

Navigating the genomes of plants and their pathogens: a strategy for the management of crop diseases

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The new sequencing technologies called NGS (Next Generation Sequencing) have enabled a huge advance over the past five years in data generation of genome sequences of many species. The probability of obtaining the complete genome of different plant varieties or genotypes of a pathogen and to compare their genetic differences is today a reality given the very affordable costs that these new sequencing technologies allow.

In the case of plant genomes we are identifying families of resistance genes and other families of genes involved in plant-pathogen interactions that we can select to include in resistance to major pathogens of commercial varieties of crop plants. As for the genomes of organisms causing plant diseases the complete genomes of the main pathogens that affect crops are today available. Analysis of these genomes has allowed the identification of families of secreted proteins, which are involved in the process of pathogenesis of these organisms. Likewise it is possible to have specific markers that easily distinguish variants, pathotypes, races and biotypes of these pathogens.

This explosion of plant genomics and pathogens information has opened up a whole range of possibilities for control of major diseases of plants by means of predicting the evolution of pathogens and the development of improved varieties based on the selection of lines containing specific resistance genes.

The Center for Bioinformatics and Computational Biology-BIOS was born as a specialist center in the analysis of this vast amount of genomic information. The Center collaborates with research groups in Colombia and Latin America who need to use the new technologies of sequencing and analysis of the data produced in research projects seeking the evolution of pathogens and the improvement of crops with new resistance characteristics against these pathogens.