

State of the World's Plants 2017

Plant Genomes – progress and prospects

Methods SOTWP Chapter 3

Identification of vascular plant species with whole genome sequences

Lists of sequenced plant species were obtained from NCBI (<https://www.ncbi.nlm.nih.gov/genome/>) and Phytozome (<https://phytozome.jgi.doe.gov/pz/portal.html>), and supplemented with a literature search (hence, the list used is likely to be incomplete). Duplicate species were removed (e.g. where synonyms had been used, when a genome had been resequenced, or when different varieties or sub-species had been sequenced), and hybrids were considered as unique species. For the report, databases were accessed up to 17th February 2017, and only sequences released or published by the end of January 2017 considered. In the online supplementary material, genomes released or published by 15th May 2017 are also listed.

Date of release/publication

For plant species with genomes accessible on NCBI, release year was obtained from NCBI. For all other species, release year was considered to be the year of the first publication associated with the whole genome sequence.

Plant uses/reason for sequencing

For each sequenced plant species, a “use” was assigned taking into account a species literature search and, where available, having read the first publication associated with the whole genome sequence. Crop wild relatives (CWRs) were identified in reference to the prioritized CWR inventory proposed by Vincent et al. (2013) *Biol. Conserv.* <https://doi.org/10.1016/j.biocon.2013.08.011>. Non-crop species that shared a genus with a sequenced crop were also considered to be CWRs.

Phylogenetic tree

The phylogenetic tree in Box 1 was created using Interactive Tree Of Life (iTOL) (Letunic and Bork (2016) *Nucleic Acids Res.* <https://doi.org/10.1093/nar/gkw290>).

For additional information for this chapter please contact sotwp@kew.org