

BREEDING BARLEY

in the New Millennium:

Proceedings of an International Symposium

H.E. Vivar and A. McNab, Editors



CIMMYT[®]
INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER

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Symposium

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in
Ciudad Obregon, Sonora, Mexico

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INTERNATIONAL CENTER FOR AGRICULTURAL RESEARCH IN THE DRY AREAS

 **CIMMYT**[®]

INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER

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Table of Contents

iv	Preface
1	Learning about Barley Breeding—D.C. Rasmusson
7	Hull-less Barley: An Overview—J.H. Helm
10	Contributions of Breeding and Crop Management to Increasing Barley Yield and Grain Quality in Chile—E. Beratto M.
18	Importance of Identifying Stripe Rust Resistance in Barley—W.M. Brown, J.P. Hill, and V.R. Velasco
25	Impact of ICARDA / CIMMYT Barley Germplasm on Barley Breeding in Ecuador—O. Chicaiza
28	Malting Barley for the New Millenium—L. Wright
34	Barley Breeding in Peru—M. Romero Loli and L. Gomez Pando
39	Accumulating Genes for Disease Resistance in Two-Rowed Barley for North Dakota—J.D. Franckowiak
47	Collaborative Stripe Rust Resistance Gene Mapping and Deployment Efforts—P.M. Hayes, A. Castro, A.E. Corey, T. Filuchkin, C. Rossi, J.S. Sandoval, I. Vales, H.E. Vivar, and J. Von Zitzewitz
61	Perspectives on Fusarium Head Blight Resistance in Barley—L. Gilchrist
72	Resistance and/or Tolerance to BYDV: Recent Advances in Barley at CIMMYT—M. Henry and H.E. Vivar
77	Two Decades of Barley Breeding—H.E. Vivar

Foreword

One aspect of CIMMYT's mandate is to develop improved barley varieties for Latin America, a task we carry out in collaboration with one of our CGIAR sister centers, the International Center for Agricultural Research in the Dry Areas (ICARDA). Our collaborative efforts are embodied in the ICARDA/CIMMYT Barley Breeding Program for Latin America, an excellent example of partnership within the CGIAR that has operated successfully since the early 1980s.

Barley can grow in extremely inhospitable environments where other crops would have a difficult time surviving—for example in the high valleys (2,700-3,500 meters above sea level) of the Andean Region in South America, where it is very cold and soils are rocky and infertile. In this region, which includes Bolivia, Ecuador, Peru, and southern Colombia, barley does well, though farmers' circumstances do not allow them to invest much in it: they do very little land preparation and do not control diseases or insect pests, despite the fact that barley provides both animal feed and food for farm families.

Regional farmers traditionally planted local barleys that were low yielding and susceptible to diseases; as a result they often suffered disastrous yield losses that seriously threatened household food supplies. Breeding to incorporate durable resistance to multiple diseases consequently became one of the main goals—and outstanding achievements—of the ICARDA/CIMMYT Breeding Program.

The approach utilized during the 20-year breeding process was to create templates for incorporating resistance to diseases endemic in the region, such as stripe and leaf rusts, scald, fusarium head blight, and

barley yellow dwarf (BYD), into a high yielding background. Resistance to scald and leaf rust was incorporated in the early stages, followed by stripe rust and other diseases. Genes conferring resistance to net blotch, spot blotch, and stem rust were added later. By applying this method, the Program succeeded in developing high yielding barleys with resistance to multiple diseases that effectively safeguard smallholder food security in the Andean Region. In essence, the Program provided farmers with an exceptional resource—greatly improved seed—that enabled them to move beyond the limitations imposed by their harsh farming environment.

The success of the Program has been such that it has produced significant spillover benefits in regions beyond Latin America. A case in point is its very impressive impact in China, where barleys developed by the Program cover 40% of the one million hectares planted to the crop. This impact is due mainly to the high yield potential of ICARDA/CIMMYT barley germplasm and its resistance to fusarium head blight and barley yellow mosaic virus.

Perhaps the most noteworthy impact of the Program is that thanks to its efforts, there is now a large pool of barley germplasm possessing good agronomic traits, high yield potential, and resistance to numerous diseases that is freely available to breeding programs all over the world. It is our hope that the achievements of this collaborative Program will be multiplied a hundred-fold by the use barley breeders—particularly in the developing world—will make of these resources.


Timothy G. Reeves

Director General, CIMMYT

Preface

These are the proceedings of an international barley symposium held on 13-14 March 2000 in Ciudad Obregon, Sonora, Mexico. The primary reason for holding this special seminar was to honor Dr. Hugo E. Vivar, who retired in February 2000 after a long and extraordinarily fruitful career. Barley researchers from Latin America, the USA, and Syria who were closely associated with Dr. Vivar were invited to make presentations at the symposium.

Dr. Vivar became the head of the ICARDA/CIMMYT Barley Breeding Program for Latin America in 1984, after working for CIMMYT for nine years. In the course of his long career, Hugo worked on different types of barley for diverse environments and uses, but made a special effort to develop barleys for marginal environments, such as those in the Andean Region of his native South America, where subsistence farmers use barley for food. The higher yields produced by new, disease resistant barleys have significantly improved farm families' food security all year round.

The main focus of the ICARDA/CIMMYT barley breeding program, under CIMMYT leadership, is on Latin America, but the barleys it has developed are also sown in other parts of the world, such as China, Pakistan, and Kenya. One of the reasons they are so widely used is that they possess resistance to multiple diseases such as

the three rusts, BYDV, fusarium head blight (FHB), scald, and net blotch. It should be noted that CIMMYT took the lead in introducing FHB resistant varieties into China through the variety Gobernadora.

There is no doubt great progress has been achieved in improving barley for food, feed, and forage. The crop has been endowed with traits such as high yield potential, multiple disease resistance, and good grain quality. However, in the future research will also have to focus on improving the quality of malting barley, a cash crop that would provide barley producers in developing countries with a promising option for earning their living.

In breeding one always builds on other people's work, and the exchange of germplasm and information is crucial to developing new varieties. We take this opportunity to acknowledge the openness and cooperation of the international community of barley breeders, especially North American barley breeding programs, whose collaboration over many years has been invaluable to ICARDA/CIMMYT barley improvement efforts. We hope these proceedings will stand as a small memorial to the accomplishments not only of Dr. Vivar, a dedicated breeder, but also of a generous group of barley scientists all over the world.



Sanjaya Rajaram

Director, CIMMYT Wheat Program

Learning about Barley Breeding

D.C. RASMUSSEN¹

Plant breeding programs are dynamic and always require change because pests, target area, markets, the plant breeder's toolbox (e.g., plot equipment, computers, and molecular-based methods), and available resources are constantly changing. Thus there is need for learning on a continuing basis. It is interesting to speculate about learning and to ponder how closely breeding success is related to learning and adopting new philosophies and new strategies. In this context I would like to share some of my memorable learning experiences with you.

In thinking about this presentation and my title "Learning about Barley Breeding," it occurred to me that many of you have had experiences similar to those I will describe. Plant breeders tend to move forward collectively in how we think about and how we do plant breeding. So those of you that are older will likely conclude that you have had a learning experience similar to my own.

I have divided the presentation into three parts:

- The formative years, when my thinking about barley breeding was shaped by advisors and more experienced mentors.

- The challenging and innovative years, when we adopted new strategies and our breeding program became productive.
- The still challenging years, i.e., ensuring gains in a mature program.

The Formative Years

Early in my career, I had the good fortune of associating with a large number of interesting and innovative plant breeders. There are too many to mention, but I would like to comment on a few. Among them were barley breeders Rollo Woodward, at Logan, Utah, and Charles Schaller, at Davis, California. I learned pedigree breeding from Rollo Woodward, my master's degree adviser. It was a small but productive barley program where hand cycling of plots was the norm. Charles Schaller, my Ph.D. adviser, did mainly backcross breeding. Together we found the YD2 gene that provides resistance to the barley yellow dwarf virus. He said that YD2 would be the largest contribution we would make in our lifetime. Coit Suneson, also a barley breeder at Davis, was a proponent of utilizing mixtures and allowing natural selection to improve populations. His hallmark paper was "An Evolutionary Plant Breeding Method." For an aspiring barley breeder, Davis, California, in the

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1950s provided a first rate learning experience. Hardly a week passed without a thought-provoking discussion about breeding methods.

The most enriching experience of my career, in terms of learning plant breeding, occurred in Ciudad Obregon, Mexico. For more than 20 years I had the good fortune of having an annual learning experience with CIMMYT staff. When I came to Ciudad Obregon for the barley harvest each year, I had the opportunity to tour the plots, view the large impressive program and, more importantly, to explore breeding philosophies and breeding methods. We tried to resolve how many crosses to make, which types of parents to use, whether or not to select on the individual plant basis and how best to breed for various mega-environments. Because it was recognized worldwide as a leading center for small grains improvement, Obregon was a gathering place for small grain researchers from all over the world. In addition to gaining valuable insights about plant breeding, I learned the importance of teamwork and of sharing ideas and germplasm.

In reflecting on my career and about learning how to do barley breeding, I always come back to colleagues whose ideas, research methods, and germplasm were available for the asking. One such colleague was Hugo Vivar. I followed his barley program with special interest. When I came to Obregon, I would visit the barley breeding plots with Hugo, and every year I obtained useful information and a valuable gift of germplasm from one sub-program or another. I was favorably impressed by the many breeding objectives and overall quality of his nurseries.

Adopting New Strategies

When I reflect on my early years in barley breeding, a few items come to mind that have contributed in a major way to our breeding effort. I am referring to four practices or innovations that we adopted between 1960 and 1970: germplasm sharing, arriving at appropriate breeding objectives, reducing development time, and the paramount role of parental germplasm.

Sharing germplasm

I learned about the value of shared germplasm when we benefited immensely from parent germplasm given to us by colleagues located at North Dakota, USA, and Brandon, Manitoba, Canada. Their germplasm was ideal since they are neighbors and they were leaders in barley improvement in the USA and Canada. Their germplasm contributed improved agronomic performance, disease resistance, and malting quality. Subsequently, we were able to return the favor when they used our varieties Morex and Robust, and their progeny, as parents in their programs. Morex was a hallmark variety quality-wise.

Arriving at appropriate breeding objectives

Upon arriving in Minnesota, I found many opportunities including the need for a sizeable breeding effort for resistance to diseases. Our germplasm was relatively low yielding, tended to lodge, and kernel plumpness was not adequate. So I concluded that it was appropriate to adopt a broad set of objectives focusing on field performance.

But, after some time, I observed that successful varieties in the Midwest six-row malting barley area had one feature

in common. They had the malting and brewing industry stamp of approval and brought a premium at the local elevator. Subsequently, our breeding efforts came to revolve around malting and brewing quality. A part of this learning experience was recognizing that malting and brewing quality is determined by a complex set of approximately 35 traits that are evaluated in three major groupings: 1) barley and malt performance ($N \simeq 14$), 2) brewhouse wort/fermentation characteristics ($N \simeq 12$), and 3) beer characteristics ($N \simeq 9$). Since mid-generation and even late-generation selection cannot be practiced for some of these 30+ traits, it was essential to limit parent choices to elite quality germplasm on both sides of the pedigree. Hence, parent building has played an increasingly important role as we attempted to incorporate desired traits into a malting barley genetic background.

Reducing development time

In most breeding programs, a barley breeder is challenged by evolving pest populations, varying environments and in some cases changing markets. These factors may mandate a rapid response by the breeding program. Another reason for shortening development time is competition among breeding programs. Acceptance of a new variety may depend on whether it is the first variety to provide new resistance or a trait of special interest to a grower or an end-point user. Yet another reason for reducing development time is the growing need for parent building, which frequently requires two to three cycles of crossing and selection. In this situation, reducing the time per cycle becomes critical.

Germplasm is paramount

I learned about value of parent germplasm slowly, and only after many years did I come to realize that parental germplasm is paramount, especially when malting and brewing quality are high priority breeding goals. Two factors were of primary importance in arriving at this conclusion. The first was recognizing that Minnesota barley variety candidates did not fare well in competition with barley lines from other breeding programs in the region. Secondly, the notion that parental germplasm is paramount was solidly reinforced when I reaped the benefits from using elite North Dakota and Canadian germplasm. Their germplasm provided a large step forward for several traits including lodging resistance, disease resistance, grain yield, and malting/brewing quality.

Additionally, I had numerous opportunities to observe a wide array of parental germplasm in our ideotype research effort. Time and time again, I observed that inferior and mediocre barley lines do not make good parents. We had to be content to do parent building for two to three cycles to obtain parents that might lead to new varieties. We needed good performing parents on both sides of the pedigree.

Ensuring Progress in a Mature Breeding Program

In the early years of a barley breeding program (perhaps a couple of decades), there are usually opportunities for improving several traits including resistance to pests, lodging, shattering, yield, and, sometimes, malting quality.

The germplasm is genetically diverse and crossing leads to populations with wide segregation that lend themselves to effective selection for several traits. But, over time, perhaps 50 years, for discussion purposes, traits receiving high priority improve substantially and the program germplasm is called elite. At this time a breeder may observe that lines in field trials have similar phenotypes and to a degree similar pedigrees.

At this point, the program can be called mature and the breeder faces a new challenge that was not present in the younger program. For future progress to occur, the breeder has two distinct challenges. Making gains for traits of choice, as in a younger program, remains a primary goal. However, there is a second major goal, that is to preserve gains that have been made over decades. One can visualize favorable combinations of individual genes scattered across the genome acting in an interactive way to produce elite phenotypes. The breeder is obliged to find a strategy that adds new alleles for desired traits, while protecting and preserving accumulated favorable alleles and gene combinations. It is not an easy task.

A new terminology describes the new type of breeding designed to build future gains upon the base of the already elite germplasm. Parent building or germplasm enhancement, terms used interchangeably, refer to introgressing desired traits/genes into an elite genetic background. In mature programs, parent building may utilize more than one-half of the crossing/selection resources in a breeding effort.

Faced with the challenge of ensuring gains in a mature program, we have gained experience with two programs

whose ultimate goal was to enhance grain yield. In the first case, we worked with individual traits that we trusted would be yield-promoting. This came under the heading "ideotype breeding." The second program was introgressing genes from elite two-row germplasm to obtain useful diversity for yield and malting quality. We call this program "open-parent cyclic selection." We used three breeding cycles. It was an open-parent strategy in that each cycle may employ different parents, i.e., the most promising lines or varieties at the time.

Ideotype breeding

The concept of an ideal plant or an ideotype, as Donald (1968) called it, was an effective elaboration on an older idea accompanied by a new terminology. The idea was that yield could be increased by modifying individual traits like height, leaf angle, and head number. The entire package of desired traits would be called an ideotype or ideal plant. Rasmusson (1987) described an ideotype for six-row spring barley and elaborated on the ideotype concept and its strengths and limitations.

The Minnesota ideotype breeding effort began shortly after Donald's hallmark paper appeared in 1968 and occupied a significant proportion of the barley breeding and genetics effort for more than 30 years. A brief consideration of two so-called ideotype traits will illustrate important aspects of the program.

Semidwarf barley. Jean Lambert, a barley breeder at Minnesota from 1948 to 1962, obtained short-stature mutants in the 'Jotun' background from Norway and began breeding with them in 1956. The aspiration was to duplicate gains

obtained in the Vogel short-stature wheats. The basic Minnesota germplasm was a three-way cross, Jotun / Kindred / 2 / Vantage. The cross to Vantage was critical as it provided the large-diameter sturdy culms that have been a distinguishing characteristic of the Minnesota short-stature lines.

Subsequently, nine cycles (40+ years) of recurrent breeding were done with the aspiration of achieving a yield breakthrough. It never came and, furthermore, the Jotun germplasm lines appeared to preclude achieving favorable malting and brewing quality, at least in the Minnesota program and target environment. Ultimately, only one short-stature variety, Royal, was released in Minnesota. The most important contribution this program made was in sharing germplasm. The Lambert Jotun short-stature lines provided parental germplasm to most barley breeders in North America.

The contribution of the ideotype approach to the barley program in Minnesota can be viewed in different ways. If ideotype-related research, ideotype-related breeding gains, and graduate education are considered, it has been a worthwhile venture. Thirty-three graduate students conducted thesis research on so-called ideotype traits within the barley breeding program, and 22 papers were published. In this context, it has been a productive and worthwhile program.

When breeding gains are measured by new varieties and enhanced germplasm (parental germplasm), the conclusion is different. The ideotype approach could not compete with the traditional ongoing breeding effort. Time and again promising gains from individual traits

were not realized because the traditional breeding effort raised the bar, so to speak. The traditional program provided the entire slate of traits needed in a new variety, while the individual trait ideotype effort too often came up short for one or more essential traits.

Wide-leaf barley. The most interesting trait in our ideotype program at present is a wide-leaf trait. The source of the germplasm was Harlan's Freak Collection. The penultimate leaf width was about 2.5 cm at its widest point. We currently have 11 lines in advanced stages of testing that have moderately wide leaves (much reduced from the source line) along with several positive agronomic traits. The pedigree, which indicates the large breeding effort, is Robust / 63-8069 (source of wide leaf) / 2 / M47 / 3 / Stander / 4 / Excel / 5 / M81. These lines have a large-diameter sturdy culm, large spike, high kernel weight, and high grain yield. We hypothesize that this attractive phenotype is the result of a gene or genes which are pleiotropic for several size-related traits. The ultimate yield level in comparison to lines from our traditional program is yet to be determined. But we are optimistic because of the combination of what appear to be yield-promoting traits.

Open-Parent Cyclic Selection

In response to our concern about lack of genetic variation, we initiated a program to introduce genetic diversity for grain yield and malting quality. The extreme narrowness of the Minnesota malting barley germplasm was described by Rasmusson and Phillips (1997). The

introgression research using open-parent cyclic selection was part of a thesis effort by Michael Peel (1998).

The objective of this research was to assess the effects of transferring genes from two-row barley cultivars to the Minnesota six-row gene pool. Our premise was that the gene combinations of the six-row cultivars should be largely maintained with a small introgression of donor germplasm. We conducted three cycles of recurrent-type breeding beginning with crosses involving five two-row donor parents. The crossing scheme led to progenies with theoretical portions of two-row germplasm of 25-50% in cycle 1, 12.5-25% in cycle 2, and 6.25-12.5% in cycle 3.

We observed the yield penalty that is commonly associated with introgression of donor genes into elite germplasm in cycle 1. In this cycle, no putative cultivar candidates were found. Furthermore, the two-row progeny were decidedly inferior in all populations, especially in the backcross and three-way cross populations. Cycle 2 populations, which theoretically contained 12.5-25% of two-row germplasm, were improved, and mean grain yield of the populations increased to 98% of the check mean.

In cycle 3, sets of lines representing three populations yielded 112-119% of the check mean in 1997 and 1998, and individual lines surpassed 'Stander', the highest yielding check in both 1997 and 1998. The highest yielding lines in each cycle were derived from populations

having the highest theoretical percentage of adapted recurrent parent germplasm, i.e., when six-row gene combinations were predominantly left intact. Results from the three breeding cycles support the proposition that a strategy that maintains favorable gene combinations while introgressing relatively small amounts of donor germplasm can lead to incremental yield gains.

Final Comments

- Barley breeding was a good career choice. It is always interesting and challenging and frequently rewarding.
- There have been many changes since I first harvested barley plots with a sickle and we obtained one generation per year. As a result, barley programs are several-fold more efficient and more productive today.
- Learning remains a high priority as we wrestle with how to utilize the new molecular tools and (for some of us) how to obtain varieties resistant to *Fusarium* head blight to save our malting barley crop.

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Hull-less Barley: An Overview

J.H. HELM¹

In the early 1970s, the CIMMYT hull-less barley program and my own program started sharing germplasm and ideas. It was a struggle in the early years, because much of our focus was on high lysine, which brought with it poor agronomics, low yield, and environmentally unstable protein quality. While nothing of commercial value came from this research approach, it did teach me a lot about protein/environment interactions and protein digestibility in the rat and pig.

By the end of the 1970s and early 1980s, most breeders had quit chasing lysine genetics, and I changed my approach to looking at environmental stability and protein and energy digestibility. Our methods of determining these were not very scientific at that time, as we had very little animal data. We pieced together some rough NIRS calibrations for protein, energy, starch, and lysine and began screening large numbers of lines. While these screenings were only very rough, we did notice that we were able to make improvements from breeding cycle to breeding cycle. I found two animal nutritionists who would work with me, Dr. Richard Beames from the University of British Columbia and Dr. B.O. Eggum from the National Institute of Animal Science, Denmark.

While they were often disappointed with the results from the samples I sent to them, I always learned a lot from their results.

It was from these early results that I changed my selection approach to selection for pig digestibility from chemical analysis. Dr. Frank Aherne from the University of Alberta got involved with our first full feed tests coupled with nylon bag tests; it was from these results that we released the hull-less variety Condor in 1988. Condor is still the predominant hull-less variety in some areas of western Canada, though I am convinced that other, newer varieties are better for all characteristics. It was Condor, however, that began the increase of the hull-less barley acreage in western Canada. The primary reason was that feed quality was superior in all environments to the hulled check varieties.

While hull-less barley acreage took off with the release of Condor, we must acknowledge that it was Dr. Brian Rossnagel at the Crop Development Centre, University of Saskatchewan, who paved the way with the release of Scout (1982) and Tupper (1984). Without that push it is doubtful that I would have put Condor forward.

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Since this beginning, the last decade has seen hull-less barley acreage rise from near zero commercial acreage to nearly one million acres. More than 16 varieties are now in production, with the pig industry as the major market. New varieties are agronomically superior, and quality is now stable with the development of Falcon (1992) and CDC Dawn (1995) as the best of the best (Table 1).

The ICARDA/CIMMYT role in this, at least from my point of view, has been the development of a diverse germplasm base that has also introduced new sources of disease resistance, early maturity, and straw strength into the program. In 1999 the predominant hull-less variety grown was Falcon. Falcon is a six-row semidwarf variety selected from one of CIMMYT's F2 populations, about 50 seeds sent to me in 1977. I was intrigued by its short stature and large head size; I played around with it for a long time before I put it into the variety registration system in 1989. The important characteristics of Falcon are its strong straw and lodging resistance under high yielding conditions. It also threshes easily; this characteristic is now the prime quality factor in hull-less barley. Falcon

Table 1. Average feed quality analysis for three hull-less barleys grown at 11 locations in western Canada, 1993, 1994, and 1995.

Characteristics	Falcon	CDC Dawn	Condor
Protein (%)	13.90	12.95	13.85
Protein digestibility (%)	79.62	80.28	78.54
Digestible energy (kcal/kg)	3507	3442	3478
B-glucan	3.8	3.5	4.5
Soluble fiber (%)	4.4	4.0	5.0
Pentosans (%)	4.2	4.0	4.1
Dietary fiber (%)	14.9	13.8	15.1
Insoluble fiber (%)	10.5	9.7	10.1

also has 5% higher protein and energy digestibility in pigs than Condor.

The future

What is the future for hull-less barley? In my opinion, we will continue to make agronomic gains equal to what is happening in the hulled barley breeding area. The ICARDA/CIMMYT program is rapidly broadening the hull-less barley germplasm. Our germplasm base, thanks to the work of Hugo, is now more than 700 entries from many backgrounds. I think the pig industry will remain the primary market; to this end we will be able to increase digestible energy by 200 Kcal (Figure 1) and protein digestibility by 5% (Figure 2).

There is a significant potential in the food industry but these are not progressing as rapidly as many think they should. I think some of the work Hugo is doing in subsistence agriculture is interesting and this is an area where we will not see the food processing industry or large companies put any effort. In my opinion, barley makes good tortillas, pancakes, muffins, soups, rice replacer, cookies, noodles, breads, and of course beer. It has potential as a source of food additives for fiber, tocols, and other fractions.

It has been an interesting crop to work on for the last 32 years when I made my first hull-less barley cross, to now when we see an expanding interest.

Breeding methodology

I would like to complete my presentation with a quick description of how we handle the breeding material in our program.

Crosses are made and F1s grown out in growth rooms or in California. The F2s from our crosses are grown out in a solid-seeded plot of approximately 4000 plants

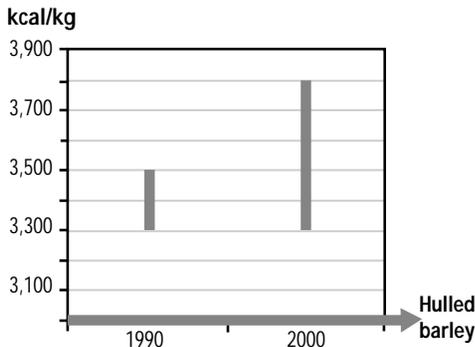


Figure 1. Range of digestible energy in hull-less barley germplasm.

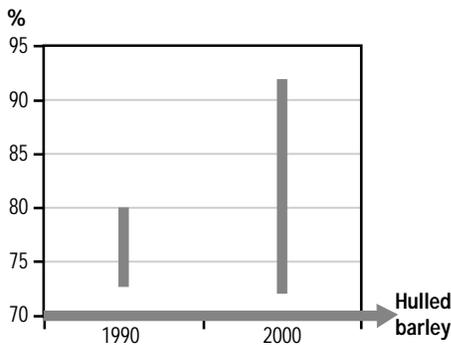


Figure 2. Range of protein digestibility in hull-less barley germplasm.

in 15.25 square meters. The F2 from Mexico is grown in a 3.5-meter row (average 65 seeds). Good populations are harvested in bulk. Seed from the large plots are screened for plump seed (6/64 in slotted screen) then run over a gravity table. The top 10% of plump, heavy seed is advanced to an F3 population grown in Southern California. We select for plant type based on pedigree in California, selecting approximately 500 heads out of a population of 4000 F3 plants. The seeds from these are bulked and 4000 random seeds planted in Alberta in a 15.25 square meter plot as are the F3 bulk from

the Mexican population. This same procedure is used in the F3 to F5. Poor populations are dropped along the way.

These large bulk populations are inoculated with scald from straw each year. The rationale is that diseased plants will produce smaller, lighter seed. By sieving to take out the small seed and using the gravity table to take out the light seed, we move the populations toward better disease resistance and larger kernels and test weights. This selection in the F2, F4, and F5 has shown to be effective for the kernel characteristics, and we have been able to select our new semi-dwarf varieties with kernel weights 30% higher than their parents. We are also seeing an increase in the level of field resistance to leaf diseases.

The F5 populations are selected for plant type by selecting a single head from up to 200 plants from the bulk population. These are grown in head/row plots and inoculated for scald. Rows with poor agronomic type or moderate to heavy disease are discarded prior to harvest. The harvested rows are weighed and scored for seed characteristics and analyzed in the research laboratory for quality. We use NIRS as a method to screen for all quality characteristics. Those rows that meet all agronomic, disease, and quality standards are entered into yield trials. We have two years of preliminary yield testing and three years of advanced yield testing. Then the best lines are entered into a cooperative testing system for two years before receiving registration as a variety and released to seed growers.

Contributions of Breeding and Crop Management to Increasing Barley Yields and Grain Quality in Chile

E. BERATTO M.¹

The first barley trials in Chile were conducted by the National Agriculture Society during the first quarter of the 20th century and later by the Ministry of Agriculture's Department of Genetics and Plant Improvement (1940-1947) and the School of Agriculture (1955-1964) of the Universidad de Chile. The trials focused on sowing date, seed rate, adaptability, and yield of varieties introduced mainly from Europe.

Research efforts in Chile up to 1976 were typically isolated trials conducted by public and private organizations; they were geographically fragmented, discontinuous, had virtually no integrated research teams, and did not persevere in pursuing established objectives. These efforts produced irrelevant results that had little impact on domestic barley production.

The National Agricultural and Livestock Research Institute (Instituto Nacional de Investigaciones Agropecuarias, INIA), through the Carillanca Regional Research Center, officially incorporated barley into its research agenda in 1976. Two years later, in 1978, a research agreement on

"Genetic Improvement and Production of Malting Barleys" was signed between INIA and the United Brewers Company (Compañía Cervecerías Unidas, CCU); the agreement is still operative 23 years later.

Initial Status

Released varieties

In 1978, when the agreement was signed, CCU was sowing the varieties Breun's Wisa, Carina, and Firlsbeck Union. Breun's Wisa was sown until 1979; Carina was withdrawn from the market in 1983, and Firlsbeck Union in 1984. Commercial cropping of the latter two varieties stopped mainly because of their susceptibility to yellow rust of barley, which greatly reduced yields (Caglevic and Herrera, 1984), grain size, test weight, and grain weight in both the northern and central parts of Chile (Caglevic and Herrera, 1982; 1983).

Barley yields

The national average barley yield in 1978 was 1.9 t/ha, but the average yields produced by commercial farmers and seed

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producers under contract to CCU were 1.7 and 2.2 t/ha, respectively.

Diseases

When the agreement was implemented, not much was known about barley diseases. Damage to yield, grain size, and test weight had not been evaluated, and no chemical control methods had been developed.

Grain size

Barley producers under contract to CCU received premium prices because of good grain size, i.e., when at least 80% of the grain was retained on 2.5-mm sieves; this cost the company 5%.

Crop management practices

Crop management practices (sowing date, seeding rate, fertilization, and weed control) used on barley at that time were similar to those recommended for wheat. This was based, with no scientific evidence, on the principle that “everything that was good for wheat was good for barley.”

Advances in Barley Improvement

New varieties

Research activities conducted by INIA under the agreement from 1978 to 1999 led to the release of five new barley varieties with good malting quality. Aramir, property of CEBECO, was introduced from Holland; Leo INIA-CCU originated from advanced lines in the ICARDA / CIMMYT nurseries. The other three, Granifen INIA-CCU, Libra INIA-CCU, and Acuario INIA-CCU, were developed by INIA’s Barley Improvement Project. The significance of these varieties

was demonstrated by their impact on yield (Figures 1, 2, and 3) and grain size, and by how often they were a part of the sowing agreements established by the CCU (Table 1).

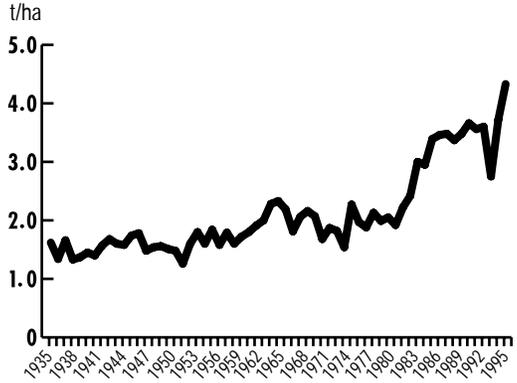


Figure 1. Progress in barley yields, 1935-97.

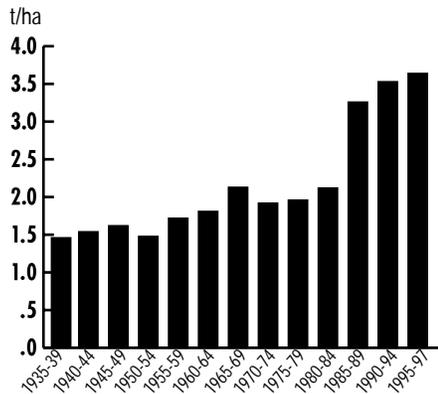


Figure 2. Progress in barley yields by five-year periods, 1935-97.

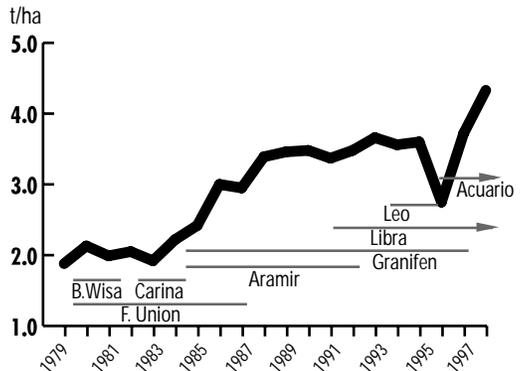


Figure 3. Progress in barley yields, 1978-97.

Table 1. Distribution of barley varieties sown by United Brewers Company (Compañía Cervecerías Unidas, CCU), 1977-99.

Year	Percentage of seed used by CCU†								Area (ha)		Percentage of total area under contract
	BW	FU	CA	AR	GA	LI	LE	AC	Under contract to CCU	Total malting barley	
1977-78	40	60							16,541	54,238	30.5
1978-79	16	84							11,163	50,804	22.0
1979-80	6	94							9,636	41,327	23.3
1980-81		83	17						13,447	39,066	34.4
1981-82		60	40						15,847	48,858	32.4
1982-83		90	10						10,984	32,436	33.9
1983-84		32		49	19				10,137	28,177	36.0
1984-85		7		76	17				12,195	29,784	49.9
1985-86				62	38				10,101	19,312	52.3
1986-87				64	36				7,889	13,914	56.7
1987-88				65	35				12,810	20,459	62.6
1988-89				51	49				14,854	20,901	71.1
1989-90				38	36	26			16,753	22,336	75.0
1990-91					38	62			12,173	26,953	45.2
1991-92					38	61	1		11,085	24,131	45.9
1992-93					35	57	8		11,080	18,946	58.5
1993-94					39	12	49		15,543	23,953	64.9
1994-95					68		32		11,083	21,399	51.8
1995-96						30		70	10,264	19,695	52.1
1996-97						30		70	11,374	18,634	61.0
1997-98						30		70	8,955	22,637	39.6
1998-99						15		85	8,028	22,527	35.6

† BW: Breun's Wisa; FU: Firlsbeck Union; CA: Carina; AR: Aramir; GA: Granifen INIA-CCU; LI: Libra INIA-CCU; LE: Leo INIA-CCU; AC: Acuario INIA-CCU.

Barley varieties sown by the CCU in 1977-99

When the agreement was implemented (1977-78), the varieties Breun's Wisa and Firlsbeck Union covered 40 and 60%, respectively, of the area sown to barley by the CCU. Two years later (1980-81), Bruen's Wisa was discontinued, and 83% of the cultivated area was sown to Firlsbeck Union and 17% to Carina. In 1983-84, Carina was withdrawn from the market, and Firlsbeck Union, Aramir, and Granifen INIA-CCU covered 32, 49, and 19%, respectively, of the barley area. In 1985-86, the area sown to barley was distributed as follows: Aramir, 62%,

Granifen, 38%, and Firlsbeck Union was discontinued. In 1989-90, 38% was sown to Aramir, 36% to Granifen, and 26% to Libra INIA-CCU. Aramir was withdrawn from the market in 1990-91 and was replaced by Libra, which occupied 62% of the barley area; the remaining 38% was sown to Granifen. In 1991-92, Granifen and Libra still covered 38 and 61%, respectively, and Leo was sown on 1%. In 1995-99, Granifen and Leo were no longer sown, and 70-85% was covered by Acuario INIA-CCU; the remaining 15-30% was sown to Libra (Table 1).

The length of time varieties introduced or developed by INIA were sown is as follows: Aramir, 7 years (1983-89); Granifen INIA-CCU, 12 years (1983-94); Leo INIA-CCU, 4 years (1991-94); Libra INIA-CCU, 10 years. Acuario INIA-CCU began to be sown 4 years ago; by 1999, 100% of the barley area was sown to it.

Progress in barley yields

National average barley yields in Chile increased from 1.5 t/ha (in 1935-39) to 3.6 t/ha (in 1995-97) within a 63-year period. This is equal to a yield gain of 149.3%, or an annual increase of 34.6 kg/ha (Table 2). Upon comparing yields during the first period (characterized by an almost complete lack of systematic barley research) (from 1935-39 to 1970-74), one comes to the conclusion that in 40 years yields increased only 31.8%, or 11.5 kg/ha annually. In contrast, between the second (1975-79) (when barley research under the CCU agreement started) and last (1995-97) periods, yield rose by 85.7%, or 73.1 kg/ha per year, over a 23-year period (Table 2). During that same period, average commercial yields obtained by the CCU increased from 1.7 t/ha in 1978 to 4.3 t/ha in 1997, a yield gain of 160.8%. Average yields of CCU seed producers rose from 2.2 t/ha in 1978 to 5.7 t/ha in 1997, an increase of 132.4%.

Table 2. Progress in national average barley yields comparing different five-year periods, 1935-97.

Period	Yield (t/ha)				Yield increase (%)	Annual increase (kg/ha)
	1935-1939	1970-1974	1975-1979	1995-1997		
Total period (1935-1997)	1.5	x	x	3.6	149.3	34.6
First period (1935-1974)	1.5	1.9	x	x	31.8	11.5
Second period (1975-1997)	x	x	2.0	3.6	85.7	73.1

The advance in annual average barley yields from 1935 to 1997 is shown in Figure 1.

Gains in barley area and production

Over a period of 63 years, barley area and production in Chile decreased by 67.8% and 20.8%, respectively (Table 3). The reasons for these reductions are as follows: about 80% of the total barley area in Chile is sown to malting barley under contract to domestic malting companies and breweries. The former have significantly reduced the area

Table 3. Progress in national average barley yields by five-year periods, 1935-97.

Five-year period	Area (ha)	Production (000 t/ha)	Yield (t/ha)
1935 - 1939	74,320	1,097	1.5
1940 - 1944	48,910	752	1.5
1945 - 1949	49,024	798	1.6
1950 - 1954	53,578	797	1.5
1955 - 1959	53,056	914	1.7
1960 - 1964	41,329	744	1.8
1965 - 1969	50,540	1,081	2.1
1970 - 1974	65,904	1,260	1.9
1975 - 1979	58,360	1,149	2.0
1980 - 1984	41,958	882	2.1
1985 - 1989	22,814	749	3.3
1990 - 1994	27,149	831	3.5
1995 - 1997	23,909	869	3.6

under contract due to the drastic reduction in the amount of Chilean malt exported to countries such as Bolivia, Brazil, Venezuela, and Peru. This reduction in exports is the result of strong competition from the European Common Market, which sells malt to those countries at a lower price. Also, local brewers such as the CCU have reduced the area they sow to barley as a result of the signing and implementation of the Free Trade Agreement between Chile and Canada, which allows the tariff-free importation of Canadian barley grain and malt into Chile. Thus it is actually cheaper to import barley grain and malt from Canada than to produce it in Chile.

Improving grain size

The basis (in place since 1978) for paying a premium for grain size was changed for the first time in 1984, from 80% of the grain remaining on a 2.5-mm sieve to 85%, as a result of genetic improvement research. In 1996, it was modified for the second time to 90%, bringing Chilean requirements to the same level as those stipulated in the European Brewery Convention.

Improving beer production efficiency

In 1978, 18.5 kg of barley were needed to produce 100 L of beer; today 16-17 kg are necessary to produce 100 L of beer (Devilat, 1988).

Advances in Crop Management

Gains in barley yields both in Chile and at the global level have been the result of improved barley varieties and the

development of better agronomic practices for managing the barley crop.

Disease management

Research on disease control measures began in 1978, when disease identification surveys in Chile's barley-producing regions were conducted by Gilchrist (1979), Caglevic and Herrera (1984), and Andrade (1986). Later studies evaluated the impact of diseases on barley yields and grain size, and identified the most economically important diseases nationally (scald, net blotch, yellow and leaf rusts, and BYDV). They also determined the most effective chemical treatments (fungicides) for controlling scald (*Rhynchosporium secalis*) in particular, since it reduces yield by more than 40% in early sown barley in years with a humid spring (Andrade, 1989). Yellow rust (*Puccinia striiformis* f.sp. *hordei*) reduced yield by 48-56% in 1980-82, and caused grain size, test weight, and kernel weight to drop dramatically in the northern and central parts of Chile (Caglevic and Herrera, 1984). At the same time, the breeding program identified genetic resistance sources, especially to scald. Most of these sources are from the ICARDA/CIMMYT nurseries (Beratto, 1983; CIMMYT, 1983).

Fertilization

The importance of applying nitrogen and phosphorus for raising barley yields and improving grain quality, especially in volcanic soils, whether Andisols (volcanic soils) or Ultisols (red clay soils), in southern Chile has been amply demonstrated in studies conducted by Peyrelongue (1983a, b; 1990; 1992) and Peyrelongue et al. (1984) (Figure 4).

Fertilization and weed and disease control

In a study conducted at the Carillanca Regional Research Center, Thomas (1997) concluded that fertilizer application and disease control were essential for producing high yields and improving barley grain quality. He also found that of these techniques, combined nitrogen/ phosphorus fertilization has the greatest impact on yield (Figure 4), grain weight (Figure 5), number of grains per m² (Figure 6), test weight (Figure 7), grain size >2.8 mm (Figure 8), and grain size >2.8 + 2.5 mm (Figure 9).

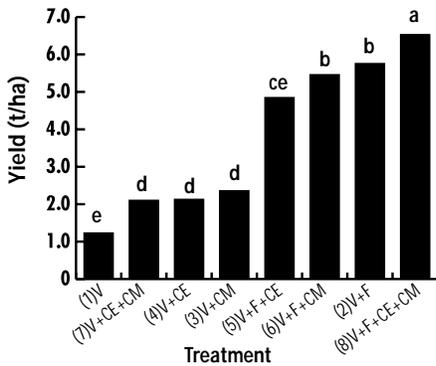


Figure 4. Effect of eight treatments on grain yield of Acuario INIA/CCU.

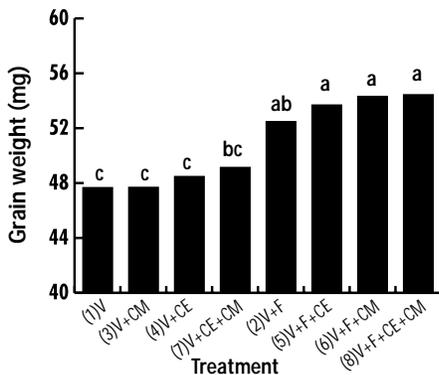


Figure 5. Effect of eight treatments on grain weight of Acuario INIA/CCU.

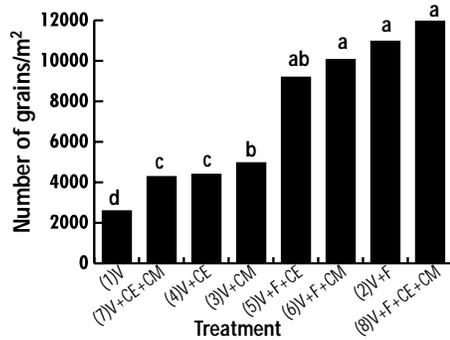


Figure 6. Effect of eight treatments on the number of grain per meter² of Acuario INIA/CCU.

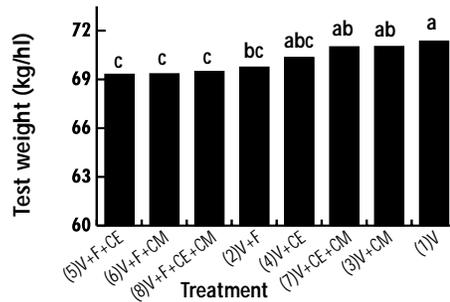


Figure 7. Effect of eight treatments on test weight of Acuario INIA/CCU.

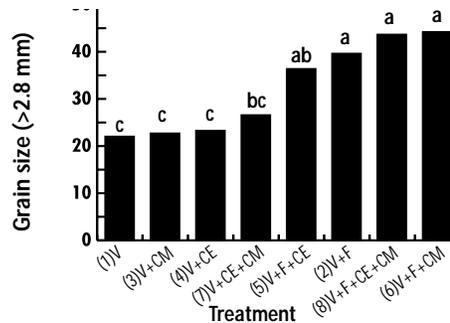


Figure 8. Effect of eight treatments on grain size of Acuario INIA/CCU.

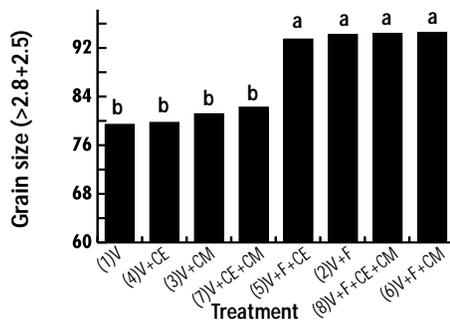


Figure 9. Effect of eight treatments on grain size of Acuario INIA/CCU.

Economic Quantification of Impacts Achieved under the Agreement

- The amount of barley grain needed for producing 100 L of beer diminished from 18.5 kg in 1984 to 17.0 kg in 1988. This has been estimated to generate a cost savings of US\$ 420,000 for the CCU (Devilat, 1988). Today only 16.0 kg are needed to produce 100 L of beer, but this has not yet been economically quantified.
- Changes in the premium paid for bigger grain size in 1978 and 1988 have translated into a higher yearly income for the CCU of US\$ 105,000 (Devilat, 1988). In 1996, the basis for paying a premium price was changed to 90% of the grain retained on a 2.5-mm sieve, but this has not yet been economically quantified.
- Campos, Ortiz, and Beratto (1989) estimated that the internal rate of return (IRR) for the 1978-87 period of the INIA/CCU Agreement was 48-50%. In a recent and as yet unpublished study, Campos and Beratto (2000) found that the IRR for the 1978-99 period of the INIA/CCU Agreement was 52%, which produced a social benefit valued at 5,350 million Chilean pesos (US\$1 = 516-520 Chilean pesos). The distribution of these benefits was 65% for producers and 53% for consumers.

Future Prospects

About 80% of Chile's barley area is currently dedicated to the production of grain for malt and beer, 15% to feed grain, and 5% to seed. In the last four years, the area sown to barley for silage production has increased, especially in the cattle-raising region in southern Chile (Goic and Ponce, 1999); this has

met with good farmer acceptance. The commercial release of facultative hull-less varieties such as *Alteza-INIA* (Beratto and Rivas, 1999), with high yield potential, resistance to economically important diseases, good agronomic traits, and very good grain and nutritional quality has paved the way for barley production in southern Chile, where it could displace maize, given that maize cropping in that region is very risky due to climatic conditions. Based on these two new alternatives, we predict that the area sown to barley for feeding livestock (both dairy and meat) will continue to rise as it has in the past two years (1998 and 1999).

The development of facultative hull-less and covered barley varieties means that farmers now have very promising genetic materials that could be sown commercially in regions with high rainfall in autumn and winter, and severe drought stress in spring and summer. Sowing spring habit barleys is not recommended in these regions (Beratto, 1990). This type of barley, besides having high yield potential, gives farmers a practical advantage: it has a longer sowing period (Salinas, 1996). As a result, barley cultivation can extend to regions, or subregions, where until recently it could not be sown due to the prevailing climatic conditions.

Future prospects for improving yield and malting and nutritional quality of both spring and facultative barley continue to be extremely good. There is still a considerable gap between the national average yield and the average yields of innovative farmers, and between the average yield achieved in research centers with the leading commercial variety and maximum yield obtained with the best advanced line (Beratto, 1999).

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Importance of Identifying Stripe Rust Resistance in Barley

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Stripe rust (*Puccinia striiformis* f. sp. *hordei*) of barley is a new disease of barley in the American hemisphere. It was recognized as a problem in Mexico and the United States only in the last 10 years (Brown, 1992; Brown et al., 1993a; Calhoun et al., 1988; Line and Chen, 1999). In South America, race 24 of the fungus was recorded near Bogota, Colombia, in 1975. Within five years, barley stripe rust was found throughout western South America causing losses of 30-70% (Dubin and Stubbs, 1984; 1986).

The fungus in recent years has spread north to Mexico (Calhoun et al., 1988), and in 1991, Marshall and Sutton (1995) reported it in Uvalde, Texas. It was confirmed in Arizona, 1993; California, 1994; Colorado, 1992; Idaho, 1993; Montana, 1993; New Mexico, 1992; Oklahoma, 1992; Oregon, 1995; Washington, 1995; and Utah, 1994 (Brown et al., 1996; Brown et al., 1993a; Chen et al., 1995; Line and Chen, 1996; 1999). Barley stripe rust is also present in western Canada. Since 1995 it has become established and on occasion causes considerable damage and concern in the northwest states of the USA. The

stripe rust fungus could pose a major threat to the industry in those areas. While there are no commercial resistant malting varieties readily available at this time, sources of resistance are becoming available.

In 1990, Dr. Darrell Wesenberg, Director of the USDA / ARS Small Grain Germplasm Collection (NSGC) Research Laboratory at Aberdeen, ID, contacted the Colorado State University barley disease research team to initiate stripe rust field trials with cooperators in South America. The authors and their Bolivian associates were familiar with the fungus and had initiated some of the first studies of the disease in the late 1970s in Bolivia (Velasco and Brown, 1982; Velasco et al., 1993).

Field work was established in Cochabamba, Bolivia, South America, in 1991 (Brown, 1992). The Cochabamba area is a high Andean valley approximately 7,500 ft above sea level. This valley shows a high endemic occurrence of barley stripe rust race 24 (BSR-24) and heavy infections are a yearly occurrence. Field germplasm and

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associated studies were initiated in the 1991 growing season (January-May) and continued through 1996. USDA/ARS NSGC staff prepared germplasm for planting. CSU and Bolivian staff carried out the field trials.

Germplasm screening trials

Trials were composed of all entries from the National Small Grain Collection and selections developed by cooperators from:

USDA/ARS (Aberdeen, ID)	University of California-Davis
North Dakota State University	Montana State University
Oregon State University	Utah State University
Washington State University	Adolf Coors
Busch Agricultural Resources	Western Plant Breeders

Selections showing some level of resistance were field tested a second year in Bolivia and also tested in Colorado, Ecuador, Germany, and eventually Mexico at different times over the period from 1993 to 2000. In 1995, Ecuador was deleted in favor of adding the Toluca Valley of Central Mexico. Field testing is now carried out at Davis, California, by University of California staff, at the Mexico site by the authors in cooperation with Dr. Hugo Vivar, and in Idaho by USDA/ARS staff.

During the period from 1991-1999, over 40,000 selections of barley were field evaluated for stripe rust resistance. Numerous sources of resistance were identified and are being incorporated into commercial lines by various barley breeding programs throughout the western U.S. All results are available on the USDA/ARS GRIN data base system. In 1999 a resistant variety, Bancroft (P.I. 605474), was developed and released cooperatively by the USDA/ARS,

Colorado State University, Idaho State University, and Oregon State University.

Race variation studies

Differential nurseries were developed in cooperation with Dr. Mareike Johnston at Montana State University. The differential nurseries were planted in Bolivia, Colorado, Ecuador, and Germany (Brown et al., 1996; Hill et al., 1995). Considerable variation was observed both between field nurseries and also under controlled conditions in greenhouse trials, where comparisons were made by Dr. Johnston (Tables 1 and 2).

Table 1. Variation of BSR-24 susceptibility in Bolivia, Ecuador, and Colorado, 1994 (field test).†

Differentials	Bolivia	Ecuador	Colorado
Emir	S	MS	MS
Mazurca	MS	MS	S
Zephyr	S	S	S
I 5	MS	S	S
BBA 2890	MS	MS	MS
Trumpf	MS	0	S
Hor 4020	R	MS	MS
Bigo	MS	R	MS
Abed Binder 12	S	S	MS
Cambrinus	S	S	S
Luttichauer Landgerste	MS	S	MS
Heils Franken	MS	MR	S
S 3170 (Hor 3209)	S	MR	S
S 3192 (Hor 2926)	MS	R	S
Grannelose Zweizeilige	R	0	S
Weisse Von Fong Tien	S	S	S
Varunda	MS	R	S
Stauffers Obersulzer	S	MS	S
Hor 1428	MS	S	MS
Morex	S	S	S
Steptoe	S	S	S
Larker	S	S	S
Abyssinian 14	MS	0	MS
Topper	S	MS	S
BBA 809	MR	R	MS
Hokkaido Chevalier	MS	R	S
Hipoly	MS	S	S

† R = resistant, MR = moderately resistant, MS = moderately susceptible, S = susceptible.

Table 2. Selected stripe rust differential reactions in greenhouse inoculations.†

Differentials	GER	GER	WPD		Utah	Colo
	24	23	93	PF94		
Mazurka	R	S	R	R		R
HOR 4020	R		R,S	I	R	S
Cambrinus	S	R	S	S	R	R
Heils Franken	S	R	R	I	R	I
HOR 1428	R	S	R	R	R	R

† R = resistant, MR = moderately resistant,
MS = moderately susceptible, S = susceptible.

Table 3. Stripe rust barley differential reactions in Montana, Germany, and Colorado, 1994 (greenhouse test).†

Differentials	Montana	Germany	Germany	Colorado
	R-24	R-24	R-23	R-24 (?)
Emir	R	R-S	R	R
Mazurca	R	R	S	R
Zephyr	S	S	I	S
I 5	R	R	R	R
BBA 2890	R	R	-	R
Trumpf	R	R	R	R
HOR 4020	R,S	R	-	S
Bigo	R	R	R	R
Abed Binder 12	S	MS	-	S
Cambrinus	S	S	R	R
Luttichauer	S	S	-	S
Landgers				
Heils Franken	R	S	R	S
S 3170 (Hor 3209)	R	R	R	R
S 3192 (Hor 2926)	R	R	R	R
Grannenlose	R	R	-	R
Zweizeil				
Weisse	S	S	S	S
Von Fong Tie				
Varunda	R	R	R	R
Stauffers	R	R	-	R
Obersulzer				
Hor 1428	R	R	S	R
Morex	S	S	S	S
Step toe	S	MS	-	S
Larker	S	I	-	S
Abyssinian 14	R	-	-	MS
Topper	S	S	-	S
BBA 809	R	-	-	R
Hokkaido	R	-	-	S
Chevalier				
Hiproly	R	R	-	R

† R = resistant, MS = moderately susceptible,
I = intermediate, S = susceptible.

Dr. Johnston also tested isolates from Colorado, Montana, and Utah against the differentials under controlled conditions. When these were compared to known races 24 and 23 in tests carried out by Dr. Walters in Germany, considerable variation was again seen (Tables 3 and 4).

Table 4. Effect of fungicide seed treatment on stripe rust race 24, at different planting times, 1994.†

Treatment	January†	April
CBG‡3.00	45 a	23 a
CBG 2.00	45 a	22 a
CBG 1.50	43 a	22 a
CBG 1.00	43 a	23 a
CBG 0.75	43 a	23 a
Captan/Baytan	40 b	19 b
Thiram/Raxil	39 b	14 c
Vitavax extra	39 b	13 c
Vitavax 200	34 c	13 c
Untreated	34 c	13 c

† Days after emergence when first pustules observed.
‡ Captan/Baytan/Gaucha.

Summary of germplasm screening

Germplasm evaluation and screening in Bolivia and elsewhere continue to identify a wide range of barley stripe rust resistance sources. Of note is that our work and that of our cooperators show considerable variation in what has been called "race 24."

Variation in race 24 is also supported by observations reported in 1994 by Marshall and Sutton (1995) and Line (Chen et al., 1995; Line and Chen, 1996;

1999). Thus it is clear that barley stripe rust in North America is a very heterogenous population.

Fungicide Trials for Control of Barley Stripe Rust Race 24

Early results in 1979² in Bolivia indicating that seed treatments might be effective led to reevaluating this approach (Velasco et al., 1995). Seed treatment field trials were hand planted twice in Bolivia (January and April) in 1998 (Table 4). Seed was commercially treated by Gustafson Corporation. The first planting in January was at the normal time for the area, a period prior to the development of high stripe rust occurrence. The second planting was much later, in April, when the fungus was very active, and under conditions of extremely high stripe rust inoculum pressure.

In all cases Baytan (triadimenol) gave significantly enhanced stripe rust protection after emergence (Table 5).

Combination seed treatment and foliar fungicide trials

Fungicide trials were initiated in 1978, when the disease was first found in Bolivia. Unfortunately at least two fungicide applications of Bayleton are required to keep the disease below a potentially damaging level (Velasco and Brown, 1982; Velasco et al., 1980). It is unlikely that under U.S. conditions two field applications of any fungicide would be economically feasible for barley stripe rust control.

Integrated trials using seed treatments and foliar spray combinations were carried out in Bolivia from January through April, 1994 and 1995. These trials demonstrated that foliar applications of Tilt, Folicur, or Bayleton applied at first sign of stripe rust were effective against stripe rust (Brown et al., 1996; Velasco et al., 1993). Other trials have demonstrated effective control with additional fungicides (Calhoun et al., 1988; Line 1998, 1999; Navarro and Zamora, 1990).

One trial of interest in Bolivia was planted with a local barley landrace and had no seed treatment other than noted (Table 5). A companion trial was planted with the variety Russell. The seed for this trial had been supplied by the ARS/USDA Small Grains Laboratory in Aberdeen, ID, and unknown to the authors had been treated with Vitavax. All plots were hand-planted and sprays applied with a manual backpack sprayer at 33 psi at label rates. No adjuvants were used.

Table 5. Barley stripe rust race 24 fungicide trial, cv. Criolla, 1994.

Treat- ment	No. of applica- tions	Rate (kg/ha)	Disease severity (%) at milk stage	Yield (kg/ha)
B/T	2	†	0.55 a	3,537.66 a
B/T	1	†	7.35 a	3,177.50 ab
Baytan		‡	12.72 a	3,140.00 ab
Tilt	2	.6	13.22 a	2,532.00 ab
Tilt	1	.6	66.77 b	2,499.16 b
Control	-	-	91.05 c	1,094.16 c

† Baytan/Tilt at 0.6kg/ha and 200g/100kg seed.

‡ As seed treatment 200g/100kg seed.

² Velasco and Brown, unpublished field observations, Cochabamba, Bolivia.

All combinations of Baytan and foliar fungicides enhanced disease suppression and resultant yield. Of considerable interest, the second trial (Table 6) with a combination of Vitavax and Baytan gave better protection than two foliar sprays without seed treatment. When compared to the efficacy of Baytan alone in the previous trial, it indicated a possible synergistic effect between Vitavax and Baytan.

Table 6. Barley stripe rust race 24 fungicide trial, cv. Russell, 1994.

Treat- ment	No. of applica- tions	Rate (kg/ha)	Disease severity (%) at milk stage	Yield (kg/ha)
Baytan		†	0.82a	3,352.66a
Tilt	2	0.600	7.90ab	3,075.83ab
Bayleton	2	1.000	8.20ab	2,715.83 bc
Folicur	2	0.750	25.45 bc	2,553.33 bcd
Manzate	2	2.000	27.47 c	2,240.83 cd
Control	-		73.77 d	2,002.50 d

† Seed treatment 200 g/100 kg seed. All seed pretreated with Vitavax.

Discussion and Conclusions

Considerable progress has been made in the identification of sources of resistance to barley stripe rust race 24 (Brown et al., 1996; Brown et al., 1993b; Hill et al., 1995; Velasco et al., 1991). The observed variability and the conclusion reached by ourselves and others that the race 24 designation is not just one race, but potentially many, brings in to question the value of searching for gene specific “vertical resistance.”

The importance of stripe rust resistance depends on all or any of several characteristics:

- location and environment
- other pest and diseases present
- total context of the cropping system
- economics

Each of the above impacts the potential usefulness of developing stripe rust resistance in barley. Barley stripe rust is favored by humid and cooler climates. These do not necessarily prevail in many of the locations where malting and feed barleys are produced.

Other pests and diseases impacting the crop, such as Russian wheat aphid and scab, may be more important. Putting a high priority on stripe rust resistance may not be appropriate or the best use of limited resources.

Looking at the whole cropping system is also important. In some areas such as Colorado, barley stripe rust is only a problem if barley is planted late and even then only in some years. Use of early planting provides a period when the fungus is not present and allows major development of the crop in the absence of inoculum.

The economics of fungicide use is also important. Effective fungicides are available for stripe rust, but in less affluent societies, are beyond the economic resources of the growers. Even in more affluent agriculture, the cost benefit ratio of the new generation strobilin-based fungicides may not justify fungicide use.

Additionally, other pest or disease problems may not be as amenable to pesticide treatment. Therefore, development and deployment of

resistance to those problems are more important in the total management context.

Use of a fungicide to manage stripe rust will not be necessary on a yearly basis due to the sporadic development of the disease in many areas. In those years when the fungus does develop early enough to become a threat, timely fungicide application may be economic and outweigh the expense and priority of developing resistance to stripe rust.

Associated knowledge gained from barley screening trials over 10 years, from field observations of the epidemiology and work with both seed and foliar fungicide trials, suggests a long-range integrated approach is best. Such an approach would emphasize the use of trace to moderately susceptible barley lines and other management techniques. Even in using such an integrated approach it is still critical to manage host plant resistance (Brown 1976; Brown 1993) by the use of:

- gene rotation, where different sources of resistance are moved in and out of the host plant population,
- gene diversity, where a range of resistance genes are present in different cultivars within an area at any one time,
- gene rotation, where continued and careful monitoring of fields are routinely carried out and initial outbreaks are detected early and spot treated with appropriate fungicides early, before the disease can spread.

Therefore a stripe rust program is recommended that uses the following integrated management tactics:

- Use a slow-rusting (TMS-5MS) line.
- Treat seed with an appropriate fungicide.
- Plant early.
- Scout and apply appropriate fungicide if 5% BSR prior to boot.

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Impact of ICARDA/CIMMYT Barley Germplasm on Barley Breeding in Ecuador

O. CHICAIZA¹

Since 1984, the barley breeding program in Ecuador started a very close collaboration with the ICARDA/CIMMYT Barley Program to develop varieties suitable for the Ecuadorian highlands. In Ecuador, barley is cultivated under rainfed conditions on mountain slopes at altitudes of 2400 to 3600 m. The highlands of Ecuador feature small subsistence farms where mechanization is limited because of the terrain, and most threshing is done by animals.

Statistical data show that the area planted to barley dropped from 100,231 ha in 1969 to 26,878 ha in 1978, due mainly to the presence of the pathogen *Puccinia striiformis* f.sp. *hordei*, which causes yellow rust. The new disease wiped out all the barley varieties in Ecuador. By the late 1970s, the barley program had released three resistant varieties (Dorada, Duchicela, and Teran) selected from materials introduced from the world collection. Yet the rapid adoption of these varieties by farmers was not enough to return barley to its previous area. Even though the varieties Dorada and Teran are still resistant to yellow rust, they have been eliminated from the barley growing area because of their susceptibility to leaf rust of barley, *P. hordei*.

Development of barley cultivars with multiple disease resistance

The main goal of Ecuador's barley breeding program has been to develop new barley cultivars with multiple disease resistance. Diseases or disease complexes determine the type of germplasm that needs to be developed for the Ecuadorian highlands. Since 1984, a breeding methodology for the incorporation of genetic resistance to major diseases was adopted by the ICARDA/CIMMYT Barley Breeding Program, because most available resistance sources, most of them in poor agronomic backgrounds, were useful only for a single disease.

The incorporation of two or more disease resistance genes into well adapted varieties or advanced lines, followed by rounds of crossing and selection, allowed the combination of resistance genes for yellow rust, leaf rust, scald (*Rhynchosporium secalis*), and BYD.

Because most sources of resistance were available at the ICARDA/CIMMYT Program, initial crosses, at least at the very beginning of the joint program, were done in Mexico. As the gene(s) was incorporated into local germplasm,

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crosses were also done by the national breeding program. In both cases, segregating populations were evaluated in both Mexico and Ecuador to speed up the selection process.

New barley varieties released in Ecuador

INIAP-SHYRI 89 was the first variety released in Ecuador in 1989. This variety originated from the cross LIGNEE 640/KOBER//TERAN 78; the original cross was made in Mexico and introduced to the national program as an F₅ line in 1985. The new variety had high levels of resistance to yellow rust, scald, leaf rust, net blotch, and BYD, but was susceptible to loose smut. It has been the most widely adopted barley cultivar in Ecuador. In 1992, the national program released another two varieties originated in the ICARDA/CIMMYT Program: INIAP-CALICUCHIMA 92 and INIAP-ATAHUALPA 92. Together these three varieties cover almost 90% of all the

barley area, which increased to 80,000 ha by 1998.

The most recent release is the variety INIAP-SHYRI 2000, generated for the national program using as parents the well adapted variety INIAP-SHYRI 89 and GRIT, introduced by the ICARDA/CIMMYT Program in 1990. The new variety will replace INIAP-SHYRI 89. The origin and characteristics of barley varieties released in Ecuador are presented in Table 1.

New barley germplasm available in the national program

The origin and yield performance of the best lines in Santa Catalina in 1999 are presented in Table 2. Yields of lines derived from crosses made by the national program are very similar to those of lines derived from crosses made by the ICARDA/CIMMYT Program. The best five lines yielded 42-75% more than INIAP-SHYRI 89. This yield increase

Table 1. Origin and characteristics of barley varieties released in Ecuador.

Variety	Year of release	Days to harvest	Plant height (cm)	Yellow rust	Leaf rust	Yield (kg/ha)
DORADA (selection from C.I. 9650)	1973	170	110	0	80S	3636
DUCHICELA	1978	180	120	30S	5MS	3700
TERAN 78 (selection from Abyssinian 669)	1978	145	105	0	60MS	2715
INIAP-SHYRI 89 LIGNEE640/KOBER//TERAN 78 CMB83A-2561-A-2M-1Y-1LAG-1E-OGH	1989	154	105	0	5MS	4937
INIAP-CALICUCHIMA 92 LB IRAN/UNA8271//GLORIA"S"/COME"S" CMB84A-1127-D-2B-1Y-6M-0Y	1992	160	110	15MS	60S	3958
INIAP-ATAHUALPA 92 SUTTER/GLORIA"S"/COME"S"/3/PI6384/ CAPUCHONA CM86-767-C-2Y-168GH-2M-2Y	1992	155	100	5MS	0	3542
INIAP-SHYRI 2000 SHYRI/GRIT E-II-93-8891-2E-1E-4E	2000	160	110	0	TR	8056

may be due to: 1) incorporation of yellow rust, leaf rust, and scald resistance genes into a single genotype, and 2) selection for high yield *per se*. Of these new lines, INIAP-SHYRI 2000 was released as a variety in 1999; the line CARDO "S" was released in the year 2000.

Performance of barley varieties in Saraguro, Loja, Ecuador

Until 1995, the average yield obtained by small poor farmers in Saraguro, Loja, was 700 kg/ha. This low yield was due to the susceptibility of the local variety Clipper to yellow rust, scald, and leaf rust; and the lack of new, improved varieties. In 1995, the breeding program decided to

introduce the variety INIAP-SHYRI 89. The high yield potential shown by this variety gave farmers enough confidence to start applying inputs such as fertilizers and herbicides in the next cycles. The results of four years of work are summarized in Table 3. The rapid increase in the number of families participating and the number of hectares planted to the new varieties is a clear demonstration that small-scale farmers have adopted new varieties released by the national program. Average yields now range from 1.9 to 3.5 t/ha, with some farmers obtaining nearly 5.0 t/ha.

Conclusions

- Barley germplasm developed by the ICARDA/CIMMYT Program has allowed the release in Ecuador of new varieties with multiple disease resistance and high yield potential.
- New barley germplasm that will allow continued progress is available in the national program.
- Seed of the new high yielding barley varieties has to be available for small-scale farmers to give them the opportunity of benefiting from the new varieties.
- Better varieties have helped small-scale farmers to develop enough confidence to apply inputs such as fertilizers and herbicides.

Table 2. Origin and yield performance of the best barley advanced lines in Santa Catalina, 1999.

Advanced line	Yield (kg/ha)	% yield increase
INIAP-SHYRI 89 (check)	4954	
ROLAND/EH11//ESC-II-72-83-3E-7E-5E-1E/3/SEN"S"/4/ALELI CMB90A-871-C-1M-1Y-1M-0Y-0E	8704	75
INIAP-SHYRI 2000 SHYRI89/GRIT E-II-93-8891-2E-1E-4E-0E-0E-0E-0E-0E	8056	62
GAL/PI6384//CN48/CI8985/3/ GLORIA"S"/COPAL"S" E-II-89-8889-1E-4E-1E-3E-0E	7569	52
CARDO "S" CMB85A-1300-E-15B-5E-0E	7153	44
GLORIA"S"/COPAL"S"//ABN/3/SHYRI CMB87-E-2Y-3B-2Y-3M-1Y-0M-0E	7037	42

Table 3. Performance of barley varieties in Saraguro, Loja, Ecuador.

Varieties	Participating families (no.)				Hectares (no.)				Mean yield (t/ha)			
	1996	1997	1998	1999	1996	1997	1998	1999	1996	1997	1998	1999
SHYRI 89	13	240	334	600	8	80	141	190	3.16	2.05	1.94	2.1
SHYRI 2000				16				6				3.5

Malting Barley for the New Millennium

L. WRIGHT¹

A brief look at the history of malting barley

What will malting barley look like in the next thousand years? What will the malting quality be? To successfully answer these questions we need to look at what has happened in the last 1000 years and perhaps from the beginning of recorded time. Around 6000 years ago, the Sumarians wrote the first references about barley and beer. During the next 5000 years the Sumarian beer recipes were refined by the Babylonians, and then by the Egyptians, by the Greeks and then the Romans.

With the spread of the Roman Empire, beer making spread throughout Europe and especially to the northern part of the Empire to the Gauls, the Teutons and into Scandinavia. By the end of the first millennium AD the art and science of malting barley and beer making were firmly established in the monasteries; each monastery had its own special sources of barleys used for malting and its special way of brewing beer. After the Reformation, brewing shifted from the monasteries to small family breweries in the towns and cities.

By the 16th century certain European regions, mainly the French and Danish areas, were prized as having better malting barley than others. Why it was better was not specifically recorded, but a statement from a 18th century brewer summed it up best: "You can't make a good beer out of poor malt". At that time plump barley, with low protein and bright hull color, was a very rough "rule of thumb" for malt quality.

The Industrial Revolution of the 19th century also revolutionized brewing science. Scientific instruments were invented to help measure the various stages of beer making. Instruments like hydrometers, attemperators, and improvements in thermometers and refrigeration made it possible to make better, more consistent beer, and in larger volumes.

Another historical event took place in 1842 in Plzen, in what is now the Czech Republic: the creation of a clear, golden-colored lager beer. Until that time lager beers were dark colored and cloudy. This clear, golden-colored lager beer became a much-sought-after standard in the making of lager beer, the most popular style of beer in the world. This beer was

¹ Busch Agricultural Resources, Inc. The opinions outlined in this talk are the author's and do not necessarily reflect those of Anheuser-Busch or Busch Agricultural Resource.

made from locally grown, low-protein barley, malted using a new British malting system that applied indirect heat and used very soft water having a very low soluble minerals content.

In North America, beer making developed in the 18th century and flourished during the 19th century. Malting barley varieties developed in the United States were higher in protein for several reasons. First, the original barley areas in North America were better suited for growing six-rowed malting barley than two-rowed barley. Second, six-rowed barleys were inherently higher in protein than two-rowed malt barley. And third, the use of supplemental starch additives in the mashing process, called adjunct, required a higher enzyme level and thus a higher protein level in the malt. All of these events, plus many more, gave us the beer and the malting barleys we have today.

Trends in current and future malting varieties

What will the trends in malting barley quality be in the 21st century? Since malting barley and the brewing industry have changed so rapidly in the past 200 years, it is impossible to accurately predict too far in the future. Also brewing techniques in the future may change some of the parameters for barley quality we have today. Yet, based on what has happened in the past 200 years, certain predictions can be made on where malting barley *could* be in the next 100 years. Much of the information used in this talk is from the American Malting Barley Association (AMBA), which recommends malting barleys for the United States on behalf of its member maltsters and breweries, Anheuser-Busch among them.

In the early 20th century, many local malting varieties evolved into regionally adapted malting varieties. In the latter part of the same century those regional malting varieties moved globally. This was driven for the most part by malting companies buying suitable malting barley for their brewing customers, who in turn had gone from being local breweries to regional breweries. These regional breweries needed larger amounts of high quality malt as they increased their size to meet regional demands. They knew which malting varieties gave them good brewing results, so they favored these varieties over several lesser known malting varieties. Thus, locally adapted varieties gave way to regionally grown varieties.

These regional varieties are now giving way to even fewer malting varieties grown in wider and more diverse regions. As malting and brewing companies source malting barley from wider and more diverse malting growing areas, malting barley varieties in the future will need to be widely adapted in terms of yield, disease resistance, and malting quality. If a malting variety is not widely adapted, it may not make it on the list of malting varieties that breweries give to their malt suppliers. Therefore, future malting varieties will be tested in more than one growing region and will have wide adaptation. If there is a slogan for the malting barley breeder in the future, it is: "Develop malting barley varieties locally, but test globally."

Malting barley must keep pace as an economically viable crop for farmers to grow. The return per acre that a crop generates will remain the factor that determines which crop the farmer will

grow in any given year. Since commodity prices have remained fairly constant, the increase in the value of the crop must come from increased grain yield. Increased grain yield comes from improved cultural practices and newer, higher yielding varieties.

In the US, new malting varieties are accepted, on average, every 10 years. This rate of acceptance has not kept pace with the introduction of varieties of competing crops. The lag in the introduction of new varieties is putting increasing pressure on the brewing industry to accept newer varieties at a faster rate. In the future, economically viable malting varieties will probably have a shorter market life and will make way for higher yielding malting varieties with very similar malting quality.

In conjunction with grain yield and wide adaptation, disease resistance also needs to be thought of globally. Disease affects not only yield but also malting quality through reduced plumpness, increased protein, and reduced malt extract. Future malting barleys will be grown in many areas and under different disease pressure. The developers of future malting varieties must be aware of which genes for resistance to minor as well as major diseases their varieties possess. This is important to determine whether a variety can be introduced into other regions.

The successful malting barley of the future will have to have a set bank of disease resistance genes to give it the extra flexibility to be sown in diverse growing areas. This is being greatly facilitated today with the advent of molecular marker assisted selection and technologies to screen for several markers at the same time.

This is just a sampling of the many important agronomic traits that the malting barley of the future will need. Yet it gives an idea of what is needed for developers of new malting varieties. The bottom line is that future malting barley breeders need to think globally when they develop new malting varieties.

Quality requirements

What will be needed in malting quality in the future? Basically, brewers want large quantities of grain of known varieties with consistent quality. Remember that malting companies are buying malting barley for their brewing customers. The brewing industry, as a whole, is very conservative and changes slowly. Breweries need consistent malting quality and approve only those new varieties that meet their needs. Yet there are some trends in malting quality that may be predicted.

Extract is the measure of everything that is put in solution from the malt at the start of the brewing process. It is a measure of soluble sugars, dextrins, soluble proteins, beta-glucans, and other compounds. Just as grain yield is money to the farmer, extract yield is money to the brewer. Generally speaking, the more extract there is in the wort, the more food for the yeast in the fermentation process. The amount of fermentable sugars in the extract is particularly important because the yeast converts these sugars into alcohol and CO₂.

In the last 40 years the extract of US varieties has increased from around 75% to roughly 80%. Will we see another 5% increase in the next 40 years? Perhaps, but we should point out that there is an upper limit for extract in the barley kernel, and we are close to reaching it. In

determining the maximum extract potential, we have to take into account not only the soluble compounds in barley malt, but also all the insoluble compounds. The hull component, the insoluble proteins, and other insoluble components have been estimated at around 15%; thus the maximum extract potential in the barley kernel is around 85%.

There are only a few ways that extract could increase beyond this limit. The author of a recent publication states that the percent extract would increase by more than 5% through the use of a hull-less malting barley. This increase in extract is very interesting to the brewers, who consider a 0.1% increase to be substantial. Will the brewing industry shift to using hull-less malting barleys? Not without changing the brewing process. Barley hulls are an important component of the wort-filtering process and contribute essential flavor to the beer. However, due to the significant jump in extract that hull-less malting barley could contribute, its use will no doubt be studied closely by the brewers. If hull-less malting barley is used in brewing, the smaller breweries will start using it first; the larger and more conservative breweries will probably not use it until all processing and flavor concerns are satisfactorily answered.

Another way to increase extract is by reducing protein. There is a reverse correlation between malt extract and barley protein. Less protein is related to more starch in the grain. From a brewer's standpoint, a high starch content in malting barley is desirable as a source of fermentable sugars. Grain protein content, on the other hand, is

important because it controls and influences many aspects of malt quality, including enzymatic activity, foam properties, and beer flavor. Therefore, a balance needs to be maintained between these factors. Higher malt protein will increase the enzymatic activity of the malt, but will also lower the fermentable sugar content in the extract. Lower malt protein will increase the fermentable sugar content in the extract, but could lower enzymatic activity below the level needed to convert the adjunct starch. A proper balance has to be maintained to accomplish both high fermentable sugars and high enzymatic activity.

Soluble protein, or wort protein, is the amount of malt protein that becomes soluble in the mashing process. Brewing yeast needs a certain level of soluble protein to provide the nutritional amino acids needed for proper yeast growth. Too little or too much protein will cause problems in the fermentation process and may lead to undesirable beer flavor compounds and beer color. Soluble protein has increased over the last 40 years. For example, the high level of soluble protein in the six-rowed variety "Stander" has caused problems in the brewing process. As a result, the AMBA has implemented new guidelines for the maximum desired level of soluble protein.

These new guidelines have brought about a progression toward lower soluble protein malting varieties. Breeding guidelines are 11.5% to 12.5% for malt protein and 4.7% to 5.5% for soluble protein. These levels may be lowered again some time in the future to 11.0% to 12.0% for malt protein and 0.0% to 5.0% for soluble protein. This reduction should maintain favorable

brewing components while minimizing unsatisfactory processing conditions, beer color, and/or beer flavor. Even lower levels may be possible if brewing processes and yeast nutrition are not adversely impacted.

Enzymatic activity of malting barley is needed to break down the starch in the kernel into sugars that in turn are converted into alcohol by the yeast. In North America, a higher level of enzymatic activity is needed to convert the starch of the adjunct as well. Enzymatic activity is generally measured using two parameters: diastatic power and alpha-amylase. Diastatic power is the measure of amylolytic enzymes levels in the malt, including alpha- and beta-amylase, limit dextrinase, and the alpha-glucosidases. This is a general measurement of the ability of the malt to rapidly break down the starch into fermentable sugars. Alpha-amylase is the major enzyme in starch conversion and is measured separately.

North American malting barleys, especially the two-rowed malting varieties, have increased both their diastatic power and alpha-amylase levels in the past 40 years. Consequently, there is concern that these higher enzymatic varieties have more spouting problems under wet harvest conditions. In addition, there are indications that the upper limit for both diastatic power and alpha-amylase may have been reached when looking at brewhouse performance. Again, the six-rowed variety "Stander" is in the center of the debate due to its higher levels of both diastatic power and alpha-amylase. After the release of Stander, breeding guidelines were changed to state that

diastatic power and alpha-amylase levels must be similar to either Harrington, a two-rowed malting variety, or Robust or Morex for six-rowed malting barley. These varieties are generally lower in these enzymes than Stander. Desired levels of diastatic power are now 120 to 150, while alpha-amylase levels are 45 to 55. These new levels should remain fairly stable or perhaps be slightly lower in the future, unless there are significant changes in the brewing process.

Application of new technologies

New technology will be developed to assist in breeding better malting barley varieties. Molecular marker assisted selection (MAS) will continue to be a tool to determine the genetic make-up of new experimental barleys. As locations of genes conferring important traits and markers for them are discovered, a library of markers will be built to enable the breeder first to test experimental malting lines in the lab and then to verify the selected lines in the field. New testing procedures and instrumentation will make it possible to screen for several hundred markers at the same time. This will greatly improve the effectiveness of the breeder in selecting successful malting lines.

Since we are speculating on future developments, there is a possibility that improved brewing chemistry could help the breeder by finding appropriate and inappropriate flavor compounds and the genes behind them. This would allow the breeder to include additional markers for these flavor genes in his library of markers. It should be stressed that the malting and brewing industry will still require barley breeders to grow

out their malting lines to determine their malting and brewing potential.

One new technology that will take more time to be accepted for use in approved malting barley varieties are genetically modified organisms (GMOs), which mean that non-barley genes have been incorporated into malting barley. GMOs are a controversial subject yet to be settled in Europe, Japan, and the U.S. It is a mixed blessing that barley has not been easily tissue cultured. By the time a truly genetically modified malting barley is ready to be tested by the brewing community, the issue of GMOs may be resolved. In the meantime, the brewing community is not ready to start

using GMO raw materials in the brewing process. However, I believe this type of research needs to be encouraged in barley while the GMO issue is being reviewed by the brewing industry.

This is a little of what may be waiting in the future of malting barley. Some researchers can already see the beginnings of new tools that may help select malting barley varieties in the future. Others researchers may already be implementing some of the ideas mentioned here. There are other new and exciting improvements in both the barley field and in the brewhouse that have not been mentioned here but we await the report of these improvements at a later date.

Barley Breeding in Peru

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Barley is a very important crop in the highlands of Peru, especially at altitudes above 3000 m (Table 1). Few crops, aside from barley, are suitable for growing under the adverse environmental conditions (such as frost and drought) that predominate in this region. Barley

contributes at least 20% of the total caloric intake of rural families.

According to national statistics, there are 3 million poor people living in highland rural areas who subsist mainly thanks to their farming activities.

Table 2 shows the barley area, production, and yield per hectare from 1977 to 1998. Barley is produced mainly by subsistence farmers as a staple food crop in relatively small plots (Table 3).

Barley grows mostly in low-fertility soils. In many cases, the use of machinery is not possible due to the steeply sloping terrain. There is virtually no flat, well-watered agricultural land. Plots are perched one above another up mountain sides rising thousand of meters. Frost, drought, hail, and other climatic factors reduce barley production at that altitude.

The rusts are the most aggressive of the diseases present in the region. Leaf rust causes damage all the way from sea level (the coast) to 2800 masl. Stem rust can be found at the same altitudes, but in recent years there have been very few outbreaks of the disease. Stripe rust is the main disease above 2600 masl, affecting 90% of the cereal area. Since 1978, it has been the most serious

Table 1. Main crops, area, production, and yield per unit area in Peru, 1998.

Food crops	Area (ha)	Production (t)	Yield (kg/ha)
Rice	269080	1548778	5756
Potato	268847	2589338	9631
Maize	214590	230450	1074
Barley	146698	165831	1130
Wheat	125894	146285	1162
Banana	117792	1321890	11222
Cassava	80708	884118	10955
Bean	75164	67563	899
Faba bean	34184	38129	1115
Pea	31415	33365	1062
Quinoa	30720	28614	931
Olluco	23523	116897	4969
Oca	21626	101639	4700
Sweet potato	17397	221609	12738
Onion	14317	315622	22045
Mashua	7244	32859	4536
Industrial			
Corn	229114	702479	3066
Cotton	73629	95262	1294
Sugar cane	52614	5705340	108438
Marigold	5507	96070	17445

Source: OIA. Producción Agrícola 1998.

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Table 2. Barley area, yield, and production in Peru, 1977–98.

Year	Harvest area (000 ha)	Yield (kg/ha)	Production (000 MT)	Malt and barley imports (000 MT)
1977	169.72	861	146.20	43.10
1978	151.54	855	129.51	38.20
1979	152.59	861	131.44	51.00
1980	109.93	890	97.87	74.10
1981	118.13	969	114.50	82.80
1982	114.82	960	110.24	61.30
1983	105.76	830	87.81	51.30
1984	108.67	946	102.80	64.70
1985	117.08	1060	124.11	95.60
1986	104.05	1130	118.14	83.90
1987	110.57	997	110.23	108.40
1988	123.70	1040	128.59	92.40
1989	120.22	1045	125.60	46.20
1990	75.10	954	71.64	84.20
1991	111.08	1028	115.22	77.70
1992†	81.76	842	68.81	80.55
1993†	101.17	1112	112.49	86.40
1994	112.50	1154	129.84	
1995	107.03	1143	131.19	
1996	108.93	1190	152.94	39.65
1997	129.91	1062	138.03	29.55
1998	149.89	1130	165.83	29.95

† Jan.-Nov. 1993/1992 (preliminary data).

Source: Oficina de Información Agraria.

limiting factor for barley production. There are many other diseases such as powdery mildew, BYDV, and foliar diseases caused by *Helminthosporium* spp. and *Rhynchosporium secalis*, which are important in the highland region during warm and wet years.

In general, very little farming technology is applied to barley production. The average barley yield was 0.8 t/ha some years ago. However, the average yield has now increased to 1.5 t/ha in some areas thanks to new varieties developed by Universidad Nacional Agraria La Molina (Pasco; Table 4).

In 1968, Universidad Nacional Agraria La Molina started a cereal breeding program that continues to this day. The program was developed in close collaboration with Malteria Lima S.A. (Backus Corporation), ICARDA/CIMMYT, Nebraska State University, and the International Atomic Energy Agency (IAEA). It focuses on cereals, but especially on barley production in the highlands.

Objectives

- To develop improved varieties with high yield potential, resistance or tolerance to abiotic and biotic stress, and good quality.
- To develop production technologies adapted to different barley production areas.
- To transfer research results to agronomy students, agronomists, and farmers.

Breeding

The breeding program has an excellent balance between conventional plant breeding, ICARDA/CIMMYT germplasm augmentation, induced mutation, and biotechnology.

Germplasm introduction and evaluation

The United States Department of Agriculture and CIMMYT have provided more than 10,000 barley accessions. This entire collection was screened for adaptability in several parts of the Andean Region. Only a few foreign accessions were adapted to such extreme environmental conditions.

National collections of local barley were put together for the highlands of Peru and Bolivia. These materials have been

Table 3. Size and number of farm units and uses of barley grain in Peru.

	Total units	Grain uses			Sold as seed
		Sold at the farmgate	Sold on the market	Home consumption	
Below 0.5 ha					
Number of units	22657	74	433	22137	73
Area	1589.75	7.93	42.28	1537.43	2.12
0.5 to 4.9 ha					
Number of units	162166	1204	7832	154624	281
Area	59279.45	545.45	3756.54	54891.77	85.69
5.0 to 9.9 ha					
Number of units	37151	499	2738	34722	89
Area	29512.47	490.68	2888.86	26069.66	63.27
10 to 19.9 ha					
Number of units	16505	250	1299	15309	53
Area	17790.38	385.7	2120.2	15206.68	77.8
20 to 49.9 ha					
Number of units	7635	131	624	7024	34
Area	10455.31	285.4	1519.99	8585.76	64.15
Above 50 ha					
Number of units	5319	89	406	3076	19
Area	7251.42	240.47	1728.94	5241.09	40.91
Total no. of units	249633	2247	13332	236892	549
Total area	125878.78	1955.63	12056.81	111532.39	333.94

Source: INEI. III Censo Nacional Agropecuario, Resultados definitivos, 1996.

used to develop and improve new varieties. The continuous introduction of new accessions through the ICARDA/CIMMYT Barley Program and other institutions is very useful to our breeding program.

Methods

Hybridization. In this method, one parent is usually a line locally developed by the cereals program; the other is generally a selected introduction. Selection is done using bulk or individual selection.

Table 4. Barley area, yield per hectare, and number of farm units in different departments in the Peruvian highlands.

Department	Barley area (ha)	Yield (t/ha)	Farm units
Ancash	6657.65	939	11005
Apurimac	3128.00	1026	7892
Ayacucho	8764.96	738	18941
Cajamarca	7011.36	986	11679
Cusco	8905.66	1250	23143
Huancavelica	20632.97	1319	31801
Huanuco	3803.27	1300	8474
Junin	8724.07	1422	16796
La Libertad	11475.12	1209	10278
Pasco	29.26	1519	191
Puno	43970.57	1003	191

Source: INEI. III Censo Nacional Agropecuario, Resultados definitivos.

Mutation induction. Mutation is used to improve the adaptability of modern, high yielding cereal varieties to make them suitable for cultivation in stress-prone areas of the Peruvian Highlands and to improve grain quality characteristics.

Doubled haploid production. Plants selected from F1, F3, or M1 are used each cycle to produce doubled haploids using anther culture.

Improved crop management practices

Studies on chemical fertilization, seeding density, seeding methods, time of seeding, and chemical weed control are conducted to develop or improve agronomic practices specifically for the region. Each year in the highlands demonstration plots using new varieties are established with the cooperation of many institutions to show farmers new crop management practices.

New improved varieties

Yellow rust resistant Zapata 588 played an important role during the severe epidemic that occurred from 1976 to 1978. Almost all barley varieties cultivated in Peru were killed by the yellow rust pathogen introduced into South America at that time.

The varieties UNA 80, UNA 8270, Yanamucllo 87, Buenavista, UNA La Molina 94, UNA La Molina 95, and UNA La Molina 96 were released between 1980 and 1996. These varieties show higher yield potential, improved yellow rust resistance, and better grain quality. Highland farmers adopted improved varieties due mainly to their good

performance (Table 5). It should be noted that UNA La Molina 95 is an early maturing hull-less variety developed by inducing mutation in the variety Buenavista using gamma rays.

Increase in National Average Barley Yields

According to statistics of the Peruvian Ministry of Agriculture, the national average barley yield increased from 859 kg/ha in 1978 to 1130 kg/ha in 1998. This considerable increase in yield was due to the use of fertilizers and other cultural practices in the highland region, which is not usual among small farmers in Peru. The increase in barley yields was of great significance for small landholders in the Peruvian highlands.

Socioeconomic Impact

The value of the annual barley production in Peru is estimated at US\$ 12 million. Barley varieties released by Universidad Nacional Agraria La Molina account for 80% of this production. From 1977 to 1998 barley production totalled US\$ 228 million, to the direct benefit of the highland population.

National statistics indicate that approximately 49.6% of Peru's total population lives in poverty or extreme poverty; three million of those people live in rural highland areas. Barley is mainly used for food and feed in Peru. In the highland region, about 70% of barley grain is used for human consumption.

Table 5. Improved barley varieties released by Universidad Nacional Agraria La Molina from 1978 to 1996.

Genealogy	Yield (t/ha)	Adaptation (masl)	Disease reaction
Zapata 588 B112(F7-1962)D2hslII/Compuesto XXI-51Cz	2 – 6	3000 – 3800	Tolerant to yellow rust
UNA 8270 CNC 203131/Compuesto XXI	2 – 5	3000 - 3800	Resistant to yellow rust Tolerant to scald
UNA 80 CNC 203346/CXXI	2.2 – 6	3000 – 3800	Resistant to yellow rust
Yanamuclo 87 UNA 8309 x Itintec 77	2.4 – 5	3000 - 3800	Resistant to yellow rust
Buenavista P71318-Row134.78 (ICARDA/CIMMYT: F3 Generation)	2.5 – 3	3000 – 3800	Resistant to yellow rust
UNA La Molina 95 Parent Material Buenavista (Gamma ray 300 Gy)	2.5 – 5	3000 – 3800	Resistant to yellow rust Tolerant to <i>Pyrenophora teres</i>
UNA La Molina 96 Gloria"s"/Celo"s"/ESCII-77-83-3E-7E-5E/1E/3/Lignee 527 (ICARDA/CIMMYT: F3 Generation)	2.5 - 5	3000 – 3600	Resistant to yellow rust, leaf rust and powdery mildew

Accumulating Genes for Disease Resistance in Two-Rowed Barley for North Dakota

J.D. FRANCKOWIAK¹

A large portion of the barley (*Hordeum vulgare*) crop in North Dakota (ND) is grown for the malting and brewing industry. Most cultivars have a six-rowed spike type and are used as malting barley based on recommendations made by the American Malting Barley Association, Inc. (AMBA). Eastern ND is generally more favorable for producing malting barley than western ND, where low yields and thin kernels are frequently production problems. During relatively dry growing seasons in western ND, two-rowed barley often yields more than six-rowed barley. Therefore, the ND Agricultural Experiment Station funded an improvement program for two-rowed barley in the 1970s.

Barley research at North Dakota State University (NDSU) is partially supported by grants from AMBA and its precursory agencies. Support for two-rowed barley improvement was based on the assumptions that two-rowed cultivars will show greater yield stability in western ND and will be suitable for production of malting barley in eastern ND. The two-rowed program complements the six-rowed program, which was started in the early 1940s.

Many of the six-rowed barley cultivars released for production in Manitoba, Minnesota, North Dakota, and South Dakota have similar agronomic traits and are often referred to as Midwest six-rowed barley. Historically, spot blotch, incited by *Cochliobolus sativus*, and wheat stem rust, incited by *Puccinia graminis* f. sp. *tritici*, are the barley diseases that have caused the greatest production losses in eastern and central ND. Barley diseases rarely cause losses in western ND.

Development of two-rowed barley for ND

In 1970, Dr. Glenn A. Peterson made crosses designed for improvement of two-rowed barley. He assumed that some traits of Midwest six-rowed barley were needed in two-rowed barley for ND. The best two-rowed cultivars from the western USA and prairie provinces of Canada were susceptible to spot blotch, wheat stem rust, and net blotch, incited by *Pyrenophora teres* f. *teres*. Crosses were made between the two types of barley and the F₁ plants were crossed to another two-rowed cultivar to increase the frequency of two-rowed plants in the progenies. In 1974, Dr. Melvern K.

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Anderson was employed as the first two-rowed barley breeder at NDSU.

Two-rowed lines selected from the initial three-way crosses were tall and lacked adequate disease resistance. To generate better material, good selections were crossed to six-rowed cultivars and the F_1 plants crossed to a two-rowed cultivar. In 1978, when selections from the second cycle of crosses were in preliminary yield trials, this author was employed as the two-rowed barley breeder. Research on barley is conducted at NDSU by a team of scientists including a two-rowed barley breeder, a six-rowed barley breeder, a cereal chemist, a plant pathologist, a geneticist, a virologist, and agronomists at the ND Research Extension Centers.

Development of 'Midwest' two-rowed barley cultivars

As two-rowed lines suitable for production in western ND were identified, phenotypic variability among the lines derived from the two-rowed by six-rowed crosses was rapidly restricted. In 1979, the line ND4994 was observed to be earlier, shorter, and stiffer than most other selections. ND4994 had large, plump kernels; acceptable levels of malt extract; and moderate values for grain protein, diastatic power, and alpha-amylase; but its yields were below average. In 1980, however, when the growing season was relatively hot and dry, ND4994 was the only early line with high yields. A reselection was released in 1984 under the name Bowman (PI483237) and recommended for production in western ND (Franckowiak et al., 1985). Bowman was classified by AMBA as a non-malting barley cultivar.

Bowman was widely grown in southwestern ND because it yielded well and often had much higher test weight values than other barley cultivars. Bowman was utilized in breeding subsequent two-rowed cultivars for ND because of its unique combination of plant height and maturity genes. Other two-rowed barley cultivars released for ND include Stark in 1991, Logan in 1995, and Conlon in 1996. Conlon was recommended as a malting barley cultivar by AMBA in 2000 and as such is the first two-rowed malting barley recommended for production in ND. These two-rowed cultivars have similar agronomic characteristics and are best adapted for production in western ND and adjacent areas of Montana and South Dakota. They can be referred to as 'Midwest' two-rowed barley.

Barley diseases in eastern ND

When released, Bowman was resistant to wheat stem rust and moderately resistant to net and spot blotch. However, its levels of net and spot blotch resistance were not adequate to recommend Bowman for production in eastern ND. Bowman is susceptible to number of pathogens of minor importance in ND. They include leaf rust, *Puccinia hordei*; barley yellow dwarf virus (BYDV); scald, *Rhynchosporium secalis*; bacterial blight, *Xanthomonas campestris* pv. *translucens*; powdery mildew, *Blumeria graminis* f. sp. *hordei*; loose smut, *Ustilago nuda*; and covered smut, *Ustilago hordei*. Bowman is resistant to barley stripe mosaic virus (BSMV) and shows some resistance to black point and common root rot, both incited by *C. sativus*.

After the release of Bowman, changes occurred in the relative importance of

several barley pathogens. In 1989, a new race of *Puccinia graminis* f. sp. *tritici* attacked cultivars previously classified as resistant (Jin et al., 1994). In 1990, a new pathotype of *C. sativus* was found to attack Bowman and many of its derivatives (Fetch and Steffenson, 1994). This pathogenicity change greatly lowered the yields of Bowman in trials at Fargo and Langdon in eastern ND (Table 1). In the early 1990s, speckled leaf blotch, incited by *Septoria passerinii* and *Stagonospora avenae* f. sp. *triticea*, returned as production problems in northeastern ND (Toubia-Rhame and Steffenson, 1999). In the 1990s, Bowman showed a susceptible reaction to new isolates of *P. teres*. However, the major event in the Upper Midwest barley production area was epidemics of Fusarium head blight (FHB), incited primarily by *Fusarium graminearum*, which started in 1993 (Schwarz et al., 1995a). The presence of the toxin deoxynivalenol (DON) reduced the value of crop and products made from infected grain (Schwarz et al., 1995b).

Table 1. Grain yields (t/ha) of selected barley cultivars in trials conducted in North Dakota from 1995 to 1998.

Cultivar	Row type	Trial locations in North Dakota				Average
		Williston 4†	Carrington 4	Fargo 4	Langdon 4	
Bowman	2	3.72	3.51	2.98	3.86	3.32
Logan	2	3.87	4.42	3.99	4.93	4.23
Conlon	2	3.57	4.12	3.52	4.53	3.84
Morex	6	3.71	3.90	3.56	4.29	3.71
Stander	6	3.79	4.60	3.75	4.67	4.18

† Number of trials.

Development of disease-resistant, Midwest two-rowed barley

Because barley is a low value crop and disease epidemics are often sporadic, many ND farmers do not apply fungicides. A few barley diseases can be controlled by clean seed programs or by seed treatments. Genetic resistance to barley pathogens is considered the best means to minimize losses caused by diseases. Thus, incorporation of genetic resistance to barley pathogens was established as a breeding goal when breeding of six-rowed barley was initiated.

The two most important diseases, wheat stem rust and spot blotch, received more attention than other diseases. Genes for resistance to loose smut, speckled leaf blotch, net blotch, and BSMV were incorporated into a few six-rowed cultivars. When other diseases occurred in field plots, highly susceptible lines and selections were discarded. When improvement of two-rowed barley was undertaken, disease testing focused on wheat stem rust, spot blotch, and net blotch.

Resistance to spot blotch

Controlling losses caused by spot blotch has been challenging. Shortly after the barley improvement program was started, the six-rowed selection ND B112 (Cího 11531) was shown to be highly resistant to spot blotch (Wilcoxson et al., 1990). Six-rowed cultivars developed from crosses to ND B112 were released in the 1960s and 1970s. Bowman has a moderate level of spot blotch resistance, which is probably controlled by two genes from its six-rowed parents (Steffenson et al., 1996).

Although this level of resistance is lower than that of ND B112, spot blotch epidemics were not observed on Bowman during the 1980s. During the 1990 growing season, however, over 80% of the two-rowed lines in nurseries near Fargo were prematurely defoliated by a spot blotch epidemic. This and subsequent epidemics on two-rowed barley were caused by a new pathotype of *C. sativus* (Fetch and Steffenson, 1994). Six-rowed cultivars are resistant to the new isolate, which was found only in ND (Valjavec-Gratian and Steffenson, 1997). This isolate continued to cause epidemics in two-rowed breeding nurseries until susceptible lines were discarded.

Finding two-rowed lines that are highly resistant to the 'old' isolate of *C. sativus* has been more difficult. Two recent observations have been helpful in selecting lines having better spot blotch resistance. First, six-rowed cultivars retain green leaves and culms longer than two-rowed cultivars in trials grown in eastern ND. Second, lines with the lowest spot blotch readings in seedling tests often have the lowest spot reactions in field tests. Using these selection criteria, two-rowed lines with better spot blotch resistance have been identified recently.

Resistance to net blotch

Two-rowed breeding lines with a moderately resistant reaction to *P. teres* f. *teres* were easy to identify with seedling tests; however, a portion of them showed susceptible reactions in subsequent field tests. These changes in disease reactions illustrate the variability associated with genetic resistance to net blotch. In the late 1980s, Midwest six-rowed barley cultivars were found to exhibit

susceptible field reactions to net blotch in eastern ND while many two-rowed lines were resistant. In the mid 1990s, Bowman and Stark showed susceptible reactions to net blotch in western ND, but six-rowed cultivars were resistant in those trials. These observations suggest that host-pathogen interactions for net blotch in ND are similar to those reported in other barley growing areas (Khan, 1982; Steffenson and Webster, 1992; Tekauz, 1990). As new genes for net blotch resistance are incorporated into cultivars, isolates of *P. teres* with different virulence patterns are identified.

Some lines selected from crosses between Bowman-derived cultivars and the two-rowed cultivar Norbert (PI 452125), bred in Manitoba and released by Agriculture Canada, have continued to show low reactions to net blotch in greenhouse and in field tests. The origin of these *Rpt* genes for net blotch resistance is unknown, but the cultivar Norbert, which was derived from a complex cross to CIho 5791 (Metcalf and Bendelow, 1981), is one possible source. Some lines derived from crosses to accessions from the ICARDA-CIMMYT barley improvement program in Mexico also have low net blotch scores. Hopefully, presence of *Rpt* genes from more than one source will permit their rapid deployment when future changes in virulence occur.

Resistance to BYDV

Barley yellow dwarf symptoms occur sporadically on barley grown in eastern ND, but production losses are often, but not always, low (Gill, 1970). Severe BYDV epidemics do occur frequently in late-planted breeding nurseries. Crosses were made in the early 1980s to introduce the *Ryd2* gene for BYDV

resistance from CIho 2376 (Rasmusson and Schaller, 1959), but BYDV resistant selections were late and susceptible to lodging. Additional cycles of crossing and selection did not improve greatly the agronomic traits of BYDV resistant lines. Thus, ICARDA-CIMMYT lines were used as an alternative source of the *Ryd2* gene. Lines with BYDV resistance and good agronomic traits have been recovered, but their malting quality is not acceptable. Malt extract values need improvement and the low protein gene from the six-rowed cultivar Karl needs to be added.

Resistance to leaf rust

Yield and quality losses caused by leaf rust of barley in ND are generally low because the crop is seldom infected before heading. The inoculum is blown northward from over-wintering sites in the southeastern USA. Rapid changes in leaf rust races are not expected because resistant cultivars are rarely grown in the over-wintering sites. Since Midwest barley cultivars do not have genes for leaf rust resistance, crosses were made to introduce the *Rph3* and *Rph7* genes from Estate (CIho 3410) and Cebada Capa (CIho 6193), respectively. Experimental lines with leaf rust resistance were selected, but they are not suitable for release as cultivars. Because the *Rph3* and *Rph7* genes are no longer effective against all leaf rust isolates worldwide (Jin et al., 1996), accessions of wild barley, *H. vulgare* subsp. *spontaneum*, were evaluated as a source of new leaf rust resistance genes. The *Rph15* gene from PI 355447 was isolated in a Bowman backcross-derived line and is being incorporated into Midwest two-rowed breeding material (Chicaiza et al., 1996). Preliminary tests indicate

accessions from the ICARDA-CIMMYT barley program may have *Rph* genes that are different from those reported in the literature.

Resistance to speckled leaf blotch

In the 1950s and 1960s, speckled leaf blotch was a problem in northeastern ND; however, severe losses were not observed again until the early 1990s. The disease develops late during the growing season and causes premature death of leaves and post-maturation straw breakage. Several genes for resistance to *S. passerinii* have been identified (Rasmusson and Rogers, 1963), but they are not present in Midwest six-rowed cultivars. In 1993, several six-rowed lines from the barley ICARDA-CIMMYT program were observed to show resistant reactions in field plots at Langdon, ND. These lines maintained green leaves and stems longer than susceptible cultivars. In trials at Langdon, delayed loss of green leaves is a criteria used to select speckled leaf blotch resistant lines. Subsequent seedling tests confirmed that selections from crosses to ICARDA-CIMMYT lines are resistant to an isolate of *S. passerinii* (Toubia-Rhame and Steffenson, 1999). Septoria resistant lines from the second cycle of three-way crosses have been identified.

Resistance to Fusarium head blight

Fusarium head blight (FHB) or scab is a frequent barley production problem in many humid and subhumid climates. Yield losses are often low, but the accumulation of toxins reduces the value of the grain. Until 1993, FHB was considered a minor disease problem in ND. Above normal rainfall during heading is believed to be partially

responsible for the FHB epidemics in 1993 and subsequent years. The best resistance to FHB has been found in accessions closely related to the two-rowed cultivar Svanhals and the six-rowed cultivar Chevron (Urrea-Flórez, 2000). Although resistance to FHB is inherited in a quantitative manner (Takeda, 1992), resistance is frequently associated with the two-rowed spike trait, controlled by the *Vrs1.b* allele at the *vrs1* locus (Prom et al., 1997; Takeda, 1990). Molecular mapping of FHB resistance in Chevron identified several QTLs of which one is associated with the *vrs1* locus in the proximal region of chromosome 2HL (de la Peña et al., 1999).

Most FHB resistant selections from crosses between Midwest six-rowed cultivars and accessions related to Svanhals have a two-rowed spike (Urrea-Flórez, 2000). FHB resistant six-rowed selections are very rare, very tall, and late. This phenomenon has also been observed in crosses to Midwest two-rowed cultivars. A close linkage between the *vrs1* locus and one of the genes for FHB resistance appears to cause the problem. The *Vrs1.b* and *vrs1.a* alleles in Midwest two-rowed and six-rowed barley, respectively, are also closely linked to a short culm gene (*hcm1.a*) (Swenson and Wells, 1944) and one or more early maturity genes. The FHB resistance locus is likely positioned in the middle of this chromosome 2HL linkage group. Thus, a double crossover is required to obtain FHB resistant lines adapted to ND. Identification of desirable recombinants is difficult because several plant height and maturity genes are segregating in crosses to FHB resistant accessions. Barley cultivars from Japan and China have

some resistance to FHB based on tests in eastern China, but that resistance is poorly expressed in ND (Urrea-Flórez, 2000), where these photoperiod sensitive cultivars head extremely early.

Multiple disease resistance in Midwest two-rowed barley

New two-rowed cultivars for ND should ideally contain a large number of disease resistance genes. However, accumulation of these genes in elite breeding material is slow because the donor parents are poorly adapted to ND. Thus, development of locally adapted material with multiple disease resistance genes consumes a large portion of the resources available for two-rowed barley improvement. The pattern using donor parents in three-way crosses, which was employed by Dr. Glenn Peterson, is still followed. Greenhouses and off-season nurseries have facilitated crossing and generation advance. A modified pedigree scheme is used to select lines with desirable agronomic traits. Seedling tests and off-season nurseries are used to identify ones that are disease resistant. The best lines become parents for another cycle of three-way crosses.

Two cycles of crossing and selection are generally adequate to recover disease resistant lines with acceptable agronomic traits. Disease resistance genes from different sources are combined in subsequent breeding cycles. However, this scheme for breeding locally adapted lines with multiple disease resistance has not been highly successful because it takes a long time. For acceptance by the malting and brewing industry, new cultivars must also have better malt quality than that of the recurrent parents.

Sources of disease resistant barley germplasm

The transfer of disease resistance genes from several landraces to elite breeding materials takes a long time. Utilization of donor parents having multiple disease resistance could shorten this time requirement. As an added benefit, accessions with multiple disease resistance might contain resistance to some minor diseases. Minor diseases become important because genetic control of major diseases alters both crop physiology and pathogen interactions. Predominant pathogens can no longer adequately suppress less aggressive ones in disease resistant cultivars. Diseases such as bacterial blight, powdery mildew, scald, black point, and root rots may need attention in the future.

Many barley lines bred by Dr. Hugo E. Vivar for the ICARDA-CIMMYT barley program in Mexico have multiple disease resistance. Although they are not well adapted to ND, they have been utilized in the development of Midwest two-rowed barley. This was, however, more by accident than by design. In 1988, several ICARDA-CIMMYT barley lines were introduced because barley stripe rust, *Puccinia striiformis* f. sp. *hordei*, was spreading into North America (Dubin and Stubbs, 1986). In 1990, control of wheat stem rust provided by the *Rpg1* gene was found to be inadequate. New genes for stem rust resistance were identified in lines from the ICARDA-CIMMYT barley program (Jin et al., 1994). Although stripe rust never became a problem in ND and the *Rpg1* gene is effective against current pathotypes of stem rust, utilization of the ICARDA-CIMMYT barley lines helped establish multiple disease resistance as a barley improvement goal.

Summary

Since most barley grown for North Dakota (ND) has a six-rowed spike type, two-rowed spring barley can be considered a new crop in ND. Drought and high temperatures in western ND and barley diseases in eastern ND are the primary factors limiting barley production. A large portion of the ND barley crop is used by the malting and brewing industry; therefore, desirable malt quality parameters are needed in elite breeding material. The two-rowed cultivars and breeding materials developed for ND have a unique combination of plant height and maturity genes and can be referred to as Midwest two-rowed barley. Multiple disease resistance was established as a breeding goal because a large number of barley pathogens can cause losses in ND. Accessions from many countries were used as sources of disease resistance genes, but lines from the ICARDA-CIMMYT barley improvement program in Mexico have been an extremely valuable source of disease resistance genes.

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Collaborative Stripe Rust Resistance Gene Mapping and Deployment Efforts

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Our collaborative stripe rust resistance research projects have multiple objectives. The first and foremost is to provide agronomically-competitive, disease-resistant varieties to our clients, who range from the Saraguro Indians of Ecuador to North American malting barley producers. A second objective is to broaden the genetic base of our barley germplasm via the systematic characterization and introgression of unique alleles. A third objective is to contribute to a better understanding of the genetic basis of durable disease resistance in crop plants.

Three key components of this research are: 1) phenotyping at the ICARDA/CIMMYT facilities in Toluca, Mexico, an environment in which the heritability of disease symptom expression is maximized; 2) genotyping with molecular markers; and 3) accelerated germplasm advance. Initially, we mapped resistance genes in ICARDA/CIMMYT germplasm and then introgressed them into North American germplasm via marker-assisted selection. More recently, we have pyramided quantitative and qualitative resistance genes and attempted to

integrate gene discovery and deployment.

The objective of this report is to summarize multiple areas of endeavor that converge on stripe rust resistance gene mapping and deployment: 1) stripe rust epidemiology, 2) quantitative vs. qualitative resistance, and 3) linkage mapping and QTL analysis efforts in barley. The results of our collaborative stripe rust resistance mapping and germplasm improvement efforts are summarized in an accompanying Figure 1 and Table 1. Because this stripe rust resistant germplasm development is an ongoing process, updated summaries will be maintained on the Internet at <http://www.css.orst.edu/barley/orbarley/collab.htm>.

Barley Stripe Rust

Barley stripe rust (*Puccinia striiformis* f.sp. *hordei*) has caused serious yield losses in Europe, the Asian subcontinent, and the Americas (Dubin and Stubbs, 1985; Hayes et al., 1996c). The disease was first reported in South America in 1975 and in

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the U.S. in 1991 (Marshall and Sutton, 1995). By 1995, it had been reported in every state of the western U.S. Commercial-scale epidemics have occurred annually in California and Oregon since 1995. Environments in the Pacific Northwest favor the disease: wheat stripe rust (*Puccinia striiformis* f.sp. *tritici*) is the most important disease of wheat in the Pacific Northwest (Line, 1993).

The two f.sp. of *Puccinia striiformis* are, however, highly specialized, and cross-infection is not of economic importance. Initially, only race 24 of *P. striiformis* f.sp. *hordei* was thought to be present in the Americas (Dubin and Stubbs, 1985). Recently, more extensive analysis has revealed considerable variation in pathogen isolates collected in the U.S. (Chen et al., 1995b; Roelfs and Huerta-Espino, 1994).

Genetic resistance is the most cost-effective and environmentally appropriate technique for crop disease management. Durability of resistance is a key consideration in disease resistance breeding. Unfortunately, durability can only be demonstrated in hindsight. Barley germplasm developed by the ICARDA/CIMMYT Barley Program in Mexico allows limited symptom development when exposed to the spectrum of virulence encountered in field tests in South America, Mexico, and the U.S. The fact that this germplasm has remained resistant over a 15-year period may be grounds for describing it as "durable." Sandoval-Islas et al. (1998) provided additional evidence for the quantitative and durable nature of the resistance of genotypes in the ICARDA/CIMMYT program.

Quantitative and qualitative resistance

There is an extensive literature on the merits of different types of resistance, and much of the debate is phrased in the context of probable durability (Johnson, 1981). The terminology of disease resistance genetics does justice to the complexity of the subject. The terms "quantitative," "qualitative," "vertical," "horizontal," "partial," and "tolerance" have precise definitions (Browning et al., 1977). Resistant phenotypes are a continuum ranging from the hypersensitive response (HR) to a modest reduction in the rate of epidemic development. Throughout the continuum, there are cases representing permutations of locus number, allele effect, race-specificity, stage of expression, and durability (Browning et al., 1977). Therefore, locus number, allele effects, stage of expression, and race-specificity need to be defined on a case-by-case basis.

In the case of cereal rusts, a large body of theory has developed regarding the risks associated with race-specific resistance genes (Johnson, 1981; Parlevliet, 1983; Vanderplank, 1978). There is evidence that pathogen virulence can evolve more quickly than plant breeders can deploy single resistance genes in new varieties (Parlevliet, 1977). Accordingly, a number of alternative disease resistance breeding strategies have been proposed and, in some cases, implemented. One approach is to pyramid multiple race-specific genes into a single genotype (Huang et al., 1997; McIntosh and Brown, 1997; Mundt, 1991).

Another approach is to use resistance genes that do not exhibit gene-for-gene relationships. Distinctions between quantitative and qualitative resistance, adult plant and seedling resistance, and

partial and complete resistance are important considerations within this general approach to disease management. At the risk of oversimplification, there is empirical evidence that non-race-specific resistance genes may be more durable than race-specific single genes (Parlevliet, 1983).

Despite the existence of considerable quantitative resistance theory, there is relatively little empirical data on the inheritance and mechanism of quantitative resistance. Molecular tools have revealed some unexpected results: unsuspected complexities in some gene-for-gene resistance systems and unsuspected large-effect determinants in some quantitative resistance systems (see reviews by Michelmore, 1995; Young, 1996). If quantitative resistance genes are to be useful, we need to understand their effects, interactions, and relationships with genes determining other economically important, quantitatively inherited phenotypes.

Characterization of plant resistance genes at the molecular level has provided information upon which to develop models involving signal detection, signal transduction, and response (Beynon, 1997). These studies (Buschges et al., 1997; Martin et al., 1993; Salmeron et al., 1994; Schulze-Lefert, 1997; Zhou, 1995) have provided molecular evidence confirming hypotheses based on whole plant data (summarized by Ellingboe, 1976; Gabriel and Rolfe, 1995) indicating that "monogenic" gene-for-gene relationships are recognition processes that turn on multiple genes in a resistance pathway.

At the same time, QTL analysis procedures have facilitated dissection of quantitative disease resistance (see reviews by Michelmore, 1995; Young, 1996). In some cases, a significant proportion of the total variance in the expression of quantitative traits may be attributable to one locus or a few loci (Chen et al., 1994; Hayes et al., 1996; Michelmore, 1995; Young, 1995), confirming classic quantitative genetic studies (summarized by Vanderplank, 1978). This may be an oversimplification due to overestimation of locus effects and underestimation of locus numbers (Beavis, 1998; Jansen and Stam, 1994; Kaeppler, 1997; Melchinger et al., 1998; Utz et al., in press; Visscher et al., 1997; Zeng, 1994). However, the overall picture is one of converging lines of evidence supporting complexity in some qualitative models and simplicity in some quantitative models.

Differentiation of qualitative versus quantitative resistance has long been a source of controversy. At one extreme is the view that these classifications represent genes with distinctly different mechanisms and race specificity (Vanderplank, 1968, 1978). At the other extreme is the view that all resistance genes are similar, but are merely expressed differently in different combinations and in different genetic backgrounds (Nelson, 1978). Unfortunately, three decades of debate have failed to resolve the issue.

Wang et al. (1994) used recombinant inbred lines of rice (*Oryza sativa*) to show that a cultivar with durable resistance (*sensu* Johnson, 1981) to rice blast (caused by *Magnaporthe grisea*) contains two race-specific, qualitative genes for resistance and ten QTLs contributing to partial

resistance (*sensu* Parlevliet, 1989). Qi et al. (1999) have presented evidence for race-specific QTLs and argued that quantitative resistance to leaf rust is an example of minor gene-for-minor gene interaction. However, the contribution of the qualitative vs. quantitative genes to resistance remains unclear.

Barley Linkage Maps and QTLs

Barley is an excellent system for genome mapping and map-based analyses. This diploid ($2n = 14$) species has seven cytologically distinct chromosomes containing approximately 5.3×10^9 bp DNA (Bennett and Smith, 1976).

Although barley is an autogamous species, there is sufficient DNA-level diversity for efficient linkage map construction in populations derived from crosses between related genotypes (Graner et al., 1991; Kleinhofs et al., 1993; Kasha et al., 1995; Becker et al., 1995; Hayes et al., 1997). The North American Barley Genome Mapping Project (NABGMP) has focused on building maps in elite germplasm to facilitate the direct application of these maps to plant breeding (reviewed by Hayes et al., 1996). Several thousand loci have been placed on these maps, providing a comprehensive catalog of markers.

Higher throughput markers, such as AFLPs, have been used for barley map construction (Becker et al., 1995; Hayes et al. 1997). Microsatellite polymorphism has been demonstrated (Saghai-Marooif et al., 1994) and used for barley germplasm characterization and map construction (Powell et al., 1996; Russell et al., 1997; Becker and Heun, 1995; Toojinda et al., 2000). The Scottish Crop

Research Institute (SCRI) has a very productive SSR development program (<http://www.scri.sari.ac.uk/SSR/>). We are currently cooperating with the SCRI in an international barley SSR characterization effort and are systematically mapping the SCRI SSRs on NABGMP populations (Toojinda et al., 2000).

Linkage maps are useful from the standpoint of understanding genome organization, establishing synteny as a platform for map-based cloning, and for QTL detection. For a review of QTL detected in barley with references and links, see Hayes et al., 1996; GrainGenes (<http://wheat.pw.usda.gov/graingenes.html>); and the NABGMP home pages (<http://www.css.orst.edu/barley/nabgmp/nabgmp.htm>; <http://gnome.agrenv.mcgill.ca>). In barley, as in other crop species, much of the activity in QTL mapping has been descriptive. The experiments required for validation of estimates of QTL number, effect, and interaction are just coming to fruition.

Larson et al. (1996), Romagosa et al. (1996), Spaner et al. (1999) and Zhu et al. (1999) have conducted marker-assisted selection experiments to verify QTLs for agronomic traits in barley. Han et al. (1997) and Marquez-Cedillo et al. (in press) have conducted similar experiments for malting quality traits. In all cases, marker-assisted selection was effective for some, but not all QTLs. For stripe rust, we have successfully introgressed resistance QTL alleles into a susceptible genotype (Toojinda et al. 1998). The limited population sizes used in many of the reported QTL detection experiments may have led to underestimation of QTL number, overestimation of QTL effects, and a

failure to quantify QTL interactions (Beavis, 1998; Jansen and Stam, 1994; Kaeppler, 1997; Melchinger et al. 1998; Utz et al., in press; Visscher et al, 1997; Zeng, 1994).

Mapping and deployment of stripe rust resistance genes in barley

Four qualitative resistance genes, *Yr1* - *Yr4*, were described by Lehmann et al. (1975). Of these genes, only the *Yr4* locus has been mapped, and it is on the short arm of chromosome 5 (1H) (vonWettstein-Knowles, 1992). We recently mapped a qualitative resistance gene to the long arm of chromosome 1 (7H) in CI10587 (Hayes et al., 1999), but the identity of this gene relative to the *Yr1* - *Yr3* genes remains to be established. We mapped resistance QTLs on chromosomes 4 (4H) and 7 (5H) in Calicuchima-sib (Cali-sib), an ICARDA/CIMMYT germplasm line (Chen et al.1994; Hayes et al. 1996c). We also mapped a major adult plant stripe rust resistance QTL on the short arm of chromosome 5 (1H) in the ICARDA/CIMMYT-derived variety Shyri and smaller-effect QTLs on chromosomes 2 (2H), 3 (3H), and 6 (6H) (Toojinda et al., 2000). At the level of resolution afforded by the available maps, the chromosome 5 (1H) QTL coincides with the position of the *Yr4* locus. *Yr4* is reported to confer resistance to race 23 (von Wettstein-Knowles, 1992) while the virulence spectrum in the Americas is described in terms of race 24 and its variants (Chen et al., 1995b).

Thomas et al. (1995) also mapped an adult plant resistance QTL in the same region in the variety Blenheim and hypothesized that it was an effect of an allele at the *Yr4* locus. We mapped a

QTL to the same region on chromosome 5 (1H) in the winter six-row variety Kold and a resistance QTL on chromosome 7 (5H) (at the same position as the chromosome 7 (5H) QTL in Cali-sib), in the CIMMYT/ICARDA spring two-row germplasm CMB643 (Hayes et al., 1999). These stripe rust resistance mapping efforts are summarized in the accompanying Table 1.

Deployment of resistance genes has involved marker-assisted selection in various germplasm advanced strategies—backcrossing in the case of the six-row variety “Tango” (Toojinda et al., 1998)—and, more recently, pyramiding. Pyramiding efforts, focused on two-row barley, are summarized in the accompanying Figure 1. The first step in construction of resistance gene pyramids involved positioning the resistance QTL alleles from Shyri and Cali-sib in a malting quality background contributed by Harrington and Galena. These resistance QTL allele pyramid lines constitute the “BCD” population. The acronym has local athletic allusions and stands for “Beavers conquer Ducks”. This germplasm has been extensively phenotyped, and its allelic structure at the target stripe rust resistance QTL is currently being defined (Castro et al., 2000).

The second step in the construction of the resistance gene pyramids involved adding a qualitative resistance gene, contributed by CI10587. Because CI10587 is agronomically disadvantaged, the qualitative resistance gene was transferred to Baronesse, the leading feed variety in the Pacific Northwest of the U.S. The quantitative/qualitative resistance gene pyramids are referred to as the “Ajo, Sal, Bu, and Ops”

Table 1. Summary of OSU/ICARDA/CIMMYT collaborative disease resistance mapping and germplasm enhancement projects.†

Two-row populations. Phase I	
Cross:	CB. Calicuchima-sib/Bowman (Yd2). AKA: 'BSR'
Parents:	Cali-sib: Stripe rust, leaf rust, scald Bowman (Yd2): Stress tolerance, BYDV
Population:	F1-derived doubled haploid. N = 94. Stripe rust, leaf rust, scald, BYDV
Mapped genes:	Stripe rust, leaf rust, scald, BYDV
Selections:	BSR45 (2-row) = Orca. Stripe rust, scald, BYDV BSR41 (6-row). Stripe rust, scald
References:	Chen et al., 1994; Hayes et al., 1996; Hayes et al., 2000
Comments:	Also mapped malting quality QTL Orca released in 1998 as a feed variety. Not recommended as a malting variety due to high protein and enzymes.
Cross:	SG. Shyri/Galena. AKA: 'D1'
Parents:	Shyri: Stripe rust, leaf rust, scald, net blotch, BYDV, FHB Galena: Malt quality, leaf rust, BYDV
Population:	F1-derived doubled haploid. N = 94. Stripe rust, leaf rust, scald, net blotch, BYDV
Mapped genes:	Stripe rust, leaf rust, BYDV
Selections:	D1-72: Stripe rust
References:	Toojinda et al., 2000
Comments:	Scald and net blotch mapping in progress
Cross:	CG. C110587/Galena. AKA: 'D3'
Parents:	C110587: Stripe rust, leaf rust, Russian wheat aphid Galena: Malt quality, leaf rust, BYDV
Population:	F1-derived doubled haploid. N = 94. Stripe rust, RWA
Mapped genes:	Stripe rust
Selections:	D3-6: Stripe rust, RWA
References:	In progress
Comments:	RWA mapping deferred until full map available
Cross:	DB. D3-6/Baronesse. AKA: D3-6/B
Parents:	D3-6: Stripe rust, RWA Baronesse: Yield
Population:	F1-derived doubled haploid. N = 100. Stripe rust, RWA
Mapped genes:	NA
Selections:	D3-6/B-23 Stripe rust, RWA D3-6/B-45 Stripe rust, RWA D3-6/B-61 Stripe rust, RWA
References:	NA
Comments:	C110587 is agronomically challenged. D3-6 was the most prepossessing line. We crossed it with Baronesse to improve agronomic type. Stripe rust and RWA resistance phenotypes were confirmed in the D3-6/B progeny.
Cross:	GA. Gobernadora/Azafran. AKA: Gobe x CMB643, Gobe
Parents:	Gobernadora: Fusarium Azafran: Fusarium, stripe rust, leaf rust
Population:	F1-derived doubled haploid. N = 144. Fusarium (I,II,III), stripe rust
Mapped genes:	Fusarium (I,II, III), stripe rust
Selections:	Gobe 24: Fusarium, stripe rust Gobe 96: Fusarium, stripe rust, scald
References:	Zhu et al., 1999b
Comments:	Stripe rust QTL not published. Maps to same position on chromosome 7 (5H) as QTL in Cali-sib.

Two-row populations: Phase II

Cross:	BCD. Orca/1*Harrington//D1-72 AKA: 'BCD'
Parents:	Orca: Stripe rust, scald, BYDV Harrington: Malting quality D1-72: Stripe rust
Population:	BC1-derived doubled haploid. N = 115. Stripe rust, scald, BYDV
Mapped genes:	Stripe rust
Selections:	BCD-12: Stripe rust, leaf rust, scald, BYDV BCD-47: Stripe rust, leaf rust, scald
References:	In progress
Comments:	Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri. BCD-47 is in regional testing and the AMBA pilot program.
Cross:	RECLA. AKA: Red Cebada Latina A complex cross involving: Gobe-24; Gobe-96; AF9216; Orca; Kredit; and Azafran
Parents:	Gobe-24: Fusarium Gobe-96: Fusarium, stripe rust, leaf rust AF9216: Leaf rust Orca: Stripe rust, scald, BYDV Kredit: Stripe rust, leaf rust Azafran: Fusarium, stripe rust, leaf rust
Population:	DH = 125
Mapped genes:	NA
Selections:	Lines advanced to breeding program
References:	http://www.css.orst.edu/recla/la_red.htm
Comments:	Objective of this population is to pyramid multiple resistance genes and to stimulate a Latin American Barely initiative. Parents selected for adaptation to various environments in Latin America.

Two-row populations: Phase III

Cross:	Bu. BCD-47//D3-6/B-23
Parents:	BCD-47: Stripe rust, leaf rust, scald D3-6/B-23: Stripe rust, RWA
Population:	F1-derived doubled haploid. N = 89. Stripe rust, scald, BYDV
Mapped genes:	In progress
Selections:	Lines advanced to breeding program
References:	NA
Comments:	Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to C110587.
Cross:	Sal. BCD-47//D3-6/B-45
Parents:	BCD-47: Stripe rust, leaf rust, scald D3-6/B-45: Stripe rust, RWA
Population:	F1-derived doubled haploid. N = 11. Stripe rust, scald, BYDV
Mapped genes:	In progress
Selections:	Lines advanced to breeding program
References:	NA
Comments:	Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to C110587.

Cross: **Ajo** BCD-47//D3-6/B-61
Parents: BCD-47: Stripe rust, leaf rust, scald
D3-6/B-61: Stripe rust, RWA
Population: F1-derived doubled haploid. N = 119. Stripe rust, scald, BYDV
Mapped genes: In progress
Selections: Lines advanced to breeding program
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to CI10587.

Cross: **Ops.** BCD-12//D3-6/B-61
Parents: BCD-47: Stripe rust, leaf rust, scald
D3-6/B-61: Stripe rust, RWA
Population: F1-derived doubled haploid. N = 108. Stripe rust, scald, BYDV
Mapped genes: In progress
Selections: Lines advanced to breeding program
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to CI10587.

Two-row populations: Phase IV

Cross: **Bub.** BCD-47//D3-6/B-23 F1//BCD-47
Parents: BCD-47: Stripe rust, leaf rust, scald
D3-6/B-23: Stripe rust, RWA
Population: SSD N = 130
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to CI10587.

Cross: **Buh.** BCD-47/D3-6/B-23, F1//He6890
Parents: BCD-47: Stripe rust, leaf rust, scald
D3-6/B-23: Stripe rust, RWA
He6890: Stripe rust, Czech malting barley
Population: SSD N = 160
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to CI10587 and the uncharacterized resistance in He6890.

Cross: **Opb.** BCD-12/D3-6/B-61, F1//BCD-47
Parents: BCD-12: Stripe rust, leaf rust, scald, BYDV
D3-6/B-61: Stripe rust, RWA
BCD-47: Stripe rust, leaf rust, scald
Population: SSD N = 149
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to CI10587.

- Cross:** **Oph.** BCD-12/D3-6/B-61, F1///He6890
Parents: BCD-12: Stripe rust, leaf rust, scald, BYDV
D3-6/B-61: Stripe rust, RWA
He6890: Stripe rust, Czech malting barley
SSD N = 130
Population:
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to C110587 C110587 and the uncharacterized resistance in He6890.
- Cross:** **Ajb.** BCD-47/D3-6/B-61, F1///BCD47
Parents: BCD-47: Stripe rust, leaf rust, scald
D3-6/B-61: Stripe rust, RWA
BCD-47: Stripe rust, leaf rust, scald
SSD N = 149
Population:
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to C110587.
- Cross:** **Ajh.** BCD-47/D3-6/B61, F1///He6890
Parents: BCD-47: Stripe rust, lLeaf rust, scald
D3-6/B-61: Stripe rust, RWA
He6890: Stripe rust, Czech malting barley
SSD N = 169
Population:
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to C110587 and the uncharacterized resistance in He6890.
- Cross:** **Sah.** BCD-47/D3-6/B-45, F1///He6890
Parents: BCD-47: Stripe rust, leaf rust, scald
D3-6/B-45: Stripe rust, RWA
He6890: Stripe rust, Czech malting barley
SSD N = 94
Population:
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to pyramid stripe rust resistance QTL alleles tracing to Cali-sib and Shyri with the single gene tracing to C110587 and the uncharacterized resistance in He6890.

Two-row populations: Phase V

Cross: **BAR12.** BCD-12/Baronesse
Parents: BCD12: Stripe rust, leaf rust, scald, BYDV
 Baronesse: Yield
Population: In progress. Target n = 500 single seed descent
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to optimize estimates of resistance gene effects and measure resistance gene interactions.

Cross: **BAR47.** BCD-47/Baronesse
Parents: BCD47: Stripe rust, leaf rust, scald
 Baronesse: Yield
Population: In progress. Target n = 500 doubled haploids
Mapped genes: NA
Selections: NA
References: NA
Comments: Objective of this population is to optimize estimates of resistance gene effects and measure resistance gene interactions.

† **Cross:** Abbreviation in bold corresponds to Figure.
Parents: Parents contribute favorable alleles for phenotypes listed.
Population: Population assayed for phenotypes listed.
Mapped genes: Phenotypes measured in the population for which genetic determinants have been mapped.
Selections: Correspond to designation in Figure. Selections contribute favorable alleles for phenotypes listed.

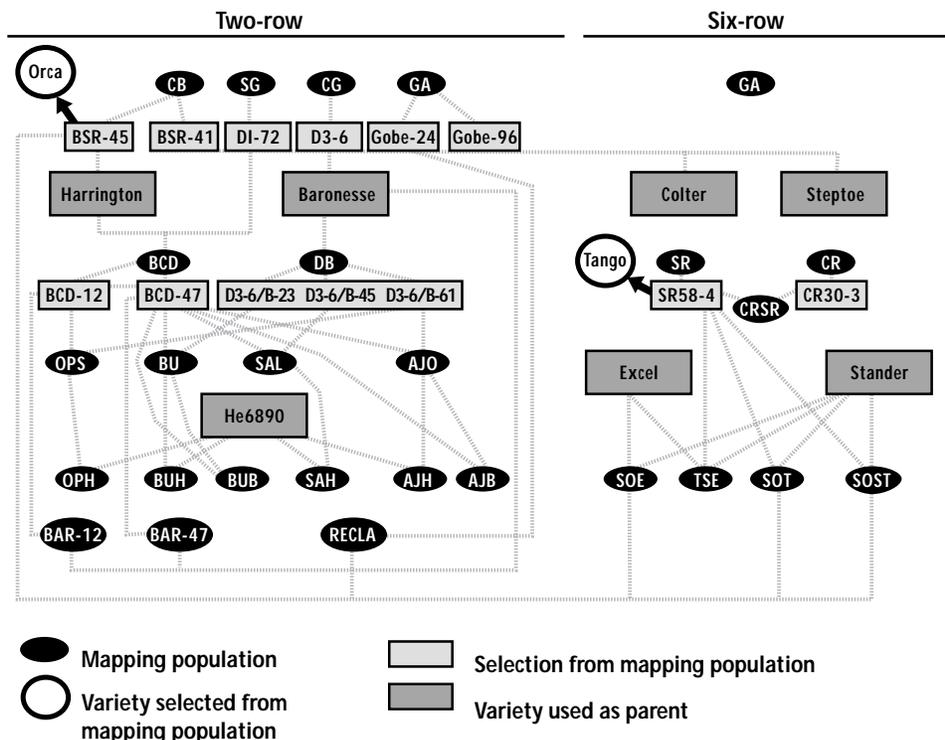


Figure 1. Construction of resistance gene pyramids in two- and six-row barley using marker-assisted selection.

germplasm. These germplasm descriptors have gastronomic allusions; the germplasm itself has been extensively phenotyped. Genotyping is in progress.

The third step in pyramid construction has involved He6890, an agronomically attractive Czech selection with uncharacterized stripe rust resistance. Our stripe rust resistance breeding effort in six-row barley is not as advanced as our effort in two-row barley. As shown in the accompanying Figure, the six-row effort is currently directed deploying resistance QTL alleles, tracing to Cali-sib, in a Midwestern malting quality background.

Conclusions

In summary, the ICARDA/CIMMYT program has been very successful in accumulating resistance to multiple diseases in single genotypes. Although this review has focused on stripe rust, this germplasm is also rich in genes conferring resistance to a range of diseases including barley yellow dwarf, leaf rust, net blotch, scald, and spot blotch. This accumulation of disease resistance alleles has been accomplished based on phenotypic data alone, and this success is testimony to Dr. Hugo Vivar's sharp eye and powers of recollection, and to the dedication of his staff. The genotypic characterization of this germplasm should be of assistance to all participants.

Faced with a field nursery of agronomically promising germplasm, all of which is phenotypically resistant to diseases, knowledge regarding the genetic architecture of each germplasm accession can be invaluable in deciding which genotypes to advance as varieties, and which genotypes to use as parents in order to continue the allele accumulation process. Knowledge regarding the genetic architecture of exotic germplasm should increase its utility, ensuring a broader germplasm base and providing an impetus for germplasm conservation.

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Perspectives on Fusarium Head Blight Resistance in Barley

L. GILCHRIST¹

Global Importance and Distribution

Fusarium head blight (FHB), or scab, has economic impact in barley-producing areas all over the world. It reduces yield and affects quality due to the toxin it produces in the grain.

Asia

Among Asian countries, China has the most extensive scab-affected area in its barley growing regions. The disease occurs mainly in the lower Yangtze River Basin (100,000 ha), where the humidity is high. Scab has also appeared in the Heilongjiang Province in recent years (Sun et al., 1999). Scab may cause 20-50% yield losses in an epidemic year (Chen et al., 1991).

Barley is produced in four provinces of Korea (Chonbuk, Chonnam, Kyungbuk, and Kyunnam). The natural occurrence of fusarium mycotoxins was surveyed in 39 barley samples collected in those provinces. Five toxin compounds were detected: deoxynivalenol (DON), nivalenol (NIV), 4-acetylnivalenol (4-ANIV), 3-acetyldeoxynivalenol (3-DON), 4,15-diacetylnivalenol (4,15-DANIV), and zearalenone (ZEA). DON, NIV, and ZEA were the major contaminants (Kim, 1993).

North America

The USA and Canada. Since 1993, scab and vomitoxins have affected barley crops in the Northern Great Plains, including North Dakota, Minnesota, and Canada. From 1993 to 1997, North Dakota farmers suffered cumulative losses due to scab and vomitoxin estimated at US\$200 million (Anonymous, 1999).

Surveys of US regional crops have shown DON to be the primary mycotoxin associated with infected barley, although ZEA and other fusarium toxins have also been detected. It is estimated that 67 and 82% of the malting barley crop have been contaminated with DON (0.6-60mg/g) during 1993 (Schwartz, 1995).

Scab is very common in the highlands of central Mexico (the states of Mexico, Tlaxcala, Hidalgo, Puebla, and Jalisco). In a first survey conducted in the states of Puebla and Tlaxcala in 1999, 33 samples of malting barley were collected and the following *Fusarium* species detected: *F. semitectum*, *F. avenaceum*, *F. sabucinum*, *F. poae*, *F. graminearum*, *F. moniliforme*, *F. dimerum*, *F. equiseti*, and *F. subglutinans*. Of these, *F. sabucinum* and *F. dimerum* are not reported in the literature. However, in this study, these two species were isolated from grains, and from root and stem lesions in blotter and germination tests (Gutierrez, 2000).

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South America

Fusarium head blight is very important in the Southern Cone and the Andean Region, including the Ecuadorian and Peruvian highlands, where barley is used for feed and food purposes. In Uruguay, Brazil, and Argentina, barley is used mainly for malting and feed (Vivar, 1997). Incipient damage has been detected in southern Chile (regions IX and X) around lakes and rivers, and wherever maize has been introduced into the crop rotation for silage production (Mellado, 1999; von Baer, 1999, pers. comm.).

In Uruguay barley was evaluated over a period of four years (1993-97) for the natural occurrence of fusarium toxins. DON and Fumonisin B1 (FB1) were predominant. Barley was second to wheat in severity of infection. ZEA levels were considerable only in barley and mixed feed, drawing attention to its use for animal consumption and its potential deleterious estrogenic effects. Locally, barley feed is used extensively in animal nutrition. The 1993-94 crop season was the first in the last decade to show severe fusarium damage (Piñeiro and Silva, 1997).

A comparative analysis of *F. graminearum* isolates from Canada, USA, Mexico, Argentina, and Uruguay confirmed that they belong to chemotype IB. There is a regional relationship between the origin of *F. graminearum* and the production of 3 or 15 Ac DON as the major isomer (Piñeiro et al., 1996).

Causal Agents

Most countries recorded *F. graminearum* as the most important scab causing pathogen. However, a broad range of *Fusarium* species was reported to cause the disease (Table 1).

Table 1. Pathogenic *Fusarium* species reported on barley by country.

<i>Fusarium</i> species	Country†				
	Canada	USA	Mexico	Japan	Poland
<i>F. graminearum</i>	+	+	+	+	+
<i>F. culmorum</i>	+	+		+	+
<i>F. avenaceum</i>	+	+	+	+	+
<i>F. poae</i>	+	+	+		+
<i>F. sporotrichum</i>	+	+		+	+
<i>F. equiseti</i>	+	+	+	+	+
<i>F. acuminatum</i>	+	+		+	
<i>F. moniliforme</i>		+	+		
<i>F. semitectum</i>	+		+		
<i>F. nivale</i>				+	
<i>F. tricinctum</i>					+

† Gordon, 1959; Clear et al., 1996. Mihuta-Grimm, 1989; Salas et al., 1999. Gutierrez, 2000. Koizumi et al., 1995; Takeda et al., 1995. Perkowski et al., 1996.

FHB symptoms and interaction with other pathogens

The first symptom of scab infection is a small, water-soaked, somewhat brownish or pinkish brown spot at the base or in the middle of the glumes or on the rachis. Water-soaking and discoloration spread in all directions from the point of infection and can cover the grain partially or completely. If conditions are favorable, spread is evident in adjacent grains. If the tissue takes on a brown color, the symptoms may be confused with those produced by other pathogens such as *Bipolaris sorokiniana*, *Rhynchosporium secalis*, *Pyrenophora teres*, and *Alternaria* spp., and saprophytes such as *Dicccum* spp. Field diagnoses can be difficult to make, and a laboratory analysis is recommended in specific cases.

If plants are affected by other diseases like the rusts and BYDV before inoculation, inoculation is not

recommended, nor should the germplasm even be evaluated. Resistant germplasm may show a susceptible reaction and produce very brownish, shriveled grain. One clear example of this is the interaction observed during the last two years in Toluca, Mexico (no stripe rust in 1998 and a heavy stripe rust epidemic in 1999), where scab resistant advanced lines from a breeding program in Minnesota, which are very susceptible to *Puccinia striiformis* f. sp. *hordei* (race 24), showed a resistant reaction to fusarium in 1998 and a susceptible one in 1999.

FHB resistance mechanisms

Understanding the different types of resistance mechanisms and their epidemiological role is necessary for breeding head scab resistance. Key points are to use specific inoculation, screening, and evaluation methods for each resistance mechanism. This is important when working with a virulent pathogen population under extreme environmental conditions. As Parry et al., (1995) reported, "Differences in resistance between cultivars could be masked, with even the most resistant cultivars becoming infected under extreme conditions."

The model proposed by Schroeder and Christensen for wheat in 1963, which suggested the existence of two components of resistance (Type I and Type II), has been accepted by most authors. Type I resistance operates against initial infection and Type II against the spread of the pathogen within the host. Type I and Type II resistances varied independently among cultivars.

Today there is evidence that this model is also applicable to barley. Field data presented in Table 2 for Gobernadora doubled haploid populations and QTLs confirmed that Type I resistance is independent of Type II, with Type II having the largest QTL detected near the centromeric region of chromosome 2 (Zhu et al., 1999).

Table 2. Relative ranking of five doubled haploid lines (out of 100) and both parents for resistance to head blight (*Fusarium graminearum*) against fungal penetration (Type I) and hyphae spread (Type II), or a combination of both. Atizapan Station, Toluca, Mexico, 1996.

Cultivar	Type I	Type II
DH-83	5	71
DH-96	8	2
DH-98	9	87
DH-52	50	1
DH-89	98	25
Gobernadora (Zhenmai 1)	1	6
CMB 643 (Azafran)	45	5

Snijder and Perkowski (1990) found a negative correlation in wheat between head blight and incubation period, given that the more resistant genotypes had longer incubation periods. This correlation makes the incubation period a potentially useful criterion for selecting for resistance.

Type III resistance was described and proved to occur in wheat by a team of Canadian researchers (Miller and Arnison, 1986). It was proposed that resistant cultivars possessed a factor that enabled them either to prevent DON synthesis or to promote its degradation. The resistant cultivar Frontana was able to degrade 18% radioactive (C14) DON into two breakdown products, while the

susceptible cultivar Casavant degraded only 5%. Snijder and Krechting (1992), also working in wheat, indicated that DON played a part in pathogenicity, as they found it to be transported from fusarium infected chaff to the young kernel, which the pathogen later colonized. The phytotoxic effect of DON can be explained by the fact that it is a very potent inhibitor of eukaryotic protein synthesis (Wang and Miller, 1988). In a resistant wheat line, DON transport was inhibited, so colonization was reduced.

To lower DON concentration in the grain is the aim of most barley breeders. Steffenson (1998) mentions that there is a fairly positive correlation ($r=0.64$; $P=0.0001$) between FHB incidence and DON concentration in barley grain.

Skadhauge et al., (1997) discovered a proanthocyanidin-free mutant of barley that shows extreme resistance to fusarium *in vitro*. This resistance is due to the accumulation of dihydroquercetin, a potent inhibitor of fusarium growth.

Type IV resistance was described as tolerance to high DON concentrations by Wang and Miller in 1988. They reported that some cultivars could tolerate high mycotoxin concentrations with no negative effects on growth. Ma et al., (1999) conducted a preliminary study where they injected pure DON solution (100 ppm) 10 cm below the spike in three different varieties [Sumai 3 (R), Norm (S), and Pioneer 2375(MS)]. They found that tolerance to DON may be independent of Type II reaction since Pioneer 2375 (MS type II) had lower average dry kernel weight. This type of research has not been done in barley.

Influence of toxins on pathogenesis and virulence factors

Inoculum composition. Today we know that different *F. graminearum* isolates have different toxigenic capacities. For this reason, it is absolutely necessary that when inoculating for different types of scab resistance, both inoculum composition and the conditions and timing of inoculation be controlled. For example, the phytotoxicity of some trichothecenes has been demonstrated (Miller and Arnison, 1986; Wong et al., 1994). A USDA team created a genetically modified strain of *F. graminearum* GzT40 that does not produce trichothecene because it does not carry gene Tri 5-, which confers virulence (Proctor et al., 1995). Eudes et al., (1998) inoculated 17 wheat varieties with specific inocula of GzT40 and of its wild parent Gz3639 in a controlled environment (Figure 1). The strain possessing toxigenic capacity (Gz3639) was virulent and produced host damage depending on the resistance present in each variety. This suggests it is essential that the composition of the inoculum used as well as the conditions during inoculation be controlled within the same year and across years, to avoid variation and incorrect interpretations.

A barley example is presented in Table 3, where two varieties [Robust (MS) and Chevron (MR)] were inoculated with nine different fusarium isolates (Evans et al., 1996). The reaction of the two varieties differed depending on the inoculated strain.

Inoculum concentration. According to studies carried out in Toluca during 1980-82 (G. Bekele, pers. comm.) on wheat, no differences were detected using 30,000-70,000 spores per ml. This

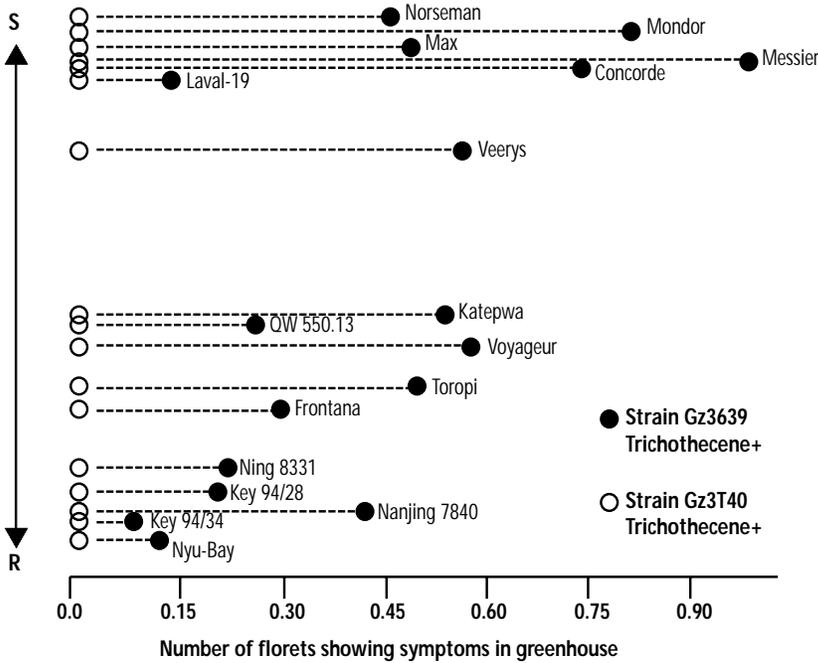


Figure 1. Virulence of the *Fusarium graminearum* genetically modified GzT40 strain (*Tri 5-gene*) and the Gz3639 wild strain (*Tri 5-gene*) on 17 wheat cultivars. Source: Eudes et al. (1998).

Table 3. Number of infected spikelets on barley varieties Robust (moderately susceptible) and Chevron (moderately resistant).

Isolate	Robust		Chevron	
	Rep I	Rep II	Rep I	Rep II
2B-2A1	17	25	12	26
3A-2A1	3	11	0	1
3A-4A1	18	23	21	16
4B-5A2	10	1	15	3
5C-3A2	4	6	4	4
6A-2A1	13	3	6	5
Butte 86-ADA-11	24	11	5	12
M66-ADA-B1-A1	3	1	13	1
94RO/STE 4	9	17	25	21
Control	0	0	0	0

Source: Evans et al. (1996).

was confirmed in barley at the same location during the 1996 cycle. Based on this information, a suspension of 50,000 spores per ml is recommended for use in inoculation.

Inoculation methods for evaluating different types of FHB resistance

At CIMMYT different plots are used to screen for each FHB resistance type.

Type I. Wheat inoculation is carried out in the evening with a hand sprayer (Bekele, 1984). A spore suspension is sprayed on 15 spikes that were selected and marked at the initial anthesis growth stage. After 10-15 days spikes are evaluated for penetration points. The precise timing of the evaluation will depend on the reaction of resistant and susceptible checks to the environment that particular year.

Barley spikes can be infected by *Fusarium* species as soon as they emerge from the flag leaf sheath, and they remain susceptible throughout the

grain filling period. Spike growth stage of resistant cultivars at inoculation affects the amount of damage observed in a particular year (Tables 4 and 5).

Type II. Inoculation using the cotton method (Bekele, 1984) is done on 20 barley spikes at the initial anthesis growth stage. Spikes are evaluated 25-30 days after inoculation. As with Type I resistance, the precise timing of the evaluation will depend on the reaction of resistant and susceptible checks to the environment that particular year.

Types III and IV. A small plot (two 50-cm rows) is sprayed with a spore suspension when 50% of barley spikes have reached anthesis. A similar plot is sprayed with

fungicide (Folicur plus) every 10 days. At harvest, a 200-g sample is used for DON analysis (Type III), and a comparison of 300-kernel weight is done between the two plots (Type IV).

Resistance Sources from All Over the World

Nearly 40 barley genotypes have been identified as having partial FHB resistance and low DON accumulation. The genetic distance between genotypes was calculated separately using morphological, agronomic, FHB severity and DON content, and foliar disease data. Five clusters were

Table 4. Inoculation using two methods (spray and cotton) at three spike growth stages (pre-anthesis, initial anthesis, and post-anthesis) and the damage produced in barley varieties. Atizapan, Toluca, 1998.

Variety	Spike growth stage [†]	Spray method	Cotton method
Shyri	PRA	6.3 (3.6-11.0)ai	39.6 (31-48.2) k
	IA	4.9 (2.6-9.1)af	26.1 (19.6-33.7)hk
	PA	1.7 (0.6-4.9)ac	21.6 (15.7-29.0) fj
Arupo/K8755// Mora (Selec 2)	PRA	7.9 (4.7-13.3)cl	23.1 (16.3-31.8)fk
	IA	6.6 (3.8-11.3)ak	11.7 (7.2-18.4)cg
	PA	9.0 (5.6-14.2)dm	3.9 (1.7-8.8)ac
Gob/Humai 10	PRA	11.1 (7.3-16.5)fo	29.1 (22.1-37.4)jik
	IA	9.5 (6.1-14.6)dm	0.3 (6.3-16.3)cf
	PA	7.0 (4.1-11.6)ck	19.1 (13.4-26.5)ej
Azafran	PRA	5.1 (2.7-9.4)ah	23.5 (16.3-32.6)gk
	IA	1.4 (0.4-4.3)ac	32.3 (25.0-40.6)jkl
	PA	1.0 (0.3-3.9)a	28.0 (21.2-36.0)ik
LP/Shyri (Selec 1)	PRA	3.5 (1.6-7.2)ad	28.3 (21.7-35.9)jkl
	IA	7.4 (4.1-13.0)bl	28.7 (21.9-36.7)jkl
	PA	10.2 (6.6-15.5)dn	22.1 (16.0-29.8) fj

† PRA = Pre-anthesis; IA = Initial anthesis; PA = Post anthesis.

Table 5. Inoculation using two methods (spray and cotton) at three spike growth stages (pre-anthesis, initial anthesis, and post-anthesis) and the damage produced in barley cultivars. Atizapan, Toluca, 1999.

Variety	Spike growth stage [†]	Spray method	Cotton method
Shyri	PRA	5.0 (2.9-8.2) cl	9.3 (5.9-14.2) ag
	IA	7.0 (4.4-10.9) gn	10.5 (6.9-15.7) ag
	PA	2.4 (1.2-4.7) bg	4.4 (2.4-8.0) a
Arupo/K8755// Mora (Selec 2)	PRA	6.1 (3.8-9.6) fm	34.3 (27.8-41.6) ln
	IA	3.7 (2.1-6.5) bk	38.7 (32.1-45.7) n
	PA	0.4 (0.1-2.2) b	24.5 (18.9-31.2) lm
Gob/Humai 10	PRA	1.6 (0.6-4.3) bf	14.7 (10.5-20.3) ei
	IA	1.2 (0.4-3.2) be	6.5 (3.8-10.9) ae
	PA	2.3 (1.2-4.7) bg	4.3 (2.3-7.7) a
Azafran	PRA	5.4 (3.2-8.9) cl	8.8 (5.7-13.2) af
	IA	9.1 (6.1-13.3) jn	8.1 (5.1-12.8) af
	PA	9.4 (6.7-13.2) ln	4.8 (2.7-8.3) ab
LP/Shyri (Selec 1)	PRA	3.2 (1.6-6.0) bf	11.8 (8.0-17.1) bh
	IA	2.8 (1.4-5.7) bh	8.3 (5.2-13.1) af
	PA	3.2 (1.6-6.0) bi	7.0 (4.3-11.2) ae

† PRA = Pre-anthesis; IA = Initial anthesis; PA = Post anthesis.

identified (Figure 2), and three genotypes did not fall into any cluster. Most two-rowed Chinese barley genotypes are grouped in cluster 1, plus Svanhals, developed in Sweden. Chevron and Chevron –derived genotype Ciho 16128 (comprising cluster 5) are the most resistant to FHB and have the lowest DON concentrations.

Most FHB-resistant, two-rowed barley genotypes are susceptible to wheat stem rust, net blotch, and powdery mildew, and all are susceptible to leaf rust. All FHB-resistant, six- rowed genotypes are susceptible to leaf rust, wheat stem rust (pathotype Pgt-QCC), and powdery mildew (Urrea et al., 1999).

Information presented in Figure 2 is useful for breeding programs, since it allows the identification of FHB-resistant cultivars whose resistance base might be different, thereby increasing the probability of accumulating levels of resistance when gene action for FHB resistance is additive. However, susceptibility to leaf blotches and rust diseases continues to be a problem that could prevent the use of these genotypes in some regions.

QTLs for FHB Resistance

Mapping QTLs for FHB resistance genes was carried out in doubled haploid populations. In Gobernadora x CMB 643 (Azafran), a QTL for type II

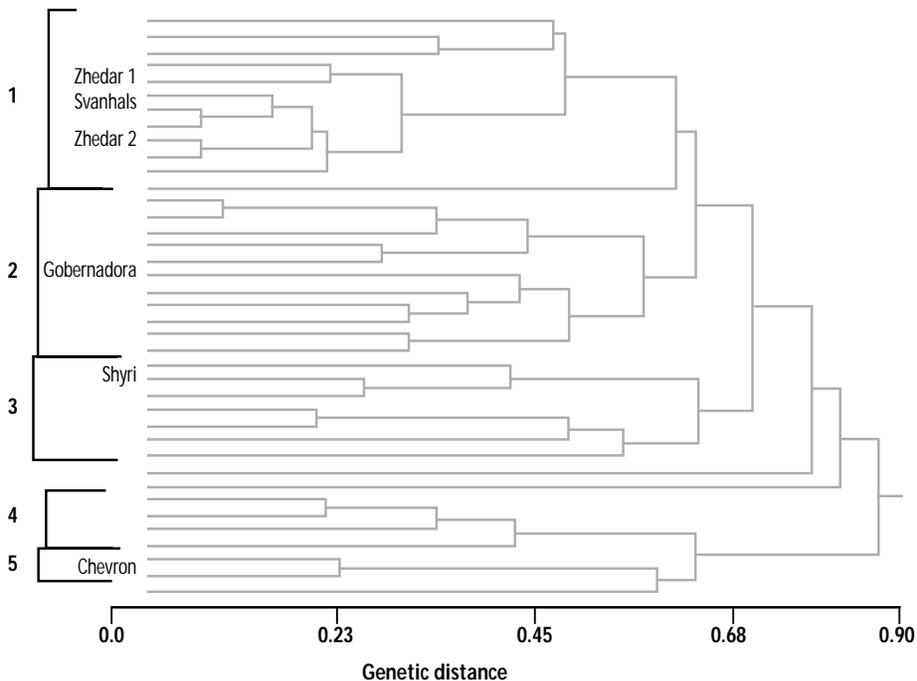


Figure 2. Dendrogram based on cluster analysis of the distance among 39 barley genotypes.
Source: Conci et al. (1999).

resistance was found in chromosome 2 (Zhu et al., 1999). Chevron and Chevron progeny have been used extensively in breeding for resistance to FHB and kernel discoloration (KD) in a Minnesota breeding program (Canci et al., 1999). Four of the QTLs associated with FHB in chromosomes 1, 2, and 4 were also associated with KD (De la Peña et al., 1999).

Evaluating Barley Varieties and Advanced Lines for FHB Resistance

In the last five years, barley varieties and advanced lines used in the CIMMYT/ICARDA Barley Program were evaluated for FHB resistance at Toluca, Mexico. The resulting data are presented in Tables 6, 7, and 8.

Conclusions

Fusarium graminearum resistance is difficult to evaluate under field conditions. Although producing symptoms is easy, it is essential to control the precise composition of the inoculum used, the method of application, and the circumstances in which inoculation is performed. Otherwise, great variability may be introduced that would make it practically impossible to interpret the observed results correctly.

The basis of FHB resistance is complex and not well understood today. The environment interacts with the host plant and the pathogen to produce a resistant reaction. The extent of the infected area in the host plant is the product of these three components (Figure 3). However, evaluating FHB reaction in the field is not enough for establishing resistance; kernel

Table 6. Characterization of fusarium head blight resistance (Types I, II, III, and IV) in nine barley cultivars.

Variety or line	Type I % infec.		Type II % infec.		Type III DON ppm.		Type IV % losses		Grain (1-5)†
	98	99	98	99	98	99	98	99	
	Shyri	4.9	7.1	26.1	10.6	3.9	16.0	5.0	
Atahualpa 92(H)	16.8	5.0	21.7	8.9	0.0	0.99	10.1	8.1	2
Arupo/K8755 //Mora (selec. 2)	6.6	11.7	3.7	38.7	1.0	2.9	13.6	4.0	2
Gob/Humai10 B89.3.1 (early)	9.5	1.2	0.3	6.5	NA‡	2.2	4.6	27.6	4
Gob/Humai10 B89.3.2 (late)	5.8	5.7	27.1	20.4	1.6	1.1	3.9	15.4	3
Chevron	5.1	4.0	11.8	26.6	1.1	2.1	2.06	40.6	4
Gobernadora	5.3	9.2	20.7	14.6	1.9	12.0	13.4	28.5	2
Azafran	1.4	9.1	32.3	8.1	NA	120.0	11.3	6.28	3
LP/Shyri (Selec. 2)	12.5	2.1	23.4	10.6	NA	2.8	15.6	14.1	4

† 1=good grain; 5=poor grain. ‡ NA=Not available.

weight losses and toxin (DON) concentration in the grain are also important.

Mesterhazy (1997) made an important and appropriate statement regarding this issue: “Without reliable methods nothing can be said about the level of resistance, factors of resistance, about their inheritance and about an appropriate selection procedure. Without adequate methods we will not have appropriate information, or what is even worse, incorrect information will be the result.”

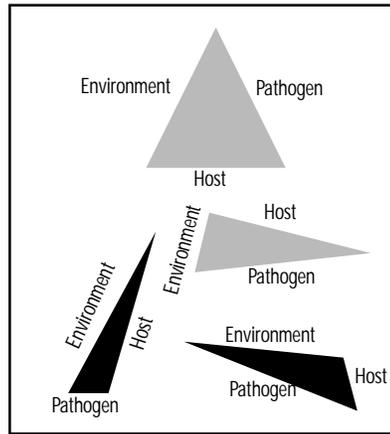


Figure 3. Area of the disease.

Table 7. Characterization of fusarium head blight resistance (Types I, II, III, and IV) in a group of advanced hull-less barley lines.

Variety or line†	Type I % infec.		Type II % infec.		Type III DON ppm.		Type IV % losses		Grain (1-5)‡
	98	99	98	99	98	99	98	99	
Tocte// Gob/Humai 10/3/Atah 92/Aleli CBSS96M00766D-B-2M-3Y	1.9	5.3	14.8	7.2	2.8	3.6	12.4	6.4	1
Tocte// Gob/Humai 10/3/Atah 92/Aleli CBSS96M00766D-B-2M-4Y	2.2	3.7	14.4	15.3	1.1	12.0	10.2	3.0	2
Penco// Chevron-Bar CBSS96Y00341s-1Y-1M-10Y	10.2	1.5	38.1	20.5	NA	9.2	2.0	6.1	1
Penco// Chevron-Bar CBSS96Y00341s-1Y-1M-16Y	–	2.6	16.9	13.2	NA	11.0	4.5	4.1	1
Ataco/Bermejo// Higo/3/CLNB/80.5138// Gloria-Bar/Copal/4/ Chevron-Bar CBSS96Y00653T-A-14Y-1M-16Y	0.9	5.1	18.7	9.3	NA	14.0	0.3	3.8	1
Ataco/Bermejo// Higo/3/CLNB/80.5138// Gloria-Bar/Copal/4/ Chevron-Bar CBSS96Y00653T-A-14Y-1M-17Y	0.9	3.7	7.3	5.1	2.3	5.3	4.7	3.9	2
Chamico/ Tocte// Congona CBSS95Y00352T-D-12Y-2Y-0M	6.8	4.6	53.1	12.6	2.0	34.0	14.8	8.8	3

† Resistance sources are in boldface. ‡ 1=good grain; 5=poor grain.

Table 8. Characterization of fusarium head blight resistance (Types I, II, III, and IV) in seven advanced covered barley lines.

Variety or line†	Type I % infec		Type II % infec		Type III DON ppm		Type IV % losses		Grain (1-5)‡
	98	99	98	99	98	99	98	99	
Gob/Humai 10/3/ Mpyt169.1Y/Laurel/ Olmo/4/ Canela CBSS95M00804T-F-1M-7Y-0M	1.0	9.7	16.3	9.4		38.0	12.9	4.3	1
Escoba/Moradilla/3/ Zhedar#2/NDB112// Mora CMB94A.595-A-2M-6Y-2M-3Y-0M	3.8	11.0	7.2	8.4		24.0	7.1	3.3	2
GOB 24 DH (Gobernadora/Azafran)	4.0	14.6	6.0	8.0		27.0	13.0	5.9	2
GOB 45 DH	5.7	19.9	6.5	19.0		26.0	2.2	15.4	2
GOB 96 DH	9.7	25.0	7.4	33.1		3.6	4.3	4.9	1
Mosquera (Fingal/F784.70/4/ Zhedar/ 3Hlla/ Gob/Hlla/Shyri)	7.3	18.2	8.2	18.1		27.0	16.3	16.4	1
Zhedar #1/Shyri // Olmo CMB93.572-A-4Y-1Y-2M-1Y-0M	2.5	23.4	5.2	11.7		31.0	7.2	4.5	2

† Resistance sources in boldface. ‡ 1=good grain; 5=poor grain.

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Resistance and/or Tolerance to BYDV: Recent Advances in Barley at CIMMYT

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Barley yellow dwarf is the most important viral disease of barley. It is caused by a complex of luteoviruses known as barley yellow dwarf viruses (BYDVs). They are transmitted in a persistent manner by aphids to all common cereals. The five serotypes PAV, MAV, RPV, RMV, and SGV differ in severity, PAV being in general the most severe and most common, followed by MAV and RPV. RMV and SGV are only found occasionally. Control of BYDV can be achieved through elimination of its insect vector by insecticide application, cultural practices, and the use of tolerant and/or resistant materials.

According to Cooper and Jones (1983), tolerance in a plant is associated with an attenuation of symptoms without reduction in virus multiplication. In a resistant plant, virus multiplication or spread is affected. The term resistance has been broadly used to refer to any type of interaction to the disease development; most field resistance reported in the literature was assessed through symptom expression in the field and is therefore tolerance. In this paper, we will differentiate the two mechanisms and refer to true resistance only when virus

concentration is affected. In some oats (Jedlinski et al., 1977) and barleys (Skaria et al., 1985, Ranieri et al., 1993), resistance has been associated with field tolerance.

The most common and effective source of tolerance to BYD in barley was identified in Ethiopian barleys (Schaller et al., 1963) and found to be associated to the major semidominant gene *Yd2* (Rasmusson and Schaller, 1959). As many authors report, this gene is associated with field tolerance and with reduction in virus concentration (resistance). It is located on chromosome 3 (Schaller et al., 1964) close to the centromere (Collins et al., 1996). It is associated with reduction in virus concentration with BYDV-PAV and MAV but not with BYDV-RPV (Banks et al., 1992; Skaria et al., 1985; Herrera and Plumb, 1989).

Recently, Paltridge et al. (1998) developed an assay based on a protein showing allelic variation that correlates with *Yd2*. Later, Ford et al. (1998) developed a PCR marker for the *Yd2*-associated allele of *Ylp* using allele-specific primer pair. These molecular markers are useful for identifying the presence of *Yd2* in barley cultivars.

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The CIMMYT-ICARDA Barley Program for Latin America holds a number of lines with high field tolerance to BYDV isolates PAV, MAV and RPV combined with resistance to foliar diseases. The objectives of the present study were to evaluate the type of resistance present in the CIMMYT barley lines, distinguish between true resistance and tolerance, and measure to what extent the gene *Yd2* was present in those lines. Some of the results presented here are still preliminary.

Materials and Methods

Virus isolates and inoculation

The BYDV PAV-Mex, MAV-Mex, and RPV-Mex isolates used in the experiment were collected in Mexico in 1993 and maintained in CIMMYT's greenhouse through transmission by aphids. The aphid species *Rhopalosiphum padi* (PAV and RPV) and *Metopolophium dirhodum* (MAV) were used for transmission.

Inoculation was performed in the greenhouse by infesting five 6-day old seedlings per line with 10 viruliferous aphids that had acquired BYDV by feeding on infected plants for 48 hours. Seedlings were isolated from each other by transparent plastic tubes. After a two-day inoculation period, aphids were killed with the insecticide Metasystox (Bayer). In all experiments, one or two plants were kept free of aphids to serve as the non-inoculated controls.

In the field, plants were infested at the three-leaf stage with aphids reared in the greenhouse on BYDV infected plants. To avoid contamination, the non-inoculated treatments were sprayed soon after emergence with the insecticide Metasystox; in the inoculated treatments,

approximately 10 aphids were deposited at the base of each seedling using a calibrated mechanical dispenser. Aphid movement was controlled through fortnightly insecticide application (Metasystox) on the entire trial, starting one week after inoculation.

Plant materials

Ninety-one lines from the CIMMYT-ICARDA Barley Program were tested in this study. These lines were selected because they showed field tolerance to one of the BYDV isolates tested. The controls were non-*Yd2* lines Atlas 57, Centinela, and Calicuchima "S" and *Yd2* lines Atlas 68, Sutter, Sutter /2*Numar.

Field evaluation of BYDV tolerance and/or resistance

Lines were tested under BYDV infection in Toluca and El Batan, Mexico, during the summers of 1997, 1998, and 1999. For each line, four 1-m double plots (20 plants) were sown adjacent to each other, to constitute the four treatments: non-inoculated, inoculated with PAV, MAV, or RPV.

Symptoms were evaluated at flowering using a 1-9 scale as described by Berstchinger (1994), 1 being the most tolerant and 9 the most susceptible. The three parameters measured were intensity of yellowing, dwarfism, and reduction in tillering. In 1999, biomass was evaluated instead of tillering because it seems to better represent the effect of BYD on plant growth.

Evaluation of resistance to BYDV using ELISA

Flag leaf-1 and roots were collected seven days after inoculation to evaluate virus titers by ELISA (enzyme-linked immunosorbent assay). Double Antibody

Sandwich ELISA (DAS ELISA) was used as described in Ayala et al. (2000). The coating polyclonal antibodies against the US PAV, MAV, or RPV isolates were provided by K. Perry (Purdue University). Optical density (OD) was measured at 410 nm using an MR 700 Microplate reader (Dynatech Laboratories). A plant was considered infected when the OD obtained in ELISA was higher than twice the one obtained with the non-infected control. The higher the OD, the higher the concentration and the lower the resistance.

Detection of the presence of *Yd2* using molecular markers

The marker pair (Ylp PCR MF and Ylp PCR MR) described by Ford et al. (1998) was used in this study following the procedure described by the same authors. A 311 base pair product was obtained after PCR of DNA from both *Yd2* and non-*Yd2* plants. After digestion of the PCR product with the restriction enzyme *Nla*III, two products of 253 and 58 base pairs were obtained with the DNA from plants with the *Yd2* gene, while a single product of 311 base pairs was obtained with plants not containing *Yd2*. The products were visualized on a 3% agarose gel.

Results

As expected, a single product of 311bp was obtained with the non-*Yd2* lines (Atlas 57, Centinela and Calicuchima "S") while a 253bp product could be visualized with the *Yd2* lines (Atlas 68, Sutter, Sutter / 2*Numar) (data not shown), confirming the usefulness of the marker for the detection of *Yd2*. The *Yd2*-associated allele (*Ylp*) was detected in 82% of the CIMMYT barleys tested (73).

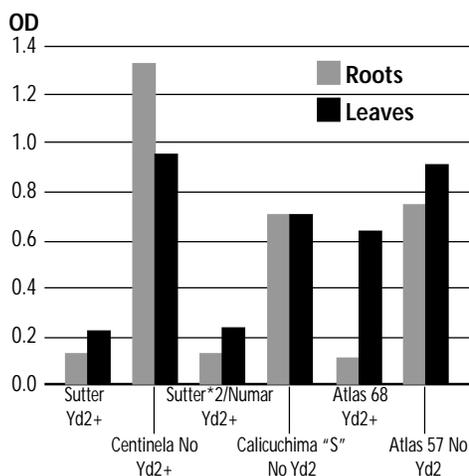


Figure 1. Virus titers in roots and leaves of barley genotypes seven days after infection with BYDV-PAV.

Effect of *Yd2* on BYDV concentration

In the lines with *Yd2*, Sutter and Sutter / 2*Numar, virus titers were low in both roots and leaves (Figure 1). However, in Atlas 68, the virus titers reached moderate levels in the leaves. According to this, differentiation between *Yd2* and non-*Yd2* lines is easier by comparing virus titers in roots.

As shown in Table 1, virus titers were lower when the *Yd2*-associated allele was present than when it was absent, confirming that *Yd2* reduces multiplication of BYDV-PAV in barley.

Table 1. Mean virus titers in ELISA measured in leaves and roots of barley genotypes with and without *Yd2*, seven days after inoculation with BYDV-PAV.

<i>Yd2</i> -associated allele	Number of lines	Average OD	
		Leaves	Roots
Present	46	0.244	0.195
Absent	16	0.682	0.998

Effect of *Yd2* on field tolerance to BYDV

Most lines carrying the *Yd2*-associated allele had a tolerant or intermediate response to BYDV-PAV and MAV (Table 2). In contrast, most lines not carrying the gene were sensitive to infection by the two BYDV serotypes. The response to BYDV-RPV did not differ greatly between lines with and without the *Yd2*-associated allele.

Table 2. Response of CIMMYT barleys to BYDV field infection.

BYDV response	<i>Yd2</i>			Non- <i>Yd2</i>		
	PAV	MAV	RPV	PAV	MAV	RPV
Tolerant	57.8†	69.6	34.8	0.0	6.7	14.3
Intermediate	22.2	13.0	30.4	7.1	6.7	28.6
Sensitive	20.0	17.4	34.8	92.9	86.7	57.1

† Percentage of lines in each category according to the presence of *Yd2* as identified by the marker pair.

Table 3. Severity of BYDV response after artificial inoculation in El Batán, Mexico. †

<i>Yd2</i> associated allele	PAV			MAV			RPV		
	Y	D	B	Y	D	B	Y	D	B
Present	1.2	0.7	0.7	1.0	0.5	0.4	1.3	0.8	0.9
Absent	3.3	3.8	5.1	1.8	1.4	1.3	2.3	0.4	0.8

† Y= yellowing, D= dwarfing, B= reduction in biomass, measured on a 1-9 scale.

Symptoms were more severe in the absence of the *Yd2*-associated allele after BYDV PAV and MAV infection (Table 3). The difference was not so marked with BYDV-RPV infection.

Germplasm with field tolerance to BYDV

Table 4 shows a list of lines with field tolerance to BYDV. The following lines combined field tolerance to the three BYDVs tested as well as resistance to BYDV-PAV: LIMON, BOLDO/MJA, GUAYABA, JACAPA, CANTUA, and CLAVO.

Table 4. Selected CIMMYT barley lines with combined tolerance to the three BYDV Mexican isolates PAV, MAV, and RPV.

Name	Selection history
PETUNIA 1	CMB93.855-G-15Y-1M-0Y
CHAMICO/TOCTE//CONGONA	CBSS95Y00352T-H-7Y-2M-0Y
DUMARI	CMB93.755-C-1Y-1M-0Y
FAIQUE	CMB93.885-A-7Y-2M-1Y-0M
MADRE SELVA	CMB92A.790-H-4M-1Y-2B-0Y
LIMON	CMB92A.655-B-7M-1Y-1B-0Y
INCIENSO	CMB92A.1264-P-1M-1Y-1B-0Y
PALTON	CMB92.391-B-3Y-1M-1Y-1B-0Y
LIMON	CMB92A.655-C-9M-1Y-1B-0Y
ARAVISCO	CMB91A.629-B-0M-1Y-1M-1Y-2B-0Y
BOLDO/MJA	CMB91A.60-1M-1Y-1M-1Y-0B
TINCTORIA	CMB91A.210-23M-2Y-1M-1Y-2B-0Y
BOLDO/MJA	CMB91A.60-1M-1Y-3M-1Y-1B-0Y
GRAMALOTE	CMB92A.893-A-1M-2Y-1B-0Y
CANTUA	CMB92.546-X-2Y-4M-0Y
CANTUA	CMB92.546-I-1Y-1M-0Y
CANTUA	CMB92.546-I-1Y-4M-0Y
PAPELILLO	CMB92A.920-A-2M-1Y-0B
CALENDULA	CMB93.947-D-5Y-1M-0Y
INCIENSO	CMB92A.1264-A-3M-1Y-0M
JACINTO	CMB92.490-E-6Y-1M-1Y-2B-0Y
MJA/BRB2//QUINA	CMB93.987-C-1Y-1M-0Y
BBSC/CONGONA	CBSS95M00144S-3M-3Y-0M
ABN-B/KC-B//RAISA/3/ALELI	CMB92.338-A-6Y-1M-2Y-1B-0Y
QUINN/ALOE//CARDO	CMB92A.1439-I-6M-1Y-1B-0Y
COMINO/3/MATICO/JET//SHYRI/4/ALELI	CMB92.494-C-2Y-1M-2Y-1B-0Y
ATACO/COMINO//ALELI	CMB92.367-E-7Y-1M-1Y-1B-0Y
ATACO/COMINO//ALELI	CMB92.367-Q-6Y-1M-0Y
CANTUA	CMB92.546-I-1Y-5M-1Y-1B-0Y

Conclusions

The CIMMYT-ICARDA Barley Program for Latin America holds germplasm with combined field tolerance to the three major BYDVs (PAV, MAV and RPV) and to other major diseases. Furthermore, some of the material is truly resistant (low virus concentration) at least to BYDV-PAV. Most lines possess the gene *Yd2*; however, it is still possible that other genes are present, because of the extremely high level of tolerance in some lines. This work is still in progress and will be completed by studying true resistance to MAV and RPV.

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Two Decades of Barley Breeding

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Plant breeders seeking to improve a particular trait, such as disease resistance, search for sources of that trait in collections stored in germplasm banks. Most germplasm bank accessions have been screened for different traits and the results published. The ICARDA/CIMMYT barley breeding program relies on this type of information for identifying cultivars to be used as parents in crosses.

The Colombian National Research Institute (Anonymous, 1984) screened 8,650 barley accessions from the world collection against race 24 of stripe rust caused by *Puccinia striiformis* f.sp. *hordei*, a disease recently introduced to the Andean Region of South America. In 1982, accessions found to be stripe rust resistant in Colombia were brought to Mexico, where they were used to launch extensive breeding efforts aimed at developing germplasm resistant to the disease. Stripe rust has since become endemic in the Andean Region.

In California, Webster et al. (1980) found 273 entries with no symptoms of pathogen virulence of *Rhynchosporium secalis* present in the state. The extensive effort devoted to finding scald resistant cultivars among 18,000 accessions from the world barley collection in the US saved us from screening a large number

of accessions in Mexico. Our work was to field test 273 resistant accessions against races of *R. secalis* present in central Mexico. Most accessions were still resistant to US and Mexican races, and only 13% proved to be scald susceptible and discarded.

In 1983, accessions from the world barley collection were screened against leaf rust at the CIANO Experiment Station located in the Yaqui Valley in northwestern Mexico. Of 11,087 accessions screened against races 8, 19, and 30 of *P. hordei*, only 285 were found to be resistant to leaf rust (Vivar, 1986).

In Japan, Takeda and Heta (1989) screened 5,000 barley accessions against *Fusarium graminearum* and found 23 entries with good levels of scab resistance.

Breeders and pathologists who have to work with resistant accessions from the world collection invariably find that resistance is in poor agronomic plant types. Therefore, they have to devote a lot of effort to transferring disease resistance genes into improved cultivars.

Multiple disease resistance

Researchers at Montana State University advanced the concept of introducing multiple disease resistance into barley using male-sterile plants to facilitate

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recurrent selection. The project required distributing several barley populations among cooperators around the world. The objective was achieved after several years of work. Plants with multiple disease resistance became available, but barley breeders were reluctant to use resistant plants in crosses with their elite cultivars because of their poor agronomic plant type.

In the 1970s, Colombian breeders carried out activities aimed at developing stripe rust resistant varieties. Their efforts culminated in the release of Quibenras, a variety characterized by its outstanding stripe rust resistance. Despite this resistance, Quibenras had a short life in farmers' fields due to its susceptibility to leaf rust, which was predominant where Quibenras was sown. Farmers who had been using expensive chemical treatments to control stripe rust were forced to continue using fungicides (Bayleton) to control leaf rust.

Both experiences pointed to the need for cultivars with multiple disease resistance to provide stability in barley production. Incorporating multiple disease resistance into high yielding barley germplasm thus became the main objective of the ICARDA/CIMMYT barley program in 1982.

This breeding strategy was implemented in several steps. The first template was achieved by crossing scald and leaf rust resistant cultivars. Once advanced lines with resistance to both diseases were obtained, they were used as parents to form a second template, to which stripe rust resistance was added. Over 18 years of breeding (two generations per year) and a total of 36 generations, we have built templates that contain resistance to BYD, net blotch, spot blotch, and head

scab, in addition to scald and the three rusts (leaf, stripe, and stem).

Several important factors were involved in the incorporation of multiple disease resistance, but a few were essential to the success of the project. First, the use of large numbers of crosses (single and top) made it possible to combine resistance to several diseases in a single plant. Second, large segregating populations were screened in the field at several experiment stations. The Toluca Station was used for screening scald, stripe rust, and head scab; the CIANO Station for leaf and stem rust, El Batán for leaf rust, and Poza Rica for spot blotch. The use of the stations helped us produce reliable artificial epidemics and effective plant selection. Third, international testing in cooperation with national program scientists spread over five continents allowed us to identify plants resistant to pathogenic races not present in Mexico.

The ability to create artificial large-scale epidemics was key for selecting against scald and the three rusts. With diseases such as barley yellow dwarf and head scab, developing artificial large-scale epidemics is cumbersome and expensive; for this reason, the identification of potentially resistant plants was done by visual selection in advanced segregating populations at the Toluca Station. The preliminary identification of potentially resistant plants required more detailed screening by CIMMYT plant pathologists Drs. L. Gilchrist and M. Henry, both of whom presented their results at this meeting.

Artificial inoculation at times creates friction between plant pathologists and plant breeders. A frequent complaint is that too much inoculum was applied, that the resistance reactions of the host

plants are blurred or that too little inoculum was applied and no differences are visible. The high rainfall (800 to 1000 mm) recorded during the growing cycle at the Toluca Station favors the development of severe epidemics of scald, stripe rust, and head scab. Since in the barley program disease epidemics develop without direct intervention by plant pathologists, complaints about the intensity of epidemics are not uncommon.

In our experience, the use of one resistant parent in a single cross does not provide an adequate level of resistance under conditions favoring disease development. This is true not only with scald, but also rust and head scab. For this reason, three-way crosses were adopted as a tool in the crossing program. All F1s are now top-crossed to a third parent so as to combine at least two resistance sources. In recent years, as the program matured, a combination of three different sources of resistance was attempted for scald, head scab, and stripe rust. For example, advanced lines (F7) from the cross Svanhals/M.Selva//Azafran/Gob24 were screened for head scab resistance with good results. Svanhals, Azafran, and Gobernadora are three sources of head scab resistance.

The combined use of three parents resistant to the same disease has resulted in cultivars showing durable resistance. The variety Shyri (released in Ecuador) was the result of crossing three stripe rust resistance sources (Motan, Kober, and Teran). Shyri has remained resistant to stripe rust since 1989 in the US, Germany, and several Latin American countries. The variety Calicuchima was selected from the cross L.B.Iran/Una 8271//Gloria/Come, all of whose

parents are resistant to scald. Calicuchima has remained scald resistant for more than 10 years in Mexico.

Partial resistance

Studies of leaf rust virulence conducted in Israel and Ecuador by Brodny and Rivadeneira (1996) showed that the virulence present in both countries was capable of rendering all major genes reported in the literature non effective. This suggests that the resistance achieved by pyramiding major gene combinations may not be durable.

Parlevliet and Kuiper (1977), working with leaf rust in barley in The Netherlands, proposed a partial resistance mechanism based on minor genes that provide varying levels of resistance against all virulences of the pathogen. Parlevliet developed barley cultivars (Vada, LP) in which several minor resistance genes were accumulated; they showed better and more durable resistance against the disease.

The use in the ICARDA/CIMMYT barley program of the sources of partial resistance to leaf rust developed by Parlevliet was hampered by the presence of other diseases, such as scald, net blotch, spot blotch, and BYD. Parental material developed in Holland was excellent for leaf rust but very poor for leaf blotches and BYD.

The program continues to breed for partial resistance against leaf rust. Several barley lines carrying good levels of partial resistance to leaf rust, stripe rust, and scald have been identified. Our aim is to combine minor and major genes to achieve durable resistance.

Head scab

In 1984 breeding for scab resistance by the ICARDA/CIMMYT barley program was not popular with ICARDA management, who argued that the disease was not considered a problem in the West Asia and North Africa (WANA) region, and that there were no reports of its presence in the Americas. I learned that breeding against a disease that is not considered a problem is a difficult enterprise. Despite early doubts about the project, breeding for scab resistance became one of the more successful initiatives of the ICARDA/CIMMYT barley program in Mexico.

Two national programs released three scab resistant varieties in two countries; Ecuador (Atahualpa and Shyri) and China (Zhenmai-1). The variety Zhenmai-1 is sown on more than 100,000 hectares in several Chinese provinces located in the lower basin of the Yangtze River, and is showing yield increases of 20-25% over the Chinese barley varieties it replaced. Dr. He Zhonghu, CIMMYT representative in China, estimates that 40% of one million hectares sown to barley in China is planted to varieties introduced from Mexico or derived from crosses between local varieties and Mexican introductions.

Head scab caused by *Fusarium graminearum* has become a major disease in North America. Since 1993, the epidemic has produced more economic losses than any other disease in US history. In areas such as the upper Midwest (the Dakotas, Minnesota), head scab has become a major problem, and extensive efforts are being invested in breeding and pathology research.

Over the last decade, fusarium toxin production in the grain has become a major concern due to the implications for human health. Toxins such as deoxynivalenol (DON) are present in grain infected with *Fusarium graminearum*. In the developed world, toxin levels in grain to be used as food or feed must not exceed 2 ppm; however, in third world countries that have no regulations on toxin content in the grain, the problem becomes more severe, especially in areas such as the Andean Region, where barley is a staple food.

Clear et al. (1997) reported that hull-less barley showed a 59% DON reduction in grain toxin content immediately after being threshed in the field. Apparently the toxin is attached to the lemma and palea, which are removed during threshing. Clear and colleagues concluded that hull-less barley may be a good option for farmers in areas affected by head scab.

After several years of testing under artificial inoculation at the Toluca Station, several hull-less, six- and two-rowed barley lines were identified as being resistant to head scab. Seed of these lines will be distributed to national programs for testing in areas prone to the disease.

Molecular markers were used to map scab resistance in the doubled haploid population Gobernadora/Azafran in cooperation with Oregon State University (Zhu et al., 1999). The doubled haploid lines were phenotyped for scab resistance in Mexico, North Dakota, and China. Type II resistance (to spread of the fungus within the spike) was mapped near the centromeric region of chromosome 2 with the largest R2 value. Lateral florets, a morphological

trait, was mapped in the same region, opening the possibilities for indirect selection for head scab resistance.

In Alberta, Canada, Dr. J. Helm selected 40 two-rowed advanced lines from a cross developed in a disease-free environment. The selected lines had never been exposed to scab during their development. The main selection objective was to find spikes lacking lateral florets. The 40 lines were sent to Mexico for screening under artificial inoculation during the summer of 2000.

Results of the screening done by Gilchrist are shown in Table 1. Five lines were found to possess Type I and II resistance (to primary infection and fungal spread, respectively). The percentage (12.5%) of head scab resistant lines selected provides a clear indication of the effectiveness of indirect head scab selection in two-rowed barley populations.

Table 1. Percent of grain infected with *Fusarium graminearum* in five two-rowed lines introduced from Alberta, Canada, and screened at the Toluca Experiment Station, Mexico, summer of 2000.

Line	Resistance (%)	
	Type I	Type II
H93123-003	5.35	5.39
H93126-002	7.23	6.23
H93125	6.88	6.83
H93123-008	5.98	7.00
H93126-011	4.44	8.30
Susceptible check (Gob-89)	13.43	27.78

Ten years of cooperation with Oregon State University has led to a deeper understanding of the genetic basis of resistance to several diseases. Stripe rust, present in Mexico and northwest USA,

has received more attention. Two Ecuadorian varieties, Shyri and Calicuchima, have been extensively studied. They carry different quantitative trait loci (QTL) for stripe rust resistance. Shyri's stripe rust resistance was mapped on chromosome 5, while Calicuchima has resistance QTLs on chromosomes 4 and 7 (Toojinda et al., 2000). The diversity of the resistance found in these two Ecuadorian varieties provides additional insurance against a sudden change in pathogen virulence.

The ICARDA/CIMMYT Barley Program has been successful in developing high yielding barley with multiple disease resistance. Record yields (11 t/ha) produced by introductions from Mexico have been reported by breeders in Chile and Peru. However, when these high yields (obtained in test plots) are compared to the national average barley yield in Peru (1.1 t/ha), it is evident that the gap between experimental and farmers' yields has increased.

In 1999, farmers were provided with fertilizer, barley seed, and herbicides as part of a project conducted in Saraguro, located in the highlands of southern Ecuador. The average yield obtained by farmers growing the new variety Shyri-2000 was 3 t/ha, compared to 7 t/ha harvested with the same variety in large seed increase plots at the Chuquipata Experiment Station. This shows that closing the gap entails more than just breeding activities.

I have described the successes of the ICARDA/CIMMYT barley program, but I have not mentioned its weaknesses. To be fair, I would call your attention to a problem exhibited by germplasm developed by the program: its

susceptibility to loose smut (*Ustilago nuda*), a disease easily controlled by applying fungicides such as Vitavax. Unfortunately, subsistence farmers with limited economic resources, who keep their grain for use as seed the following year, could decide to skip the seed treatment and run into a potentially serious production problem.

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