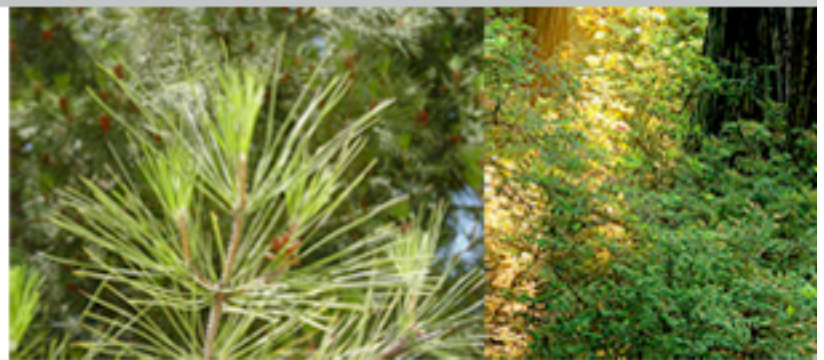


The conifers include over 500 species worldwide and are the dominant plant type in most temperate forest ecosystems. The conifers also include many of the most economically important forest tree species. The Pine Genome Project proposes to advance the understanding of the genomes of this very important branch of the tree of life. A comparative genomic approach is recommended to capture the wide genetic and functional diversity in this plant group. The Five Year Strategic Science Plan has four major elements.



www.PineGenome.org/PGP



GENOME STRUCTURE AND ORGANIZATION

The structure and organization of conifer genomes can be determined by DNA sequencing of the expressed genes (ESTs) and gene-space sequencing of genomic DNA (\$12M/yr)

FUNCTIONAL GENOMICS

The function of conifer genes during development and in response to biotic and abiotic stresses can be determined through transcriptome, proteome, and metabolome analysis (\$8M/yr)

TRANSLATIONAL GENOMICS

Genetic mapping, quantitative trait locus (QTL) mapping, and association genetics can be used to understand the relationship between phenotypes (economic and adaptive) and natural genetic variation (\$8M/yr)

BIOINFORMATICS, DATABASE, & GENETIC STOCKS

Bioinformatic tools, public access databases, and a genetic stock center must be developed and curated to support a large and integrated Pine Genome Initiative (\$2M/yr)

