

The SharCo Plum pox virus Database

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The EU FP7-funded SharCo project develops several strategies to study and control the *Prunus* sharka disease. In this frame, SharCo partners have developed an unprecedented collective effort to analyse the variability of *Plum pox virus* (PPV). To ensure efficient data dissemination and usage, standardized origin and sequence information on several hundred PPV gathered as a consequence of this effort have been organised in a web queryable database (http://w3.pierroton.inra.fr:8060/).

The database allows on-line submission of isolates data (origin, typing results, sequence...). Mandatory fields have been specified together with a curation process to allow consistent data searches. Subsequent sequence or chromatogram files submission for an existing isolate is also possible. A semi-automated import procedure of Genbank accessions to centralize all known PPV isolates has also been developed.

Multi-criteria searches of the database or direct access to an isolate and to its sequence information via their identifiers allow for easy data retrieval. Cross-links to available Genbank accessions are displayed for fast navigation and information about the availability of the isolate in the Sharco centralized collection of lyophilized isolates has been implemented.

Several tools like blast, geographical mapping, custom fasta sequence and basic statistics have been developed and integrated on the database website to help researchers to understand the geographic dynamics and the genetic evolution of the PPV population, which is crucial for an efficient management and control of the disease.

The current database release (November 2010) contains 1277 sequences from 777 isolates, over 60% of which have been developed by the SharCo partners. Preliminary analysis reveals new divergent clusters and host preference of some PPV strains.

At the moment, the database access is restricted to the SharCo partners and collaborators but plans are to rapidly share it with the scientific community.

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