of the crop are important considerations for experimental design of a mutation breeding programme. This presentation will highlight collaborative research led by the Plant Breeding and Genetics Laboratory to develop and adapt genomics tools aimed at facilitating mutation breeding projects in the FAO and IAEA Member States. The focus has been on using open-source approaches while keeping assay costs as low as possible. This includes amplicon and whole-genome sequencing methods for the discovery and use of natural and induced genetic variation. Applications and future prospects for seed and vegetatively propagated crops will be presented.

Country or International Organization

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