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Most of my research has focused on species where only modest effort is spent on crop improvement, methods development, and genomics. In this statement, I will illustrate how my efforts are moving these goals forward in sunflower and other oilseeds, as well as my research vision.

### *Development of sunflower marker/genomics resources*

Through discussions with key sunflower stakeholders, I initiated a partnership of USDA, several seed companies, and a third-party laboratory, Biodiagnostics, to co-develop a 10,000 SNP Illumina Infinium array that could lower costs to both public and private sunflower breeders through bulk purchase. I led development of the linkage mapping populations needed to map the SNPs, and interacted with industry on goals of the work, specifically downstream trait mapping work that could be done. We completed development of the array and published the resource with two important disease resistance genes mapped (CV publications 22 and 27). I also led the effort to combine this map with another, independent SNP map that was released from embargo, allowing for collaborative work across maps (36).

Because the USDA breeding program is the only public release sunflower program in the world, many of our released inbred lines are used by colleagues for genetic studies. Most of our lines were resequenced to 10x depth by John Burke's and Loren Rieseberg's groups. Nolan Kane and I took this further and resequenced additional parental lines and all of my  $F_4$  and greater experimental lines from the last 10 years. Through trio imputation, we have nearly completed development of a rich resource for mapping and genomic selection in our sunflower breeding program (45; unpublished data).

### *Genomic selection/Association mapping*

We developed and genotyped an association mapping population of open pollinated varieties from the National Plant Germplasm System, which we also phenotyped for reaction to three necrotrophic diseases: Sclerotinia stalk rot (caused by *Sclerotinia sclerotiorum*), Sclerotinia head rot, and Phomopsis stalk canker (caused by *Diaporthe helianthi*; 25, 26). Using our 10,000 SNP array, we found resistance to all three diseases was due to many, moderate-to-low effect loci, which sometimes formed tight clusters. Additional resolution is necessary to learn more, and resequencing of the panel is currently underway. In the meantime, our preliminary association model information has been given to commercial breeders through a material transfer agreement.

We have also partnered with Loren, John and others on a GWAS project to understand abiotic stress resistance in sunflower using another GWAS resource known as the SAM panel. My lab is conducting flood tolerance in the field using a case-control design with nested RCBD and partially balanced lattice, with other labs conducting similar studies for other stresses. Preliminary results are showing discrete targets for breeding with logical candidate genes underlying them. The SAM population is also the centerpiece of our fatty acid genetics project, in which we profiled the fatty acid content of the SAM population at 6 locations from Vancouver, to Fargo, to Athens, GA. Our goal is to combine traditional mixed model GWAS analysis with models for genotype-by-environment analysis such as AMMI to better understand small to moderate effect modifier genes and their interaction with the environment. This genotype-by-environment interaction is known to be a factor in rejection of high oleic contract sunflower at delivery for some hybrids, and it would be helpful to breed against this effect.

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### *Sunflower variety development*

Our breeding program is central to our lab, as much a “sandbox” for our breeding methods and genomics research as a means to improve sunflower. I have led development of 20 sunflower inbreds and assisted in development of several more (11, 12, 28, 35, 42, 43, 44, and unpublished). Of particular interest right now is ‘RHA 476’, which results in hybrids with very early maturity and high yield. The yield advantage of one such hybrid, which we call ‘Honeycomb NS’, is about 300 kg/ha over the best commercial hybrid sold in western Canada. This hybrid may also have a fit in double crop systems in Colorado, Nebraska, and Kansas, which we are investigating. Our program also released two restorer (male) lines, ‘RHA 485’ and ‘RHA 486’, which have oil content around 45% of total seed weight and very good resistance to *Phomopsis* and *Sclerotinia*.

### *Perennial crop domestication for sustainable agroecosystems*

Two years ago, we received a grant from the Malone Family Foundation and the Land Institute to study the potential of interspecific hybrids between *Silphium integrifolium* and *S. perfoliatum* for hybrid oilseed crop varieties, similar to the sunflower system. The concept relies on normal plant behavior, pollination, and seed development without sterility, and our data indicate that this is the case, at least for some hybrids. Further, the hybrids express increased partial resistance to *Silphium* rust (*Puccinia silphii*), larger floral diameter like *S. integrifolium*, and compact branching like *S. perfoliatum*.

Lewis flax (*Linum lewisii*; a Colorado native plant) and Eurasian perennial flax species are members of the *Adenolium* section of the *Linum* genus. These species produce short, shrubby plants that can persist for several years and bloom twice each growing season under agricultural management. Working with Minnesota’s Forever Green Initiative, our selection work to reduce seed dormancy and encourage upright habit has been very successful. Genomics-assisted methods are possible, but the genome differs from domesticated annual flax in that the former are  $2n=2x=18$  generally, and annuals are  $2n=2x=30$  species. With a genome sequence of annual flax available, we are interested in sequencing Lewis flax and/or *Linum perenne* from Europe, but have yet to propose it for funding.

### *Future directions*

The ingredients for a healthy lab include having happy, motivated people; reporting results in a timely manner; and pursuing opportunities to do new science. I am fortunate today to work with great people that allow me to succeed in this way (see [www.hulkelab.org/people](http://www.hulkelab.org/people)). We recently submitted proposals for new projects in unmanned aerial vehicle (drone) phenotyping of sunflower with John Nowatzki’s group at NDSU and rhizosphere analysis of our sunflower OPV diversity panel to understand the tri-trophic interactions between sunflower, root associated microflora, and *Sclerotinia* in a root infection scenario with Nolan Kane and Jason Corwin at CU-Boulder. After meeting with human nutritionists at a conference last summer and speaking with sunflower industry contacts, I developed an interest in flavor profiles and nutrition enhancement of confectionery sunflower, to increase value or add markets for this important crop to Colorado and the West. I am interested in developing a multidisciplinary NIFA-SCRI proposal around this idea. I am also interested in doing more at the intersection of agroecology and oilseed genetics, because I am certain such knowledge can enhance sustainability of cropping systems on western landscapes. My goal for this position is to use the latest in genomics and quantitative genetics to add value to new and underutilized oil crops for Colorado producers and end markets.