Editorial

Genomics of the gene bank necessitates and benefits!!

Crop genebanks available across the globe are always served as valuable resources for economically important genes. These gene banks give out valuable raw material for the crop improvement through the augmentation, conservation and sharing of unique germplasm among the researchers. The world population is increasing with the alarming rate and is 7.8 billion as of January 2021 and will continue to grow day by day. To meet the food supply to this large population we need bumper crop production. Are plant breeders ready to take this challenge? Does existing accessions conserved and maintained in the gene bank is sufficient to feed the world by planning systematic crop improvement programme? Do we all know the extent of the variability conserved? Is there any necessity to add the variation from alien sources in the crop plants? Do crop breeders meet all the requirements from the exiting crop gene banks? Urgent need for the effective utilization of the available germplasm is augmentation, characterization and systematic evaluation of the accessions for the identification of the trait specific material which could be utilized in the crop breeding programme. Most of the germpalsm curator across the world have opinioned that only a small fraction of the naturally occurring genetic diversity available in the world's germplasm repositories has been explored to date, which means large extent of the variability conserved, is unknown.

Many curators believe that the advent of new genomic tools and genome-scale technologies like high-throughput genotyping and sequencing may elucidate the insight of the variability among the germplasm and their effective utilization in the coming years. Many researchers started working and utilizing the genomics tools for increasing the understanding about the accessions available in their holdings. Researchers are on the verge of integrating the genotyping and sequencing into the activities of a modern gene bank to revolutionize the way scientists document the genetic identity of their accessions; molecular passport data generation, identification of the seed lots, varieties, and alleles; find and remove duplicates; and rationalize active collections etc. The question is how the availability of genomics data are likely to motivate innovative collaborations with the larger research and breeding communities to engage in systematic and rigorous phenotyping and multilocation evaluation of the genetic resources in gene banks around the world. Many of such studies have already been published in various crops like rice, wheat, maize etc. and many more yet to come.

While utilizing the genomics approach one should keep in the mind the cost effectiveness, the efficacy of the genomic tool and easiness in the handling the technology. As plant breeder, we should not be satisfied with effective utilization of the genomic tools, but we should strive for a deeper understanding of how genomic information stored in seeds is translated into plant performance and ultimately for the improvement of the crops.