



# 2019 BREWERS ASSOCIATION FUNDED RESEARCH GRANTS

## BARLEY

### BUILDING A WINTER MALTING BARLEY MARKET FOR THE GREAT PLAINS

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- **Partner(s):** University of Nebraska-Lincoln
- **Principal:** Stephen Baenziger
- **Primary goal(s):** The outcome and impact will be new cultivars and an expanding barley market for malting barley (as well as feed and forage) in a region with generally few diseases (very little Fusarium head blight) but known for abiotic stresses (harsh winters and heat/drought) and aphid pressure. The short-term impact will be identifying European winter malting barleys suitable for production in the Great Plains and the sharing of better characterized germplasm within the larger winter barley community and identifying which available winter malting cultivars can be grown to foster the Great Plains malting barley industry.
- **Background:** Winter barley is known to be more drought tolerant than winter wheat and with water restrictions and changing weather, winter barley has the potential for further expansion. The Great Plains, with its dry climate coupled with the potential for irrigation, is favorable for the development of malt and food grade grain with minimal disease. Traditionally, winter barley in the Southern Great Plains is grown primarily as a feed grain with grazing potential, or for forage. While neither of these uses are related to malting barley quality, we believe it is critical to have a barley market before you can have a malting barley market. Having a barley market provides a ready market for malting barley grain that does not meet malting quality specifications.
- **Additional Information:** Barley was once widely grown throughout the Great Plains but almost all of those acres have been converted to winter wheat or summer annuals (corn and soybeans). Alternative production areas must have the knowledge base, familiarity with the crop, and maintain the equipment to produce the crop for the alternative production area to be successful.

### CHARACTERIZATION OF GENOTYPE BY ENVIRONMENT INTERACTION FOR MALTING QUALITY IN NEW YORK STATE

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- **Partner(s):** Cornell University Department of Plant Breeding and Genetics
- **Principal:** Mark Sorrells
- **Primary goal(s):** The objectives of this project are to characterize GxE (genotype by environment) interactions for yield and malting quality in spring two-row malting barley in New York, identify the most informative testing locations to improve resource use allocation, and identify genetic material that is broadly adapted to New York as well as material that has high potential in specific regions.
- **Background:** New York is the fourth largest brewing state in the country with over 400 operational breweries. Malting barley production is growing in New York with much of the growth stemming from the passing of the state Farm Brewery Bill in 2012. This legislation gives economic incentives to brewers who use local malt and hops in their beers, spurring the creation of over 150 new farm breweries and a dozen malthouses in New York.
- **Additional Information:** A comprehensive GxE study for malting barley has not been conducted in this region. Identification of either regionally superior lines or a broadly adapted line would decrease grower risk and further establish a consistent malting barley crop for malting and brewing in the Northeast.

### STABLE AND SUSTAINABLE DRYLAND PRODUCTION OF HIGH-QUALITY MALT BARLEY

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- **Partner(s):** Montana State University
- **Principal:** Jamie Sherman
- **Primary goal(s):** 1) Development of a greenhouse system to study roots as well as make more efficient selections. 2) Genetic dissection of drought tolerance in a population varying for stay-green and the low-protein gene. 3) Confirmation of greenhouse methods as a tool to select for root architecture through a field study. 4) Improved efficiency of breeding for

drought tolerance through markers and new phenotyping tool. Outcomes: Knowledge gained from this study will improve understanding of genetic control over drought tolerance. Genes identified, providing drought tolerance, will be deployed in new varieties that will improve yield and quality stability for the all-malt industry.

- **Background:** This proposal will continue the investigation of the genetic control of stable, high quality malt under dryland production, which is necessary to meet the needs of the all malt industry in the Western U.S. Although barley is well adapted to dryland farming, historic production of malting barley has been in higher moisture to ensure malt quality. In dryland conditions, current barley varieties have an increased risk of rejection due to poor malt quality, resulting in a significant economic loss to farmers of more than half of the potential crop value. Therefore, growers are often reluctant to plant malting barley due to the increased risk, resulting in an unstable malt barley supply for end-users.
- **Additional Information:** Long-term Impacts: 1) Growers' risk in raising malt barley will be mitigated by the creation of lines with stable quality under dryland production. 2) Genetic dissection of drought tolerance and quality stability will allow for the more efficient release of lines. 3) Malt barley production will be more sustainable and more stable benefiting end-users.

## INTERACTION BETWEEN BARLEY GENETICS AND MALT PROCESS IMPACT ON FLAVOR

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- **Partner(s):** Montana State University
- **Principal:** Hannah Turner
- **Primary goal(s):** We propose to utilize nine different malt processes to malt four barley varieties, which have been characterized to make chemically diverse malt through an earlier study. The malts will be characterized for malt quality and chemical profiles will be determined. Twelve of the malts will be taste tested to determine if variation in chemical profile can be tasted. Twelve will also be nano-brewed and chemically analyzed to determine if chemical differences in wort predict chemical difference in beer. In the future, select malts, identified through this study, will be made into larger batches of beer to determine if chemical differences result in taste differences.
- **Background:** The basis for success in the all malt brewing industry is the creation of high-quality products each with individual profiles. Therefore, an important focus of the craft industry is flavor. Historically, unique flavors due to malt have been provided by changes in the malt process rather than by the different barley varieties making the malt. While there is some evidence that barley variety can contribute to flavor, little to no research has been completed that investigates the interplay between barley variety and malt process on flavor.
- **Additional Information:** In future years, varieties and malt protocols with promise will be replicated in large malt and brew batches to confirm results. Outcomes: Determine the interplay between barley genetics and malt process on flavor potential. If the interaction between genotype and malt process is significant then it will change the way breeders, maltsters and brewers think about flavor.

## WINTER AND SPRING 2-ROW MALT FOR CONVENTIONAL AND ORGANIC SYSTEMS

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- **Partner(s):** Montana State University
- **Researcher:** Jed Eberly
- **Primary goal(s):** 1) Test 25 winter barleys in tilled and no-till systems to determine the impact on important traits, including winter survival, yield, and malt quality. 2) Continue building the winter barley breeding pipeline for Montana by making crosses, inbreeding and testing about 8,000 lines resulting from winter crosses for winter survivability and malt quality. 3) Compare spring barley in conventional and organic systems to identify varieties particularly suited to organic management and/or to identify varieties with agronomic and malt stability across conventional and organic management systems..
- **Background:** Barley is the second most widely grown grain crop in Montana. Initially, barley was grown primarily as an animal feed, but more recently malt barley has dominated the state. Barley also has value as a rotational crop with wheat, sugar beets and, most recently, pulse crops. Spring barley has been the focus in Montana, even though winter barley can have significantly higher grain yields and lower grain protein. Winter barley could provide more sustainable malt production in the state by making better use of early spring moisture and requiring fewer inputs per amount of malt produced.
- **Additional Information:** Through this work, we will determine the barley traits necessary for improved performance under different management systems. Long-term goals of this project include the development of winter malt lines and lines adapted to organic systems for Montana, and to establish a system to breed for high-quality malt under a variety of agricultural systems. Maltsters and brewers can benefit from both winter barley and barley that would perform in organic systems due to improved marketability and sustainability.

## IMPROVING MALTING QUALITY IN TWO-ROWED BARLEY BY REDUCING GRAIN PROTEIN AND $\beta$ -GLUCAN CONTENT THROUGH MARKER ASSISTED BACKCROSSING

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- **Partner(s):** University of California, Davis
- **Principal:** Alicia del Blanco
- **Primary goal(s):** Introgress, via marker assisted backcrossing, the low GPC (grain protein content) allele from malting variety "Karl" and the low  $\beta$ -glucan allele from mutant M351 to our elite malting barley variety UC Tahoe and advanced line UC1390. Backcross to recurrent parents and start genotyping of backcross generation for donor alleles (low GPC/low  $\beta$ -glucan).
- **Background:** Malting quality traits are key factors in producing value-added malt and beer. Moderate protein levels in the grain, as well as  $\beta$ -glucan content no higher than 100 ppm are required in malting barley grains. The American Malting Barley Association (AMBA) guideline for all malt two-row protein content is  $\leq 12\%$ , with a total malt protein of  $\leq 11.8\%$ , which implies lower N fertilization of barley crops to meet these standards, with a consequent reduction in grain yield potential.
- **Additional Information:** Crosses and backcrosses will be made under greenhouse conditions, to advance 3 or 4 generations in 1 year. The primary crosses and first backcrosses between UC Tahoe and UC1390 to Karl have already been made and we are currently genotyping. The primary crosses between UC Tahoe and UC1390 to M351 have been made. Therefore, creating the populations and increasing the seeds will take approximately 2 years. Backcross generations will be genotyped with barley CAPS specific markers (Distelfeld et al., 2008), and SSR markers Bmag369 and Bmag564 (Hu et al., 2014) selecting only the plants carrying the low GPC and  $\beta$ -glucan alleles, respectively. We will also start using these lines as parents in our regular malting barley crossing blocks.

## DEVELOPMENT OF TWO AND SIX-ROWED WINTER MALT BARLEY VARIETIES FOR THE EASTERN U.S.

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- **Partner(s):** Virginia Polytechnic Institute and State University
- **Principal:** Carl Griffey
- **Primary goal(s):** Develop improved malting barley cultivars for the mid-Atlantic and southeastern U.S. to benefit the local economy by providing farmers with a new profitable crop to add to their operations. Local maltsters can provide brewers with malt grown nearby, which significantly reduces the effects of shipping malt from across the country or from Europe.
- **Background:** To support the craft beer and malt industry in the mid-Atlantic and southeastern US, farmers must have access to barley cultivars that are well-adapted to the hot, humid growing conditions (disease, pre-harvest sprout, and lodging resistance, while fitting the soybean double crop rotation) and have superior malting qualities (low  $\beta$ -glucan, balanced enzyme package, low protein, and desirable flavors). To most efficiently develop these improved malting cultivars, we must understand the genetic architecture and have DNA markers associated with improved quality that can be readily deployed to enable informed selections much earlier in the breeding cycle.
- **Additional Information:** Virginia Tech has been releasing barley cultivars since the 1940's, therefore we are poised to take on the challenge of developing cultivars optimized for this new agricultural system.

## EVALUATING A MULTI-STATE BREEDING PROJECT TO PRODUCE LOCAL MALTING BARLEY FOR THE CRAFT BREWING INDUSTRY

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- **Partner(s):** University of Minnesota
- **Principal:** Kevin Smith
- **Primary goal(s):** The primary deliverable from this proposed project will be a variety prediction tool that can select breeding lines that should perform well in specific environments. The data and modeling tools will be publicly shared public through a repository on the Triticeae Toolbox (<https://triticeaetoolbox.org/barley>) so that other researchers can use them. In addition, we will share the results of our analysis in the form of prediction reports and reports on the evaluation of the tool itself.
- **Background:** The University of Minnesota, with support from the Brewers Association, recently coordinated an effort with 16 breeders/researchers across 14 states/provinces to create and utilize a data infrastructure to support upstream barley breeding across the U.S. This initiative produced a dataset of observations on many barley varieties for several important agronomic and malting quality traits. These observations were made across 20 locations from 2015-2017, providing a powerful dataset that spans diverse environments and growing conditions.
- **Additional Information:** Craft brewers are increasingly looking to obtain the raw material for their products from local sources. This trend has created a demand for malting barley cultivation in regions and locations proximal to craft breweries. Such a shift in market preference has the obvious benefit of reducing transportation costs from current centers of production, but brewers may also receive a premium for sourcing ingredients locally. With this change in the industry landscape, barley breeding and cultivation must adapt to fill this demand.

## THE CONTINUING QUEST FOR FLAVOR: FROM THE OREGON PROMISE TO THE ROMP OF OTTERS

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- **Partner(s):** Oregon State University
- **Principal:** Pat Hayes
- **Primary goal(s):** 1. Directly contribute to the development of winter 2-row barley varieties with competitive agronomic performance and unique flavor contributions to beer. 2. Generate publicly available agronomic, malting quality, and sensory quality data on agronomically relevant winter 2-row barley germplasm. 3. Contribute to the fundamental body of knowledge regarding the genetics and biochemistry of barley contributions to beer flavor. 4. Stimulate a national network of barley and barley flavor research.
- **Background:** There is increasing awareness of the contributions that barley can make to beer flavor and that these contributions can be made by barley germplasm with requisite agronomic and malting quality profiles. Thanks to support from the Brewers Association (BA) and Flavor Pack, we have developed a path for developing barley varieties of potential interest to the craft industry based on unique flavor, quality, and agronomic attributes. The path starts with development of doubled haploid germplasm from cross combinations that allow for simultaneous breeding progress and contributions to fundamental genetics. Using the Oregon Promise germplasm (Golden Promise x Full Pint) we have shown that barley genotype and growing environment can make differential contributions to beer flavor (Herb et al., JASBC, 2017a). We have built on this foundation to address the role of malt modification on barley contributions to beer flavor (Herb et al., JASBC, 2017b). Currently, we are extending this work to confirm that flavor is quantifiable by trained sensory panels in pilot (two-barrel) brews and that a large consumer panel can detect flavor differences and identify preferences for experimental barley germplasm.
- **Additional Information:** The Romp of Otters is a set of 47 winter habit 2-row doubled haploids developed from crosses of Maris Otter with a contemporary German variety (Violetta) and an experimental German variety (Ackermann 04-028-36).

## ENHANCEMENT OF WINTER HARDINESS IN TWO-ROWED BARLEY GERmplasm FOR THE CRAFT BREWING INDUSTRY

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- **Partner(s):** University of Minnesota
- **Principal:** Brian Steffenson
- **Primary goals(s):** First, we will evaluate and genetically characterize the winter hardiness of populations derived the six most elite VIR (Vavilov genebank) accessions identified from previous multi-site and multi-year testing. This germplasm may become the foundation for winter barley breeding programs across the northern tier states and beyond. Second, we received funding to procure additional barley germplasm from VIR for winter hardiness testing. Third, we will provide important new outreach information on the potential of winter barley production in the U.S. Interest in winter barley production is growing rapidly across the country as new breeding programs have been started in several northern states.
- **Background:** The Upper Midwest is the largest producer of malt in the U.S. Yet, barley acreage in the region has dropped to historic lows. Despite this downward trend, there is increased optimism for a recovery of barley acreage due to several factors: i) the dramatic upsurge of craft breweries creating a demand for locally produced malting barley, ii) increasing ecological pressures on the predominant corn/soybean cropping system that threatens its sustainability, and iii) changes in cropping systems toward autumn-sown cover crops that could evolve to prominently include winter barley as the main grain crop. Autumn-sown (i.e. “winter”) barley has many advantages over traditional spring-sown barley that is currently grown in the Upper Midwest and other regions of the country including, i) higher yield potential, ii) enhanced malting quality, iii) higher nitrogen and water use efficiency, iv) escape from major “summer” diseases, and v) various ecological services.
- **Additional Information:** This proposal addresses the Brewers Association goal of developing public barley varieties and aligns with its sustainability priorities of: i) increasing the usage efficiency of energy, water, and other natural resources; ii) protecting the long-term viability of watersheds; and iii) promoting more sustainable growing practices.

## IDENTIFYING SPRING MALTING BARLEY VARIETIES FOR THE CRAFT BREWING INDUSTRIES

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- **Partner(s):** North Dakota State University
- **Principal:** Richard Horsley
- **Primary goals(s):** Deliverables include a final report provided to cooperators that includes field, barley, and malt data from each individual ESNB (Eastern Spring Barley Nursery) site. Data can then be used by local scientists to determine varieties that may be candidates for production in their area. Preliminary results suggest a group of varieties from Europe may be good candidates for larger scale field, malting, and brewing evaluations in 2019 and 2020.
- **Background:** Barley used for malting and brewing must meet specific requirements on nearly 20 different end-use quality traits. Barley grown outside of its area of adaptation often fails to meet the specifications needed for malting and brewing, which include grain free of pre-harvest sprouting, grain protein less than 12%, plump kernels > 80%, and germination  $\geq$  95%. Additionally, un-adapted varieties often have lower yields and are susceptible to local diseases that are not present in the area where they were developed.
- **Additional Information:** The 25 ESNB varieties/lines are grown in replicated trials in MI, OH, PA, VT, ME, MA, NY, and NY. Data are collected by local experiment station or extension personnel. A composite sample from each entry from every location are sent to North Dakota State University (NDSU) for determining barley quality (kernel plumpness, protein, pre-harvest sprouting damage, and mycotoxin levels). Data from field and lab evaluations are compiled and analyzed at NDSU and a final report is sent back to cooperators.

## EFFECTS OF VARIETY BY MALTING INTERACTIONS ON THE MALT AND BEER METABOLOME

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- **Partner(s):** Colorado State University
- **Principal:** Adam Heuberger
- **Primary goal(s):** This investigation will result in comprehensive chemical description for how malt metabolites are influenced by kilning, and if/how this process is different among barley varieties. We expect many malt flavor metabolites to vary, including Maillard reaction products that can be influenced by varying levels of amino acids and sugars in the barley grain and produced during seed germination. Further, we will validate which of these chemical differences are important for flavor. This can provide chemical targets for higher-throughput screening of malt samples, which can be used to provide a new layer of quality control/assurance within the malting and brewing industry.
- **Background:** There is a considerable consensus on the importance of malt on beer flavor, however the impact of barley variety on flavor is less understood. Recent studies at Colorado State University (CSU), Montana State University (MSU), Oregon State University (OSU), and others have demonstrated that barley varieties can be distinguishable (via sensory) when evaluated in highly controlled malting and brewing systems. However, the mechanism of how barley genetics affects flavor is still unclear. Research at CSU has shown that different barley varieties produce grains with different metabolite chemistry (i.e. small molecules such as amines, amino acids, lipids, organic acids, alkaloids), and that this distinct metabolite chemistry is maintained after malting.
- **Additional Information:** An important outcome of this research can include identifying target chemicals to track during breeding, malting, and brewing to predict malt flavor. This research supports the Brewers Association funding priority of “understanding the beer sensory outcomes of barley malt flavor deciders.”

## METABOLOMICS AND GENOMICS ANALYSIS OF THE ‘ROMP OF OTTERS’ BARLEY FLAVOR PROJECT

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- **Partner(s):** Colorado State University
- **Principal:** Adam Heuberger
- **Primary goal(s):** 1) Perform metabolomics analysis of five malts and five beers from the Oregon State University (OSU) barley flavor project. 2) Perform genomics analysis of barley from the OSU barley flavor project. 3) Develop statistical models to integrate chemical, genetics, and sensory information provided by OSU. For this research, 14 barley samples will be profiled using SNP genomic profiling, and a subset of barley varieties will be profiled for chemistry 5 malts and 5 corresponding beers). The barley genetics and malt chemistry will be associated with beer chemistry and corresponding sensory data using multivariate statistical modeling. This information can improve our understanding of the molecular basis of a barley variety’s effect on beer flavor.
- **Background:** The contribution of barley and malt to beer flavor is an important area of research in the craft beer industry. At Colorado State University (CSU), we have demonstrated how barley varieties can be distinguished as sensory differences in the finished beer and describe a chemical basis for this phenomenon. Parallel studies at Oregon State University demonstrate flavor differences in barley within the Oregon Promise breeding program (Golden Promise x Full Pint; Dr. Pat Hayes). Further, the Oregon Promise germplasm studies revealed that that the beer flavor differences can be mapped in the genome (Herb et al. 2017). These varieties are now being developed and evaluated as the ‘Romp of Otters’ project.
- **Additional Information:** This proposed will perform metabolomics profiling and genetics analysis of a subset of varieties developed at OSU (Romp of Otters). This supports the long-term goal to identify the genetic and chemical determinants of flavor, which will be used for developing new barley varieties of interest for the craft industry at a much faster pace. This proposed project will also serve as the foundation for a new collaboration between CSU (Heuberger, Munoz-Amatriain) and OSU (Hayes) to combine our expertise in metabolomics, genomics, and barley breeding with a focus on malt and beer flavor.

## HOPS

### MULTIFACETED IMPACTS OF NITROGEN AND SULFUR FERTILITY ON HOP PRODUCTIVITY, QUALITY, AND BREWING CHARACTERISTICS

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- **Partner(s):** US Department of Agriculture; Oregon State University
- **Researcher:** David Gent
- **Primary goal(s):** 1) Characterize the association between nitrate and sulfur content in commercial hop lots. 2) Determine the interaction of nitrogen and sulfur fertilization rate on nitrate accumulation in cones, cone yield, and quality factors. 3) Quantify the impact of sulfur fertilization rate on brewing characteristics of dry hopped beers. 4) Disseminate results to growers, brewers, and others.
- **Background:** Nitrate levels in raw products and beer are recognized as a potential quality defect when levels are excessively high. We have established that there is a strong, positive relationship between the rate and timing of nitrogen fertilization and resulting nitrate levels in hop cones, with subsequent nitrate transfer from hops during brewing proportionate to hopping rate. Further, we have also quantified interactions between nitrogen fertilization and levels of alpha acids, sensorial characteristics of hop cones, and practical aspects of pest management in the field. In this project, we will build on these findings and investigate how nitrogen and sulfur fertilization jointly influence nitrate accumulation in cones and multiple phases of crop yield and quality in the field, laboratory, and brew house.

- **Additional Information:** Based on the behavior of nitrogen and sulfur in other plant systems, we expect that increasing sulfur fertilization may decrease nitrogen stored as nitrate but potentially alter aroma and flavor characteristics of hops and beer due to changes in thiol containing compounds and other mechanisms.

## MAPPING NOVEL LOCI FOR POWDERY MILDEW RESISTANCE IN HOPS

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- **Partner(s):** University of Minnesota
- **Principal:** Gary Muehlbauer
- **Primary goal(s):** 1. The wild hop germplasm collection (~7,200 accessions) encompassing North American genetic diversity will be phenotyped with two races of powdery mildew and resistant accessions will be identified. 2. A germplasm panel consisting of 480 accessions will be assembled and resources (plant materials and genetic information) will be made available to hop scientists. 3. Genetic markers that are associated with powdery mildew resistance loci will be identified and will be provided to interested breeding programs. 4. Mapping populations containing powdery mildew resistance will be generated that can be used for breeding and additional phenotyping of traits not captured within the scope of this study.
- **Background:** Crop improvement relies on identifying and utilizing genetic variation. In hop (*Humulus lupulus* L.), most varieties have been derived from only a handful of genotypes resulting in limited genetic variation. Previously, utilization of wild relatives of hop has been a rich source of genetic variation and has since allowed for the development of novel hop varieties that are tolerant or immune to various pathogens.
- **Additional Information:** To control powdery mildew, growers apply multiple applications of fungicide, resulting in added expenditures along with environmental and consumer concerns. Therefore, “built-in” genetic resistance is the most economical and environmentally-friendly approach to controlling hop powdery mildew. Wild hop collections have a wealth of genetic diversity and have been invaluable sources of novel alleles for disease resistance.

## DEVELOPMENT AND APPLICATION OF COST-EFFECTIVE DNA-BASED MARKERS FOR HOPS

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- **Partner(s):** USDA-ARS National Clonal Germplasm Repository
- **Principal:** Nahla V. Bassil
- **Primary goal(s):** We will develop an economical DNA-based fingerprinting test for assessing variety purity. A set of 242 cultivars and accessions from the world collection will be tested along with regionally collected accessions from Nebraska. A reference fingerprinting database will be produced and made available to testing labs. A set of SSR (simple sequence repeat) markers with the ability to discriminate varieties will be developed.
- **Background:** DNA-based markers are important for molecular breeding, genetic mapping, variety discrimination, testing purity of genetic stocks, and assessing genetic diversity, relationships, and population structure. Several genetic tools exist for hops, but their use is limited to specific populations, applications, or are costly. We propose developing, testing, and applying an economically viable set of DNA-based markers for fingerprinting 242 hop cultivars and accessions from the National Clonal Germplasm Repository world collection. The fingerprinting set will also be used to resolve relationships among central Great Plains wild collected germplasm.
- **Additional Information:** The developed test will contribute to quality control of hop production and germplasm maintenance benefiting hop producers, protecting cultivars, and craft brewers expecting performance benchmarks of specific hop cultivars. Additionally, the fingerprinting set will be applied to resolve relationships of central Great Plains collected germplasm by the University of Nebraska-Lincoln. The markers will additionally benefit the breeding program by identifying redundancy in the wild germplasm collection.

## DEVELOPMENT OF THIOLS AND THIOL PRECURSORS IN DIFFERENT HOP VARIETIES DURING HOP HARVEST AND THEIR IMPACT ON BEER FLAVOUR

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- **Partner(s):** Nyseos, Barth-Haas Group
- **Researcher:** Laurent Dagan, Christina Schoenberger
- **Primary goal(s):** This project aims to evaluate the variation in concentration of free and bounded thiols in 6 different popular hop varieties. In a second step the researchers plan to investigate how the free thiols correlate with specific sensory properties in craft beers.
- **Background:** Some aromatic hop varieties contain free and bounded thiols in form of precursors. Their aroma properties are very important to brewers as they impart many different fruity flavours into beer during dry hopping. Analysis of these compounds (3MH, 4MMP and 3MHA) is challenging and currently only offered by very few laboratories. The existence of these compounds and their sensory relevance in hops is relative new knowledge to the brewing world. In order to have a controlled impact of these compounds in the brewing process a lot of information needs to be gathered.
- **Additional Information:** The topic of thiols as a resource for fruitiness in craft beers presents many opportunities to develop new beer profiles and a better flavour consistency management of all relevant beer styles as IPA, pale ales, IPL etc. The challenge is to identify and manage the hop samples and the hopping parameters during brewing allowing brewers to optimize the transfer and release of fruity thiols in desired concentrations.