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## Genomics of Sunflower

<b>Status</b>	Approved
<b>Competition</b>	Applied Genomics in Bioproducts or Crops
<b>Sector</b>	Agriculture
<b>Genome Centre</b>	Genome British Columbia
<b>Project Leader</b>	Loren Rieseberg, University of British Columbia

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### Project Description

The sunflower family (Compositae; so-called because their flowering heads are made up of many tiny flowers), is the largest plant family on earth, with over 24,000 described species, roughly 10% of all flowering plant species. They include economically important crops (sunflowers, lettuce, artichokes), beautiful wildflowers (daisies), common allergens (ragweed, goldenrod), valuable medicinals and costly invasive plants and rangeland weeds (thistles, dandelions). Despite the wide diversity and economic importance of plants in this family, there is no genome sequence for any of these species, or even any plants from closely related families. This has delayed genetic research and crop breeding.

Despite the rather large genome size of Compositae, recent advances in DNA sequencing technology (so-called “next-generation” sequencing) now make it practical to sequence their genomes. Our project will use both these new technologies along with more conventional sequencing methods to obtain the DNA sequence of the entire cultivated sunflower genome.

Having an entire genome sequence will facilitate scientific research across this diverse plant family, with applications ranging from crop improvement to weed control to the development of wood-producing sunflower varieties. For example, it will allow us to characterize genetic and morphological variation among domesticated sunflower lines, relating genetic differences to important crop characteristics. This will facilitate molecular breeding programs for the improvement of commercial crops. A second application will be the development of sunflower as a new fuel (biofuel) source with unique advantages as an annual woody plant. Biofuel development will exploit wood-producing ecotypes of two extremely drought tolerant, wood-forming, desert-dwelling wild species: silverleaf sunflower (*H. argophyllus*) and Algodones dune sunflower (*H. tephrodes*). This will allow farmers to grow small, woody trees (a source of biofuel) in a single year while simultaneously using the sunflower seeds for edible oil. Such a dual-use crop has great economic potential.

Our project will increase the speed and precision of sunflower-breeding programs by identifying molecular markers for beneficial genes that encode important agricultural traits such as seed-oil content and flowering time. We will exploit Canada’s strong genomics infrastructure and

leadership in Compositae genomics and use this infrastructure and expertise to full advantage in collaboration with experts world-wide.