

## ASSESSMENT OF BARLEY CROP VULNERABILITY IN THE UNITED STATES

### A Report from the Barley Crop Germplasm Committee

September 30, 2004

#### Executive Summary

Barley (*Hordeum vulgare* subsp. *vulgare*) is an important component of the US economy. The estimated value of the crop as a raw agricultural commodity is over \$800 million. Value added components from barley (i.e. beer, brewing industry activities, feed, and food) contribute an additional \$146 billion to the economy. Barley is cultivated on about 5 million acres in the US. The vast majority of the crop is cultivated across the northern tier states from Minnesota in the east to Washington and Oregon in the west. Crop or genetic vulnerability in US barley is of concern because of the potential for losses due to diseases, insects, or other production hazards. Analyses of state barley cultivar surveys across the Upper Midwest and Western production regions indicate that one or two cultivars usually predominate, sometimes exceeding 70% of the acreage in a given region. This trend is especially apparent in the Upper Midwest region where malting cultivars predominate. The malting barley crop in the US has a high degree of genetic uniformity, especially in the Upper Midwest production region. The stringent quality requirements imposed by the brewing industry for malting cultivars have forced breeders to narrow their germplasm base by using closely related parents that already possess superior malting characteristics. This trend will likely not change in the near future. The number and genetic diversity of feed barley cultivars is much greater than for malting types, particularly in the west. The major disease threats to US barley and their order of significance include, 1) the rusts (both stem and stripe rust); 2) Fusarium head blight; 3) the three leaf spot diseases of net blotch, spot blotch, and scald; and 4) barley yellow dwarf. The National Small Grains Collection (NSGC), housed at the USDA-ARS National Small Grains Germplasm Research Facility (NSGGRF) in Aberdeen, Idaho, is a valuable source of genetic diversity for countering disease and other production threats. The NSGC maintains over 27,000 *Hordeum* accessions and is one of the largest working collections of barley in the world. The present barley component of the NSGC is reasonably adequate and represents broad genetic diversity in *H. v.* subsp. *vulgare* from nearly 100 countries. However, continued acquisition is encouraged especially of germplasm originating from areas of the world that are not well represented, e.g. China, Central Asia, and Latin America. Collections of non-cultivated *Hordeum* species should also be broadened, particularly for the wild barley progenitor, *H. v.* subsp. *spontaneum*, which can be easily hybridized with barley and is a rich source of valuable disease resistance genes.

## **General Introduction**

Crop or genetic vulnerability in US barley (*Hordeum vulgare* subsp. *vulgare*) is of concern because of the potential for losses due to diseases, insects, or other production hazards. Crop loss figures are not readily available, but US barley production is annually threatened by diseases caused by fungi (e.g. rusts, smuts, scald, scab, leaf blotches, root rots, and powdery mildew), viruses (e.g. barley yellow dwarf), and bacteria (e.g. bacterial blight). The crop is also threatened by insect pests, including greenbug, Hessian fly, cereal leaf beetle, corn leaf aphid, English grain aphid, bird cherry-oat aphid, Russian wheat aphid (RWA), wireworms, and others. The two major climatic constraints to barley production are drought and temperature extremes, especially untimely freezes. Each of these disease, insect, and climatic constraints is capable of causing severe economic losses to producers.

## **Barley Production Regions in the United States**

There are two major barley production areas in the US: one in the Upper Midwest consisting of Minnesota, North Dakota, and South Dakota and the second in the west consisting of California, Colorado, Idaho, Montana, Oregon, Washington and Wyoming. These ten major barley-producing states planted over 4.2 million acres in 2004 or about 90% of the US barley acreage (USDA National Agricultural Statistics Service, USDA NASS; see link <http://www.usda.gov/nass/>). The same states produced an estimated 248 million bushels of barley or just over 90% of the total US production in 2004. The Upper Midwest region accounted for about 38% of both the planted acreage and production in the country. The seven western states had 52% of the planted acreage and nearly 53% of the US barley production in 2004. The three leading western states of Idaho, Montana, and Washington accounted for 44% of the US barley production in 2004.

The Southern (Texas) and Mid-Atlantic regions (Delaware, North Carolina, Maryland, Pennsylvania, and Virginia) of the US produce a small, but important amount of barley that is mainly used for winter grazing pasture and feed grain production. In 2004, these states planted 210,000 acres of barley (USDA NASS).

Specific information related to genetic vulnerability of the barley crop and germplasm of major breeding programs in the two major production areas is given below.

## **Composition of Barley Cultivars within Regions and Germplasm in Breeding Programs**

### **Upper Midwest Production Region**

Six-rowed malting barley predominates in the Upper Midwest region. In 2003, cultivars of this barley class comprised over 94% of acreage in Minnesota, 80% in North Dakota, and 50% in South Dakota. Reports from the 2003 USDA NASS and State Statistical Services indicate that in Minnesota, North Dakota, and South Dakota two six-rowed malting cultivars, 'Robust' and 'Lacey,' account for nearly 71% of the three-state total of 2,375,000 acres. This same trend has occurred for many years. For example, in 1985, 'Robust' and 'Morex,'

accounted for about 67% of the three-state acreage. 'Robust' and 'Lacey' are from the Minnesota improvement program and represent a very narrow germplasm base in that Morex or Morex-related germplasm are common parents. The first two-rowed cultivar ('Conlon') recommended for malting in the Upper Midwest was released in 2000 and comprises from 2% (Minnesota) to 12% (North and South Dakota) of the acreage in the respective states. South Dakota has the highest percentage of feed barley (all two-rowed types) in the region at 25% and Minnesota the lowest 1.5% (a six-rowed type). The heaviest concentration of feed barley is in the western Dakotas.

There are three public breeding programs in the Upper Midwest: two in North Dakota and one in Minnesota. Additionally, Busch Agricultural Resources, Inc. (BARI), a proprietary program based in Colorado, also breeds six-rowed malting cultivars for the region.

#### **Minnesota**

**University of Minnesota—St. Paul. University of Minnesota—St. Paul.** The Minnesota program is focused on breeding six-rowed malting cultivars for the Upper Midwest region. The germplasm is very narrow as just seven ancestors (Lion, Manchuria, Oderbrucker, Chevron, Trebi, Clho7117, and Mich1807) account for 80% of the germplasm base in the breeding program based on pedigree analysis data (F. Condon and K. Smith, unpublished). Morex and Morex-derived progeny comprise the bulk of the genetic background in the Minnesota program. Severe epidemics of Fusarium head blight (FHB) have forced the introduction of exotic germplasm with resistance to this devastating disease. At least 70 % of new breeding lines developed in this program now trace to exotic sources of FHB resistance greatly increasing the diversity of the program. However, it will be at least five years before new disease resistant varieties tracing back to exotic sources of resistance could be released. Recently, a program aimed at exploiting wild barley (*Hordeum vulgare* subsp. *spontaneum*) for useful traits, especially disease resistance, was initiated.

#### **North Dakota**

**North Dakota State University—Fargo.** North Dakota has two barley breeding programs: one focused on spring six-rowed types and the other on spring two-rowed types. The goal of both programs is the development of cultivars with acceptable malting quality, but a portion of the effort is devoted to feed barley. Barley is grown in all areas of the state, and most growers plant cultivars recommended for malting. 'Robust' has been the most popular cultivar for nearly 20 years. The new six-rowed cultivars 'Drummond', 'Lacey,' and 'Tradition' are expected to increase in acreage in the future. 'Conlon' is currently the most widely grown two-rowed cultivar.

Currently grown six-rowed cultivars have 'Traill' and 'Morex' in their parentage. Traill ('Kindred'/'Trebi') released in 1956, introduced a set of genes for local adaptation. Cultivars derived from crosses to Traill show improved performance stability under variable production conditions such as spring frosts, waterlogged soils, drought, disease pressure (leaf spots, root rots, and head blights), and post-anthesis heat stress. 'Morex,' released in 1978, introduced improved malting quality from the Canadian cultivar 'Bonanza.' The two-rowed cultivars

released for North Dakota have yield stability genes derived from Midwest six-rowed barleys. Stem rust, spot blotch, and net blotch are the most important barley diseases in North Dakota. Partial resistance has been incorporated into released cultivars; however, race changes in the pathogens have occurred frequently. The devastating FHB epidemics of the 1990s in the Red River Valley region caused a dramatic westward shift in barley production in North Dakota. North Dakota barley cultivars have little resistance to sporadic diseases such as barley yellow dwarf, leaf rust, scald, smuts, bacterial blight, kernel blights, and root rots.

Breeding of six-rowed barley for North Dakota was initiated in 1947 using accessions from China, Russia, and Turkey and cultivars from Wisconsin and Canada. Other accessions have contributed genes for resistance to stem rust ('Peatland' or 'Kindred'), net and spot blotch (NDB112), and loose smut ('Jet'). The two-rowed program was started in 1973 using western two-rowed cultivars such as 'Klages' and 'Hector' in crosses to Midwest six-rowed barleys. Key agronomic characteristics of two-rowed cultivars were derived from Midwest six-rowed barley. Accessions from China with FHB resistance (Rudd et al. 2001) and those from the ICARDA/CIMMYT program with stem rust and Septoria speckled leaf blotch resistance (Toubia-Rahme and Steffenson 2004) are being used to develop cultivars with multiple disease resistance.

Over 700 barley genetic stocks having the two-rowed cultivar 'Bowman' as the recurrent parent were developed to study morphological mutants and disease resistance genes (Franckowiak and Lundqvist 2002). New semi-dwarfing and short-day response genes from East Asian accessions are being evaluated to control lodging of barley in irrigated areas of western North Dakota. Finally, resistance genes (e.g. *Rph15* for leaf rust resistance) from the wild progenitor of barley, *H. v. subsp. spontaneum*, are being introduced into the breeding program.

**Busch Agricultural Resources, Inc.** The specific focus of the BARI program for the Upper Midwest is to develop spring six-rowed cultivars that fit the North American malt quality profile. The current six-rowed malting cultivars developed by BARI for the Upper Midwest were derived using germplasm from three US development programs (North Dakota State University, University of Minnesota, and BARI) as well as breeding lines from Canada. The BARI program, like other Upper Midwest programs, has a narrow germplasm base, derived largely from the Minnesota cultivar Morex.

#### **Western Production Region**

In general, the commercial barley crop across the western US is quite diverse; however, as is the case in the Upper Midwest, one or two cultivars usually dominate in certain locales or states (USDA NASS and State Agricultural Statistics Services). More than 50 different cultivars were grown over approximately 2.5 million acres in 2003 and 2004 in the six western states that conduct annual cultivar surveys (Colorado, Idaho, Montana, Oregon, Washington, and Wyoming) and California and Utah. This accounts for about half of the total US barley acreage. Among the more than 50 cultivars named in the 2003 and 2004 surveys, the percentage of single-cultivar acreage in various states ranged from <1 to 73%. 'Harrington' has dominated in Montana (44%)

and Idaho (34%), 'Baronesse' in Washington (70%) and Oregon (28%), 'B1202' in Wyoming (35%), and 'Moravian 14' in Colorado (51%). All of the dominant cultivars are two-rowed, and all but one ('Baronesse') are malting types. There is a preponderance of two-rowed spring barleys cultivated in the west, with a relatively even split between malting and feed types.

Most of the six-rowed spring cultivars were from the Midwest or derived from Upper Midwest malting and western feed type germplasm. The two-rowed spring cultivars were derived from a broader germplasm base that includes sources from western Canada, Europe, and the Upper Midwest as well as Intermountain and Pacific Northwest states. European or western North American germplasm provided the primary genetic base for the western two-rowed germplasm (both malting and feed types). Studies on the genetic diversity of North American barley cultivars has revealed that breeding for malting types has resulted in a narrowing of the germplasm base, due to the need to maintain linkages that contain favorable malting quality genes (Eslick and Hockett, 1974; Martin et al., 1991). However, in the last 20 years a wider range of germplasm from worldwide sources has been introgressed into western breeding programs.

There are six public breeding programs in the six western states of California, Idaho, Montana, Oregon, Utah, and Washington. All are state funded, except for the Federal program in Idaho. In addition to the public programs, there are four proprietary programs located in Montana (Western Plant Breeders), Idaho (Coors and Plant Breeding 1), and Colorado (BARI). In the sections below, more detailed information is given on the genetic background comprising the breeding germplasm in the 10 major breeding programs of the western US.

### **California**

**University of California–Davis.** Spring feed types are the predominate barley class grown in California, although six-rowed malting types are occasionally cultivated in the Klamath basin on a contract basis. The cultivars UC 937 and UC 933 occupy the greatest barley acreage in the state. Both are six-rowed types that carry stripe rust resistance. The germplasm in the California breeding program was developed over the last sixty years in the Central Valley with new inputs from the CIMMYT/ICARDA program based in Mexico and from other breeding programs in the Pacific Northwest and Intermountain states. The breeding program has recently changed to include the development of malting barleys as well as feed barleys.

### **Colorado**

**Busch Agricultural Resources Inc.–Ft. Collins.** The specific focus of the BARI program for the western US is to develop spring six-rowed and two-rowed cultivars that fit the North American malt quality profile. The current BARI six-rowed malting cultivars released for the west are Midwestern malting cultivars adapted to the western growing conditions. The current BARI two-rowed malting cultivars were developed using germplasm from three development programs: University of Saskatchewan, USDA-Idaho, and Busch Agricultural Resources.

### **Idaho**

**USDA-ARS–Aberdeen.** This program currently emphasizes development of both

malting and feed barley cultivars. Parental germplasm was derived from the Upper Midwest, Southern Great Plains, and Intermountain regions, as well as various European countries. The program includes both spring (80%) and winter (20%) types. Included within each of these growth habits are several classes: 1) malting (70%), 2) hulled feed (10%), 3) hulless feed (10%), and 4) specialty types such as high beta-glucan, waxy (10%).

About 600 crosses are made in the program each year. At Aberdeen, there are 3,000 breeding lines in storage as well as segregating populations in various stages of inbreeding. ARS-Aberdeen has recently incorporated resistance to RWA from NSGC accessions into improved barley germplasm (Bregitzer et al. 2003) and a new RWA-resistant barley, 'Burton,' has been released from the program. Also, adult plant resistance to stripe rust has been incorporated into cultivars such as 'Bancroft.' Stripe rust resistance remains one of the primary goals of the breeding program. Stripe rust screening of NSGC accessions and breeding materials is being done in cooperation with UC Davis and ARS-Pullman.

**Coors, Inc.–Burley.** This program develops two-rowed malting types with a European quality profile and germplasm base.

**Plant Breeders 1–Moscow.** This program started breeding barley in 1979 utilizing diverse germplasm mostly from North America and Europe. About 75% of PB1's effort has been on two-row feed types with 25% effort on six-row feed types. Recent cultivar releases have emphasized high yield and test weight. PB1 is also developing cultivars with stripe rust resistance and low kernel phytic acid composition.

#### **Montana**

**Montana State University–Bozeman.** The Montana State University barley improvement program borrows strongly from European germplasm and from landrace lines worldwide. The program has focused primarily on dryland barley cultivars for feed, malt, and hay. The NSGC has provided crucial genes for the feed quality improvement program and expanded the genetic base of the program. 'Baronesse,' a remarkable two-rowed feed barley cultivar from Germany, has contributed to a dramatic yield increase in four of the six new cultivars (three malting, two feed, one hay) in the process of release.

**Western Plant Breeders–Bozeman.** This program is quite diverse, developing feed cultivars of spring (mostly) and winter growth habit that are adapted to dryland and irrigated production areas. Waxy hulless types for feed, food, and processing are also in the program.

#### **Oregon**

**Oregon State University–Corvallis.** The Oregon program works with a factorial set of 12 barley germplasm classes: three growth habits (winter, facultative, and spring) x two germplasm groups (two-rowed and six-rowed) x three end uses (food, feed, and malt). As a consequence, exotic germplasm accessions are constantly introgressed into the core-adapted base. Additionally, the project has made judicious use of alleles from the wild progenitor of barley, *H. v. subsp. spontaneum*.

**Utah**

**Utah State University–Logan.** There are two independent breeding programs run by two different breeders for spring- and fall-planted barley, respectively. For a long period (1970-2000), the spring program emphasized six-rowed types for feed only. This program generated high yielding cultivars that were, in many ways, different from those (mostly two-rowed malting types) released from other western breeding programs. A renewed involvement in two-rowed types has been occurring in the last few years and now accounts for 20% of the research efforts. Also, a similar allocation of effort towards breeding of malting types has been made for both six- and two-rowed types. The breeding strategy addresses yield potential in water-limiting and saline conditions, lodging resistance, and loose smut resistance. For winter barley, only six-rowed types for feed have been bred. In 2004, crosses between two-rowed spring types and six-rowed winter types were made in order to introduce the two-rowed trait in fall-planted germplasm. Lodging resistant and winter hardy lines are actively pursued in the breeding program.

**Washington**

**Washington State University–Pullman.** This program has a diverse germplasm base with parental material represented from the Midwest, Intermountain, and Pacific Northwest states, western Canada, Europe, China, South America, Australia, as well as the international breeding center of CIMMYT/ICARDA based in Mexico. The program emphasizes spring barley development (both two-rowed [80%] and six-rowed [20%]) for malting (70%), feed (25%), and food/industrial (5% i.e. waxy and hulless types) purposes. Specific vulnerability traits of importance in the breeding include disease (barley stripe rust, *Rhizoctonia*, *Fusarium*, and *Pythium* root rots), insect (Russian wheat aphid and Hessian fly), and drought resistance. Mutation breeding has been part of the breeding strategy with about 50 M<sub>2</sub> and M<sub>3</sub> populations in storage on site. There are also about 3,500 cultivar, breeding line and genetic stock accessions in permanent storage on site as well as about 5,000 breeding lines available on a three year rotation.

**Genetic Uniformity of Barley in the United States**

As documented in the sections above, the US malting barley crop has a high degree of genetic uniformity, especially in the Upper Midwest production region. There are several reasons for this condition. One of the most important is the stringent quality requirements imposed by the brewing industry for malting cultivars. This has forced breeders to narrow their germplasm base by using closely related parents that already possess superior malting characteristics (Wych and Rasmusson 1983). Second, the brewing companies usually prefer to source only a few malting cultivars for beer production at any one time, thereby effectively limiting the number of cultivars grown. Third, the popularity of certain cultivars (i.e. due to their high yield or premium for quality) among producers ensures that only a few will predominate in a given region. Fourth, the fortunate history in the US is that limited genetic diversity has not led to serious and sustained losses in production. This latter observation ignores the fact that today extensive barley production is limited to relatively few states, due to previous outbreaks of diseases and insects in other regions. For example, barley was once

widely grown in the eastern and central Corn Belt states, but severe epidemics of FHB contributed to the virtual elimination of crop in the region. The same trend also occurred in Wisconsin and southern Minnesota several decades later. In the 1990s, barley production in the Upper Midwest has shifted westward toward north-central North Dakota due to a series of severe FHB epidemics.

The narrow germplasm base of barley cultivars in the Upper Midwest shows little indication of change in the near future. For example, in the 2003 Mississippi Valley Barley Nursery, at least 21 of 25 experimental selections had Morex-related germplasm in their parentage. Similarly, Klages-related germplasm is prominent in the parentage of western two-rowed malting barleys; however, cultivars grown in the west exhibit significantly more genetic diversity than those of the Midwest.

### **Diseases of Highest Impact on Barley in the United States**

The most threatening diseases on barley and their order of significance include 1) the rusts (both stem and stripe rust), 2) FHB, 3) the three leaf spot diseases of net blotch, spot blotch and scald, and 4) barley yellow dwarf. Additionally, there are other diseases currently not present in the US that could be potential threats to barley production.

#### **Rusts**

The rusts have historically been the most important diseases of cereals worldwide because they cause significant yield loss, are easily disseminated by wind, and have explosive reproductive capacity. These same attributes have made the cereal rusts potential bio-warfare agents in several countries, including the US (Peterson 2001). Barley is host to four different rusts in the US: stem rust (caused by *Puccinia graminis* f. sp. *tritici* and *P. g.* f. sp. *secalis*), leaf rust (*P. hordei*), stripe rust (*P. striiformis* f. sp. *hordei*), and crown rust (*P. coronata* var. *hordei*) (Mathre 1997). Of these four pathogens, stem rust and stripe rust have the greatest potential to cause widespread yield loss. Stem rust occurs primarily in the Great Plains region and is mostly a threat to the Upper Midwest production area, while stripe rust occurs primarily in the Western and Intermountain states. In addition to threatening the western production area, stripe rust could also thrive in the Mid-Atlantic region if it was ever introduced there.

The most effective means of control for rust diseases is the deployment of resistant cultivars. Fungicides are also effective for control, but are not always cost effective. Success in controlling stem rust has been achieved in the Upper Midwest production area. All of the major barley cultivars carry the resistance gene *Rpg1*, which has protected barley from serious damage due to stem rust since the mid-1940s (Steffenson 1992). However, rust pathogens are extremely variable and races with new virulences arise periodically. Such was the case in 1989 when race QCC appeared in the Great Plains region. Race QCC carries virulence for *Rpg1* and threatened barley in the Upper Midwest region. Isolated epidemics were reported in the early 1990s, but race QCC never caused widespread damage on the crop (Steffenson 1992). From the evaluation of over 18,000 *H. v.* subsp. *vulgare* accessions from the NSGC, only one (Q21861) was found to exhibit a high level of adult plant resistance to race QCC (Jin et al.



1994). Resistance genes from Q21861 are being incorporated into advanced breeding lines in the Upper Midwest to protect against race QCC.

Stripe rust is a relatively new disease of barley in the US. The disease was first reported in the Western Hemisphere (Colombia) in 1975 and then spread across many South America countries in the succeeding decade (Mathre 1997). In 1991, stripe rust was first detected in the US in Texas. Four years later, the pathogen could be found in every state of the western production area. In response to this new disease threat, the NSGC collection was evaluated for stripe rust resistance, and several highly resistant accessions were identified (Brown et al. 2001). Efforts to breed barley cultivars with resistance to stripe rust were initiated before the pathogen was found in the US. As a result, several stripe rust resistant cultivars have already been released from the ARS program in Aberdeen, Oregon State University, University of California-Davis, and Washington State University.

#### **Fusarium head blight**

FHB is one of the most devastating and insidious diseases of barley. It is caused by a number of different *Fusarium* species, but the most common one in the US is *F. graminearum* (teleomorph: *Gibberella zeae*) (Steffenson 2003). Precise yield loss estimates are difficult to obtain for FHB in the field, but may exceed 40%. In controlled field inoculation tests, infection by *F. graminearum* resulted in yield reductions of 41%. Most FHB pathogens produce mycotoxins that are hazardous to humans and animals. The most common one produced by *F. graminearum* is deoxynivalenol or DON. Mycotoxin contamination of grain is the most insidious aspect of this disease because a seemingly good barley crop with high yield, test weight, and plump kernels can be severely discounted at the elevator because of the presence of mycotoxins (Steffenson 2003). FHB also can affect seed quality. Producers who save seed infected with *Fusarium* for the sowing of next season's crop may experience reduced seed germination and a higher incidence of seedling blight and root rot.

FHB was considered a relatively minor and sporadic disease problem of barley in the United States for many years. Over the past decade, however, it has re-emerged as the most important factor reducing the yield and quality of the crop in the Upper Midwest region (Steffenson 2003). The FHB epidemics of the 1990's in the Upper Midwest region were particularly devastating and caused severe economic losses, grain processing problems, food/feed safety concerns, and human hardship. The United States General Accounting Office (GAO) estimated that about \$200 million in revenues were lost by barley farmers in North Dakota alone from 1993-97 (Anonymous 1999). Because of FHB, the Upper Midwest region is no longer considered a reliable producer of premium malting barley.

FHB is an extremely difficult disease to control. An integrated approach using host resistance, management of infected crop residue, and fungicides offers the best means for ameliorating the deleterious effects on grain yield and quality as well as reducing the levels of mycotoxins such as DON. Extensive evaluations of *Hordeum* germplasm (including a portion of the NSGC) have been made in an effort to identify resistance to FHB (Steffenson and Scholz 2001). Unfortunately, only a few accessions with moderate FHB resistance were identified

from this work. Breeding for FHB resistance and low DON accumulation is a major focus of breeding programs in the Upper Midwest. The barley-FHB pathosystem is subject to extreme variability due to various factors; thus, one of the great difficulties in FHB research is obtaining reliable phenotyping data. Moreover, genetic studies have revealed that resistance is complex being controlled by many quantitative trait loci of small effect scattered across the genome (Steffenson 2003).

Three major leaf spot diseases occurring on barley in the US include net blotch caused by *Pyrenophora teres* (anamorph: *Drechslera teres*), spot blotch caused by *Cochliobolus sativus* (anamorph: *Bipolaris sorokiniana*), and scald caused by *Rhynchosporium secalis*.

#### **Net blotch**

Net blotch is one of the most widely distributed foliar diseases of barley in the US. It is known to be severe in the Upper Midwest, western (particularly California and Montana) and Mid-Atlantic production regions. Many areas have reported an increased incidence of net blotch in the last several decades, caused in part by the more common practice of growing barley continuously in one field, and/or in conjunction with irrigation (Mathre 1997). Minimum tillage practices may also contribute to an increase in net blotch because more inoculum is retained in the additional crop residue left in the field. Yield losses due to net blotch can approach 100% in severely affected fields of highly susceptible cultivars, but more typical losses range from 10 to 40%.

The net blotch fungus persists from one growing season to the next as seed-borne mycelium or as pseudothecia in infested host residue. Seed-borne inoculum can be important in initiating net blotch epidemics, but it serves more often to introduce the pathogen into fields previously free of net blotch. Conidia and ascospores are probably the most important sources of primary inoculum because both are formed on straw (Mathre 1997).

The destruction of primary inoculum is the first step toward controlling net blotch. Use of pathogen-free or fungicide-treated seed will eliminate seed-borne inoculum and prevent the introduction of *P. teres* into fields that previously were not infested with the pathogen. Destruction of host residue infested with *P. teres* is also recommended, but is often difficult to accomplish because the pathogen can survive on this debris for at least two seasons after cropping. Rotation with non-susceptible crops for at least two growing seasons can also reduce the incidence of net blotch. Several foliar fungicides have shown good efficacy against net blotch, but an economic return on this additional input may not always be realized.

The most effective means of controlling net blotch is through the use of resistant cultivars. A large portion of the NSGC has been evaluated for net blotch resistance, resulting in the identification of many sources of resistance. Genetic studies have revealed at least five major resistance genes, which confer a qualitative type of reaction (i.e. a small or incompatible lesion) to the pathogen. Quantitative resistance, that recognized by a reduction in the leaf area affected by the pathogen, also has been described in barley (Mathre 1997). Variation for virulence in *P. teres* has been reported from most areas where net blotch is a problem. Because

resistance in the host is often overcome by changes in virulence in the pathogen, barley cultivars should be bred with broad based resistance to *P. teres*.

#### **Spot blotch**

Spot blotch is found in nearly every region where barley is grown, but is most severe in areas with a warm, humid climate. Spot blotch has been especially damaging in the Upper Midwest region where yield reductions over 30% can occur. Inoculum of *C. sativus* may be seed-borne or may arise from existing mycelium or conidia on plant residue or from conidia in the soil. Initial leaf infections in the spring result from airborne conidia produced either on wild grasses (many are hosts for the pathogen) or on plant residue in or above the soil.

Because *C. sativus* can be seed-borne, the use of pathogen-free or fungicide-treated seed may be beneficial. Primary inoculum in crop residue can be reduced by rotating with non-susceptible crops (i.e. non-grass species) or by using tillage practices that either bury or facilitate the rapid breakdown of the residue. However, the value of each of these management strategies may be negated by soil-borne inoculum. Foliar applications of fungicides can significantly reduce the level of spot blotch infection in barley and increase yields; however, several applications are sometimes necessary to achieve adequate control. The economics of this control measure can vary with the severity of disease, cost of the fungicide, number of applications necessary, and market value of the harvested grain (Mathre 1997).

The use of resistant cultivars is the most economic and environmentally sound means for controlling spot blotch in barley. Six-rowed malting barley cultivars in the Upper Midwest region have remained resistant to spot blotch for over 40 years (Steffenson et al. 1996). This durable resistance was originally derived from the breeding line NDB112. Two-rowed barley cultivars in the region do not possess the same level of resistance as found in six-rowed cultivars and have been damaged by some races of *C. sativus*. Other sources of resistance to spot blotch have been described in cultivated and wild species of *Hordeum*, but have not been exploited in breeding programs (Fetch et al. 2003; Wilcoxson et al. 1990).

#### **Scald**

Scald is another common disease of barley in the US. It is particularly prevalent in California, the Pacific Northwest states, and Montana. Yield losses as high as 40% can occur under epidemic conditions, although losses under 10% are more common (Mathre 1997).

Infected residue is the principal source of primary inoculum for initiating epidemics. In the absence of infected host residue, infected seed can be an important source of primary inoculum. The scald fungus requires moisture (especially splashing rain) for the dispersal of its conidia; thus, the disease is most severe during seasons with frequent rain episodes.

Scald can be controlled by destroying sources of primary inoculum (i.e. infected seed and residue), applying fungicides, and deploying resistant cultivars. Many qualitative acting resistance genes with major effects have been reported in barley. Due to the extreme pathogenic variability of *R. secalis*, qualitative resistance genes have not been durable.

Therefore, more broad-based resistance strategies have been investigated, including the use of composite cross populations and male-sterile recurrent selection schemes for combining major (race-specific) as well as minor (non race-specific) resistance genes in cultivars.

#### **Barley Yellow Dwarf**

Barley yellow dwarf (BYD), caused by the *Barley Yellow Dwarf Viruses (BYDVs)*, is the most important and widespread virus disease of barley in the world. BYD was first discovered in California in the 1950s and remains a disease problem there. Periodic epidemics have also been reported in the Upper Midwest production region (Edwards et al. 2001). Losses approaching 100% can occur if infection starts early in the developmental stage, but losses of about 15% are more common under natural conditions. *BYDVs* are transmitted by aphid vectors in a persistent (circulative) manner. Wild and cultivated grasses, volunteer cereals, and other monocots can serve as over-seasoning hosts for *BYDVs*. Spread of *BYDVs* depends entirely on vector movement. In the Great Plains region, viruliferous aphids can be carried from the south to the Upper Midwest along low-level jet stream winds (Mathre 1997).

The best control for BYD is through the use of resistant cultivars. One of the most effective resistance genes identified to date is *Ryd2*, which was derived from an Ethiopian accession.

#### **Other Diseases**

There are many other diseases of barley that could adversely affect the crop, but are currently not found in the US. Two potentially damaging diseases of note include *Ramularia* leaf spot, caused by *Ramularia collo-cygni* and barley yellow mosaic caused by the *Barley Yellow Mosaic Virus (BaYMV)*. *Ramularia* leaf spot has recently increased in prevalence and severity across Europe and other regions. *BaYMV* is soil-borne and found in East Asia and parts of Europe (Mathre 1997). The virus is transmitted by the soil-borne fungal vector *Polymyxa graminis*.

Blast, caused by *Magnaporthe grisea* (anamorph: *Pyricularia oryzae*) is one of the most devastating diseases of rice in many regions of the world and is present in the US. Isolates of *M. grisea* with virulence for barley are known (Chen et al. 2003; B. Steffenson, unpublished). If such isolates become endemic in the US, significant losses to barley could occur under favorable weather conditions.

Soil-borne pathogens often go unrecognized, but can cause substantial losses in barley. The root rot pathogens of *Rhizoctonia*, *Pythium*, and *Fusarium* have increased in importance across the Pacific Northwest states. Of these three pathogens, *Rhizoctonia* is most problematic because no clear resistance has been identified. Root rot diseases have been particularly severe under reduced or no-till seeding (Cook 2001; Smiley 1996), a practice that has been widely adopted in the Pacific Northwest in recent years (Cook 2001; Schillinger et al. 1999).

#### **NSGC: An Important Source of Genetic Diversity for Combating Disease Threats**

The NSGC is housed in the USDA-ARS National Small Grains Germplasm Research Facility (NSGGRF) at Aberdeen, Idaho and maintains over 27,000 *Hordeum* accessions in its working collection of barley germplasm, backed up in the base collections held at the USDA-ARS National Center for Genetic Resources Preservation (NCGRP) in Fort Collins, Colorado. The current holdings in the NSGC make the barley collection one of the largest working collections in the world. The number of accessions for various species and subspecies of *Hordeum* in the collection are shown in Table 1. In the NSGC barley collection, approximately 25% of the accessions are improved breeding materials and cultivars, 4% are genetic stocks, more than 50% are landraces, and 11% are wild species. Within the cultivated accessions (*H. v.* subsp. *vulgare*) 68% are spring habit, 7% are facultative, and 25% winter; 32% have two-rowed spikes, 67% six-rowed, and 1% other; and approximately 15% have hullless kernels. In addition, large bulk samples of a number of barley composite crosses are stored as part of the NSGC.

The primary gene pool of cultivated barley consists of *H. v.* subsp. *vulgare* and *H. v.* subsp. *spontaneum*. Genes from these sources are readily available for introgression in cultivated barley because no hybridization barriers exist. The *H. v.* subsp. *vulgare* accessions represent a large diversity of cultivated barleys from nearly 100 countries, and thus, is a fairly complete collection. Nearly 70% of the *H. v.* subsp. *spontaneum* accessions in the NSGC is from Israel; thus, a wider geographic representation (e.g. from Iraq, Iran, Syria, Lebanon, Turkey, etc.) of this subspecies is needed.

The secondary gene pool consists of the single species, *H. bulbosum*. Introgressions of chromatin from *H. bulbosum* into *H. v.* subsp. *vulgare* have been achieved and contributed unique disease resistance alleles to the cultivated species (Pickering 2000). Accessions of *H. bulbosum* in the NSGC are from more than 20 countries, but are over-represented again by Israel.

The tertiary gene pool consists of the remaining ~30 *Hordeum* species, which some researchers have advocated moving to the genus *Critesion* (von Bothmer et al. 1991). These species show little pairing in crosses with *H. v.* subsp. *vulgare*; therefore, their contribution to donating genes for barley improvement may be limited. Representatives of most species in the tertiary gene pool are present in the NSGC; however, some species are still lacking.

The adequacy of species and geographic representation in the collection needs to be viewed with regard to the three gene pools in the genus *Hordeum*. Moreover, the NSGC barley accessions would benefit from attention to the actual diversity available, both in terms of geographic diversity represented and adequacy of sampling within geographical areas. A number of germplasm collectors have indicated that inaccessibility may have resulted in collections being limited to marketplaces and roadsides. Furthermore, small samples sizes may not have adequately represented available diversity in landraces. Qualset (1975) and others have pointed out that we have almost certainly not discovered or captured all the important genes in existence.

The systematic evaluation of barley accessions in the NSGC was initiated in 1983 under the direction of ARS staff at Beltsville, Maryland. Currently, the NSGC evaluation program is coordinated by the National Small Grains Germplasm Research Facility (NSGGRF) staff at Aberdeen, Idaho, in consultation with the Barley Crop Germplasm Committee, interested barley researchers, and ARS administrators. The NSGGRF staff has attempted to respond to the most critical needs of US barley researchers relative to evaluation and enhancement of barley germplasm. Priorities are ever evolving. During the recent outbreaks of stem rust (race QCC), stripe rust, FHB, and RWA, the NSGGRF staff identified cooperators to evaluate the collection for resistance to these disease and insect pests and provided them supplemental funding. These evaluations have resulted in the identification of resistant accessions, some of which are being utilized in US barley improvement programs.

Several evaluations of NSGC material also revealed the vulnerability of the *H. v.* subsp. *vulgare* gene pool. For example, from the evaluation of over 18,000 *H. v.* subsp. *vulgare* accessions, only one was found to exhibit a high level of adult plant resistance to pathotype QCC (Jin et al. 1994). Evaluations of barley germplasm (>10,000 accessions) for resistance to FHB have been made over the past eight years, and less than 1% of the tested accessions exhibited a useful level of resistance (Steffenson and Scholz 2001). The level of diversity for leaf rust resistance in cultivated barley also appears quite narrow. Sixteen major leaf rust resistance genes have been described from *H. v.* subsp. *vulgare*, but none of them is effective against all of the known virulence types of *P. hordei* in the world (Fetch et al. 1998; T. Fetch and B. Steffenson, unpublished). These examples indicate that an extremely narrow level of genetic diversity exists in *H. v.* subsp. *vulgare* for resistance to some pathogens.

Wild species are an important alternative source of disease resistance genes for crops, especially when there is limited or no genetic variation in the cultivated species. Wild barley, *H. v.* subsp. *spontaneum*, is the progenitor of cultivated barley. These two taxa are closely related and can be easily hybridized; thus, gene transfer from *H. v.* subsp. *spontaneum* into barley is routine. Introgressions of *H. bulbosum* chromatin into barley have also been successful, making this member of the secondary gene pool a source of potentially useful genes for barley improvement. The long co-evolution of *H. v.* subsp. *spontaneum* and *H. bulbosum* with various pathogens in their natural range makes them important sources of novel resistance genes for diseases such as the rusts, FHB, net blotch, scald, Septoria speckled leaf blotch, and powdery mildew (Fetch et al. 2003; Moseman et al. 1980; Pickering 2000; Weibull et al. 2003). Several accessions of *H. v.* subsp. *spontaneum* from Israel were found to possess resistance to six different diseases of importance to the Upper Midwest production region (Fetch et al. 2003). The same was true for accessions of *H. bulbosum* from the Middle East region (B. Steffenson, unpublished). These studies highlight the importance of wild *Hordeum* species as sources of valuable disease resistance genes.

The present barley component of the NSGC is reasonably adequate and represents broad genetic diversity in *H. v.* subsp. *vulgare*. However, continued acquisition is encouraged especially of germplasm originating from areas of the world that may not be well represented, e.g. China, Central Asia, and Latin America. It is important to acquire newly developed unique

improved cultivars from around the world as well. The NSGGRF staff should maintain strong relationships with the staff of other national and international collections. It is recommended that the non-cultivated *Hordeum* species collection be broadened. Broadening the collection of *H. v.* subsp. *spontaneum* is of greatest urgency. In this regard, agreements are being established to procure diverse collections of *H. v.* subsp. *spontaneum* from across the Fertile Crescent in association with ICARDA based in Aleppo, Syria and the N. I. Vavilov Institute based in St. Petersburg, Russia. Additionally, a proposal was submitted to the USDA Plant Exchange Office to collect wild barley germplasm in southern Turkey in 2005. These actions should significantly increase the geographic representation and diversity of *H. v.* subsp. *spontaneum* accessions in the NSGC.

Accessions included in the NSGC and other barley germplasm collections find use principally as parental germplasm in the development of improved cultivars that efficiently produce high quality grain in environments variable for biotic and abiotic stresses. However, despite the diversity of germplasm available to breeders and other researchers, the current spectrum of cultivars grown in the major barley producing states exhibit limited genetic variability. The US malting and brewing industry, for example, currently depends on a very narrow germplasm base. Expanded efforts to more fully characterize accessions in the NSGC may lead to increased utilization of diverse germplasm. Likewise, efforts to facilitate more effective germplasm exchange among breeders and geneticists in the US and other nations may help increase genetic diversity and reduce the vulnerability of barley.

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Table 1. Number of accessions of *Hordeum* species in the National Small Grains Barley Collection in Aberdeen, Idaho.

<u>Taxonomy</u>	<u>Site Code</u>	<u>Count</u>
<i>Hordeum arizonicum</i>	NSGC	1
<i>Hordeum bogdanii</i>	NSGC	19
<i>Hordeum brachyantherum ssp. brachyantherum</i>	NSGC	8
<i>Hordeum brachyantherum ssp. californicum</i>	NSGC	2
<i>Hordeum brevisubulatum</i>	NSGC	14
<i>Hordeum brevisubulatum ssp. nevskianum</i>	NSGC	1
<i>Hordeum brevisubulatum ssp. turkestanicum</i>	NSGC	1
<i>Hordeum brevisubulatum ssp. violaceum</i>	NSGC	30
<i>Hordeum bulbosum</i>	NSGC	210
<i>Hordeum capense</i>	NSGC	1
<i>Hordeum chilense</i>	NSGC	10
<i>Hordeum comosum</i>	NSGC	4
<i>Hordeum hybrid</i>	NSGC	7
<i>Hordeum jubatum</i>	NSGC	31
<i>Hordeum lechleri</i>	NSGC	2
<i>Hordeum marinum</i>	NSGC	9
<i>Hordeum marinum ssp. gussoneanum</i>	NSGC	11
<i>Hordeum murinum</i>	NSGC	17
<i>Hordeum murinum ssp. glaucum</i>	NSGC	30
<i>Hordeum murinum ssp. leporinum</i>	NSGC	19
<i>Hordeum muticum</i>	NSGC	5
<i>Hordeum parodii</i>	NSGC	2
<i>Hordeum procerum</i>	NSGC	3
<i>Hordeum pusillum</i>	NSGC	10
<i>Hordeum roshevitzii</i>	NSGC	2
<i>Hordeum secalinum</i>	NSGC	4
<i>Hordeum sp.</i>	NSGC	58
<i>Hordeum stenostachys</i>	NSGC	13
<i>Hordeum vulgare ssp. spontaneum</i>	NSGC	1,501
<i>Hordeum vulgare ssp. vulgare</i>	NSGC	25,242
SUMMARY		27,267