

Developing high yield plants optimized for changing environmental conditions is a cornerstone of meeting our food, textile and bioenergy needs. Using genomic information to shape agricultural processes is key to accomplishing this challenge.

CONIFERS *members of the order Pinales*

Genome size (millions of bases) >20,000 Mb
Number of Genes ~ 30,000

Conifers are a family of cone-bearing, primarily evergreen plants that include the cedar, fir, pine and spruce. Researchers are identifying networks of genes involved in wood formation as well as adaptation to temperature change and pest resistance. A key part of forest management is replanting harvested lands with seedlings with superior growth characteristics, high wood quality and environmental adaptability. Genomics offers a rapid way to identify the best candidates for high-performance trees.

BREAD WHEAT *Triticum aestivum*

Genome size (millions of bases) 17,000 Mb
Number of Genes ~ 124,000

The wheat genome is almost six times larger than the human genome and largely consists of repetitive chunks of non-essential DNA. Determining agriculturally useful genetic variants is challenging. Researchers from Kansas State University have developed a wheat diversity catalog of genetic variation present in 62 varieties from around the world. This helps identify DNA changes associated with key traits.

TOMATO *Solanum lycopersicum*

Genome size (millions of bases) 900 Mb
Number of Genes ~ 34,000

Commercially-grown tomato plants are limited to 16 hours of light per day or they suffer a fatal form of leaf damage. Researchers have linked the CAB-13 gene to light tolerance but commercial tomatoes have a partially inactive version of CAB-13. When the wild version was crossed into domesticated varieties, plants thrived under continuous light, and tomato yield increased by 20%.

POTATO *Solanum tuberosum*

Genome size (millions of bases) 844 Mb
Number of Genes ~ 39,000

Potatoes are an important source of starch, protein, antioxidants and vitamins but are susceptible to a wide range of pests and disease such as *Phytophthora infestans*, which caused the Irish Potato Famine in 1840. When the potato genome was sequenced, researchers identified over 800 genes associated with disease and pest resistance. The functions of these genes are under study, in the hopes of creating hardier, less susceptible varieties of potato.

Agricultural Genomics

APPLE *Malus domestica*

Genome size (millions of bases) 745 Mb
Number of Genes ~ 57,000

In February 2015, the USDA approved the commercial planting of genetically engineered apples that resist browning when sliced or bruised. Scientists silenced the activity of a set of apple genes that produce the enzymes involved in browning. The so-called "Arctic apple" will be available in small, test-market quantities in late 2016. It will be many years before the nonbrowning fruit is widely distributed.

CORN *Zea Mays*

Genome size (millions of bases) 2,300 Mb
Number of Genes ~ 32,000

Plant growth is controlled by a complicated network of genes and their interaction with the environment. Determining which genes are activated under different conditions helps scientists decipher the relationship between genes and the environment. Many of these networks have been determined for corn, including those that influence leaf and ear size, water control and drought responsiveness. These findings open the door to selecting optimal genetic combinations for future varieties.

COTTON *Gossypium hirsutum*

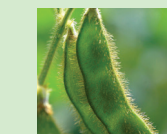
Genome size (millions of bases) 2,300 Mb
Number of Genes ~ 70,000

The fluffy fibers harvested from the cotton plant are in fact hair-like structures that originate from the seeds enclosed in the cotton boll. There are over 20,000 fibers per seed. Cotton researchers want to understand the genetic and environmental regulators of fiber production. Scientists and farmers hope to identify genetic variants that optimize fiber length, quantity and quality and use them to guide the development of new cotton strains.

HudsonAlpha Genome Sequencing Center

The HudsonAlpha Genome Sequencing Center (HGSC) at HudsonAlpha is led by faculty investigators Jeremy Schmutz and Jane Grimwood, PhD. Over the last 10 years, this team of researchers have worked on the genomes of more than half of all the plants sequenced to date. The HGSC is a partner in the Joint Genome Institute, which is funded by the US Department of Energy and focused on initiatives related to clean energy generation. Additionally, research in the HGSC lays the foundation for genomics-enabled breeding across several important crop species.

Below are some of their accomplishments.



Soybean

The HGSC led the effort to sequence the soybean reference genome in 2010 and have recently assembled a diversity catalog showcasing genetic variation for more than 70 ancestral and current

soybean cultivars. This effort seeks to broaden the genetic base of commercially available soybeans. Modern soybean strains represent only a fraction of the genetic variation present across the entire species. During domestication, breeders selected plants using a very narrow set of criteria, like higher yields. Valuable traits for pest resistance and climate hardiness were inadvertently tossed aside. Identifying the full spectrum of genetic diversity allows important ancestral traits to be reclaimed.

Citrus



The HGSC was part of an international team that analyzed and compared the genome sequences of 10 diverse citrus varieties, including sweet and sour orange, mandarin and pumelo.

Modern citrus has very little genetic diversity and is vulnerable to the effects of disease and environmental stress. By inferring past events that gave rise to these common citrus varieties, researchers hope to identify strategies that restore genetic diversity, producing healthy and high-yielding trees.

Sorghum



Sorghum is gaining recognition as an important feedstock source for biofuel production. It is an excellent candidate because it doesn't require as much water or fertilizer as other grasses.

The HGSC, in collaboration with several research centers, was awarded a grant from the US Department of Energy to catalog the natural variation in sorghum DNA.

Once researchers identify genes that regulate water and nutrient use, they can develop next-generation feedstock plants that maximize growth, producing large amounts of biomass for energy conversion.

