

Ancient Plant with Modern Potential – crops could build better cars or improve health

June 29, 2011 – Researchers at University of Alberta (U of A) have deciphered the genetic code for flax, an ancient plant with modern potential.

Mike Deyholos, project researcher U of A, explains the historical significance of the TUFGEN or Total Utilization Flax Genetics project, “Canada is the world leader in linseed production – flax – but higher profile crops like canola, wheat and corn have typically received more research investment. When petroleum products largely replaced linseed oil following the Second World War, flax crop production declined and that meant years of minimal research taking place. We just didn’t have access to as many resources as we had for those other species.”

First Canadian led whole genome project for a complex organism

Using a highly-efficient sequencing procedure developed by the Beijing Genomics Institute, Canadian researchers now have the genetic information to accelerate improvements for flax and to identify ways to adapt this ancient plant to modern uses.

Flax is the first crop sequenced using de novo (Latin for *from nothing*) assembly of Illumina whole-genome shotgun sequencing (WGS). The Illumina WGS technology is much less expensive than previous genome sequencing approaches, but has been proved by researchers to be as valid the earlier technologies that were applied to crops such as rice. From an agricultural perspective, breeders had access to only a handful of flax DNA markers until this successful genome project. There are now over a thousand DNA markers for flax. Having the flax genome sequence and associated data will help breeders and scientists recoup those lost research years and accelerate improvements for flax.

More complete genome sequence equals better environmental and economic picture

According to surveys conducted by the Flax Council of Canada, flax growers face big problems managing fibre and stems. The stem produces a very strong fibre (bast) difficult to use or get rid of. Unlike their counterparts in Europe, growers can’t make linen from flax stems because the growing season here is too short and the fall is too cold. That leaves growers with fields of almost indestructible material. *Straw management* is the term used to describe the problem with flax stems – too hard to get rid of, costly to transport to facilities that could process, hard on the farm machinery and eventually a source of discouragement for flax growers. Traditionally flax is grown for oil or linen but currently Canadian crops are only used for oil. Applying genetic research to those troublesome bast fibres could actually generate economic and environmental benefits (becoming a natural alternative to materials like fiberglass) or if the fibre can’t be used – grow a crop with stems that can be more easily worked back into the soil. Most importantly, having the genome info will help better utilize all the plant. For Canadian flax growers it introduces a new viability for their crop.

Funding Details

Funding for the total \$12M TUFGEN project, of which flax sequencing is a small part, came from Genome Alberta, Genome Prairie, Genome Canada and National Institute of Agricultural Research (INRA, France) .

Background

Excerpt intended for scientific publication, 2011

The genome of flax (Linum usitatissimum) assembled de novo from short shotgun sequence reads

Flax is an ancient crop still widely cultivated as a source of fiber, oil, and medically relevant compounds. To accelerate crop improvement, we conducted whole-genome shotgun sequencing (WGS) of the 350Mbp nuclear genome of flax. Seven paired-end libraries ranging in size from 350bp to 10kb were sequenced using an Illumina Genome Analyzer. Computational prediction found 44,453 protein-coding genes. Within the predicted proteome we found many examples of lineage-specific genes. Together these results show that de novo assembly, based solely on WGS short sequence reads, can be an efficient means of obtaining nearly comprehensive genome sequence information for some plants.

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Additional images are available at: <http://picasaweb.google.com/MikesGene/Flax#>

Image – harvesting the flax seed for research Kernens Crops Research Centre. Photo Credit: Ken Jackle



About Genome Alberta:

Genome Alberta is a publicly funded organization that initiates, funds, and manages genomics research and partnerships. We are based in Calgary but lead projects around the province and participate in a variety of projects across the country. We are one of Canada's six Genome Centres and work closely with these centres to advance the science and application of genomics, metabolomics, and many other related 'omics'. Apart from the scientific contributions and advances that come from our research, we contribute directly to the economy and have put almost 20 million dollars into salaries, benefits and consumables since we were created in mid 2005.