Breeding Programs and Viromes

Breeding programs can benefit from virome analysis for testing that germplasm is free of viruses, and for identifying virome profiles for testing which genotypes show resistance or tolerance, to provide recommendations for further breeding and propagation.

Considering virome information in breeding programs could be especially important for breeding of vegetatively propagated crops where the viral load accumulates in the host over time, reducing the productivity or seed quality of crops (Gibson and Kreuze, 2015;Thomas-Sharma et al., 2016;Jacobsen et al., 2019;Andrade-Piedra et al., 2022).

Sharing of germplasm among breeding programs in regions where different viruses are present could benefit from virome analysis to add an additional screening method to ensure known or novel viruses are not also exchanged.

For crops that are propagated via true seeds, exchanging germplasm among breeding programs is similarly complicated by seed transmissible viruses (Dombrovsky and Smith, 2017).

Developing systems to ensure virus-free germplasm may be exchanged is particularly important for breeding programs that are attempting to develop resistance, or at least tolerance, to viral diseases that impact crop production.

Virome data can be used in qualitative (presence/absence) as well as quantitative evaluations in crop breeding programs.

Using viral sequence abundance as an additional phenotype in variety evaluation may help identify varieties that suppress viral replication or resist infection altogether.

When corresponding genotype data are also available for crop varieties, this phenotype can be associated with genetic markers to infer resistance to a particular group of viruses.

Phenotype data from breeding populations will provide the genetic parameters crop breeders need to quantify the impact selection may have on the development of disease resistance.

Providing virome data from breeding programs established across diverse planting environments would also allow for selection of genotypes that are resistant to the combination of viruses that are particularly problematic in certain regions.

Virome analysis provides a unique opportunity to combine sequence data from both the virome and host in unified prediction models to estimate the relative importance of differences in virome composition and host resistance mechanisms for crop productivity.

Implementation of HTS techniques to screen large germplasm collections and seeds that are exchanged among breeding programs, are prerequisites to using crop genetic diversity for the development of improved varieties.

The development and implementation of high-throughput phenotyping will facilitate such new approaches.