

**When a genome is sequenced, do the benefits accrue to just the research community or do they trickle down to the everyday grower?** Many of the benefits of research will trickle down to the everyday grower. For example, in corn the benefits have been at least 90% to growers. Using the research, companies have been able to develop corn that is better able to withstand insects, cold, heat, wind etc.

The following are three examples of research scientists could conduct using the “lowpass” genome sequencing for dahlias.

**1.** Scientists could compare dahlia DNA to other flower species. An example of this might be comparing the various pathways that plants use to fight pests; not all plants have all of the pathways. **2.** Scientists could determine which pathways actually exist in dahlias. This would aid efforts to breed dahlias more resistant to specific pests. In particular, several “plant-specific” pathways exist that can silence viruses or prevent viruses from moving from organ to organ in an infected plant. Knowledge of which pathways exist would aid in strategies to breed virus-resistant lines. **3.** The low pass genome provides a tool kit for assessing which genes are present in any given cultivar: during domestication and breeding, some varieties may have lost specific pathway genes. Knowing what’s missing, allows a scientifically rational approach to restoring genes in a particular variety by conducting crosses with a line that contains a functional copy of the missing information.

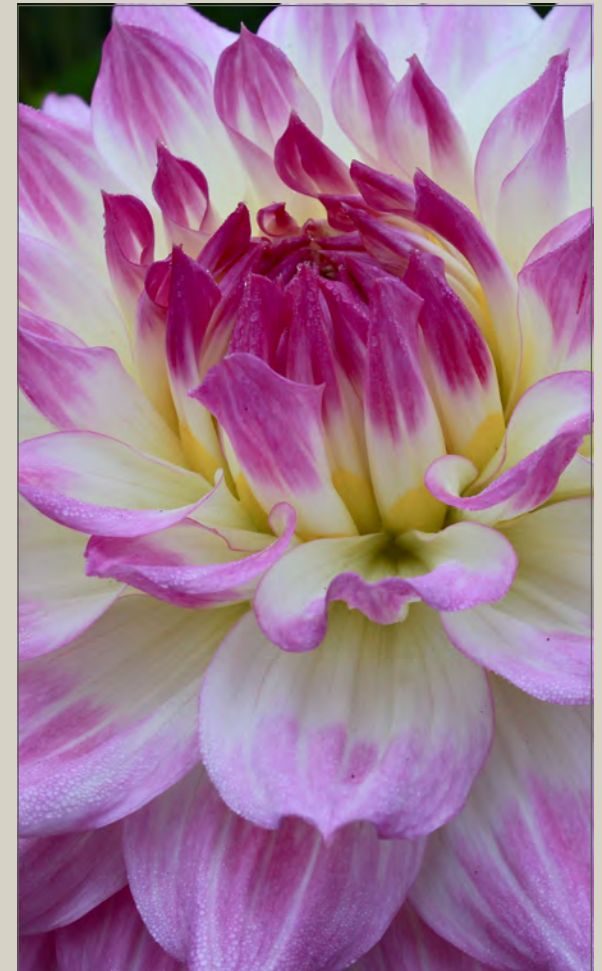
Down the line, when funds are raised for a “highpass” sequencing project in which genes are placed in the correct order on each dahlia chromosome, breeding efforts could be greatly accelerated. For example, identifying the neighboring genes that might affect the outcome of a breeding experiment. What if an important disease resistant gene is close to a non-functional copy of a gene required for certain pigment in flower? In a cross, the pair of genes – one favorable for disease resistance and one limiting color production – will almost always be co-inherited. Knowing this in advance, a laboratory test can be established to screen hundreds or thousands of progeny to find the breeding pathways that will result in plants containing the good disease gene and a more favorable color gene. Such “molecular breeding” relies first on knowledge of the DNA composition of each gene and then on the order of genes.

Without either sequence completed, it would be unlikely that scientist would raise the funds for the genome sequence themselves and study dahlia genetics. Only crops like sunflowers, that have a cash crop potential, would incentivize companies to invest in genome sequencing to make the outcomes better and the crop stronger or more resistant.

\$30,000 is needed for a “low pass” sequencing. It is our hope to fund the first “lowpass” genome sequencing from “original” dahlia DNA through fundraised gifts.

## AMERICAN DAHLIA SOCIETY

### Dahlia Genome Project



# The Dahlia Genome Project

**What is genome sequencing?** A laboratory process that determines the complete set of genes or genetic material in a cell or organism.

**What are the benefits for the research community?** Sequencing the dahlia genome would provide a road map of the locations and “composition” of all its genes. In lay terms it’s like having a road map for a trip from San Francisco to New York. Without the map, researchers don’t know what roads lead to the result they are seeking. With genome sequencing, scientists could determine what genes have changed (evolved) and could explain how various floral forms came to be. Genome sequencing also allows comparison among species. For example, dahlias are a composite, like a sunflower. After sequencing, scientists could determine what genes are common to both sunflowers and dahlias. They could also identify genes that are novel in dahlias.

**The American Dahlia Society is currently funding Washington State University research on viruses in dahlias. Could genome sequencing tie in with that research?**

Yes, sequencing the dahlia genome could pinpoint where genetic viral defenses might be found. It could increase the likelihood of breeding plants with enhanced viral resistance.

**If the genome is sequenced, what are some long term and short term projects that scientists might undertake?** Comparing dahlia DNA to other flower species would interest scientists that study flower and plant evolution. Longer term projects could involve building tools for breeders.

**Are there any examples of other cultivars that have had their genomes sequenced? After sequencing what research resulted for those cultivars?** There are thousands of sequenced flowers and vegetables. Work on corn, for example, has allowed scientists to pinpoint precisely which genes contribute to specific traits: growth habit, drought resistance, photoperiod sensitivity, contributions to height, ear properties, yield, etc. A genome road map will ensure future projects are faster and more likely to produce a precise result.

**Who might do the sequencing? What might their role in this project be?** A scientist familiar with dahlias would have to identify a key dahlia to sequence – perhaps one of the original Mexican species that led to all modern dahlias. The chosen plant would have a specimen made and deposited into a plant collection, most likely at the Missouri Botanical Garden. The work would then

shift to a commercial sequencing company. It is more efficient and less expensive to send the sample to a large DNA sequencing center to be sequenced on a variety of machines. The data is then combined for the best possible outcome.

Donations can be made to the American Dahlia Society. Any and all donations are welcome. Please indicate on the memo section of your check that you would like the funds to be used for the genome sequencing project. Mail your check to:

ADS Genome Project  
American Dahlia Society  
16816 Country Road 10  
Bristol, IN 46507  
Please make checks out to:  
American Dahlia Society.

The American Dahlia Society is a 501(c)(3) non-profit organization and donations are tax deductible. Tax id #: 23-2123580

**How long does it take to sequence the dahlia genome?** Sequencing typically takes a week to a few months once material is sent to the lab. The length of time is dictated by the size of the genome and to what level of accuracy we choose to fund.