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Review Article

Breeding Barley for Yellow Rust Resistance: Conventional and Molecular Pursuits

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Abstract

***Puccinia striiformis* f. sp. *hordei* (*Psh*) causing barley stripe or yellow rust is a serious threat to barley production. The most cost-effective and long-lasting strategy for combating this disease is using genetic resistance. Stripe rust resistant genes providing both qualitative and quantitative resistances to *Psh* have been documented and resistance breeding has adeptly developed numerous barley varieties employing both conventional and molecular methods. The creation of high-yielding, disease-resistant cultivars necessitates the identification of resistant sources, comprehension of genetic inheritance, and subsequent hybridization and selection. A significant challenge in barley breeding remains the pyramiding of multiple disease resistance genes into high-yielding germplasm. Historically, barley breeders utilized fundamental genetic approaches, mutation breeding, and hybridization. To hasten resistance breeding advanced methodologies such as doubled haploidy and molecular techniques are also adopted.**

Keywords: *Hordeum vulgare, Puccinia striiformis* f. sp. *Hordei*, genetic resources, genetics, QTL*s*

Introduction

Barley (*Hordeum vulgare* L.) an ancient crop, cultivated in more than 100 countries, is the fourth most important cereal crop in the world. Overall, global barley production hovers around 150 million tonnes. The major barley producing areas are Russian Federation, Australia, Europe, North America, Canada UK, and Asia (Harwood, 2019). Barley has diversified uses as livestock feed, food stuffs (sattu/roasted barley, porridge, and chapattis) and religious purpose, besides it is an important industrial crop used for production of malt for brewing and distillation, and in health drinks. The crop is short seasoned, early maturing and is cultivated mostly in neglected areas with low and unstable productivity, where wheat can't be grown, thereby, known as "poor men's crop" (Verma *et al.*, 2010). Barley has several health benefits and has good nutritional and even medicinal properties due to high content of bioactive compounds such as -d-glucan, tocotrienols, tocopherols, and phenolics such as benzoic and cinnamic acid derivatives, quinones, proanthocyanidins, chalcones, flavonols, and flavones (Holtekjolen *et al.*, 2008).

Climate change, have potential to bring about severe epidemics and affects the agricultural productions adversely thereby, threatening the global food security. According to Oerke (2006), plant diseases and pests could passively deprive humanity for over 50% of the attainable yield. Barley productivity, throughout the world, is affected by economically different diseases; however, yellow rust or stripe rust caused by *Puccinia striiformis* f. sp. *hordei* (*Psh*) severely decreases grain quality and yield thereby curtailing barley production. The most economical and long-lasting component of yellow rust management is genetic resistance which focus on using resistant cultivars, especially those with durable resistance, to combat yellow rust disease.

Resistance breeding has been very successful in the past, and, many resistant or tolerant barley varieties/lines/genetic stocks have been developed using conventional and molecular breeding approaches (Nelson *et al.*, 2018; Patial *et al.*, 2021; Patial *et al.*, 2023). Marker Assisted Selection (MAS) have been widely used in commercial barley breeding programmes for effective and efficient incorporation of yellow resistance genes derived from adapted and non-adapted germplasm. Moderately dense genetic maps have been constructed (Graner *et al.*, 1991; Kleinhofs *et al.*, 1993) which has led to an increased accuracy of locating QTL to specific chromosomal regions. The identification and introgression of yellow rust resistance genes through MAS leading to pyramiding of different resistance genes into barley cultivars have sustained the disease resistance mechanism. This review provides an insight on conventional and molecular breeding aspects for yellow rust resistance breeding which will be an important for breeders working in barley improvement programme.

Genetic Resources and Pre-breeding for yellow rust resistance in barley

Genetic diversity is an important source of *de novo* beneficial alleles and is paramount for the progress towards a breeding goal. Many of the barley cultivars grown today shares related pedigrees with one-parental inheritance in certain cases (Martin *et al.,* 1991; Wych and Rasmusson, 1983; Sjakste *et al.*, 2003). For example, most of the present-day high yielding Turkish barley cultivars had developed from '*Tokak*' landrace (Kilian *et al.*, 2006).

Due to ongoing erosion of resistance genes in cultivation, discovery of novel sources of resistance is crucial. For barley yellow rust resistance, Mathur and Siradhana (1990) screened 700 cultivars under natural epiphytotic of *Puccinia striiformis* of which only fifteen were disease free and 11 showed traces of the rust and considered as resistant. Chen *et al.* (1995) reported barley genotypes - Hor 2926, Hor 1428, Hor 3209, Abyssinian 14, BBA 2890, Stauffers Obersulzer, Grannelose Zweizeilige to be resistant to all barley yellow rust races. Nover and Scholz (1969), Toojinda *et al.* (2000) and Castro *et al.* (2003) established a number of transiently designated genes for stripe rust resistance from barley germplasm. Gyawali *et al.* (2018) in 336 barley genotypes revealed eleven (AM-14, AM-177, AM-37, AM-120, AM-300, AM-36, AM-103, AM-189, AM-291, AM-275 and AM-274) resistant sources of stripe rust against six races and 89 Adult Plant Resistance (APR) sources for barley yellow rust race. Verma *et al.* (2018) revealed twelve resistant genotypes (ARAMIR/COSSACK, C8806, Astrix, C9430, Gold, CLE 202, Gull, Isaria, Piroline, Lechtaler, Stirling and Trumpf) at adult-plant and seedling stages. Patial *et al.* (2023) studied genetic variability of yellow rust resistant advanced lines and identified potential lines for yield enhancement. The characterization of sources of yellow rust resistance and the exploitation of the allelic richness of landraces, wild progenitors, and breeding lines in barley has facilitated their utilization in breeding programs.

Gene, genetics and QTLs for yellow rust resistance

In barley, stripe rust can be caused by either the rust that infects wheat (*Puccinia. striiformis* f. sp. *tritici*, *Pst*) or barley (*P. striiformis* f.sp. *hordei, Psh*). Barley stripe rust/yellow rust can cause yield losses of up to 70% under epidemic conditions (Dubin and Stubbs, 1986) and occurs in cool and wet climate. Resistance is classed as seedling and adult-plant resistance (APR). Seedling resistance is also known as 'all stage resistance'. This type of resistance is expressed at all growth stages, is often race specific and is conferred by a single 'major effect'. On the other hand, APR is expressed in adult plants, controlled by multiple 'minor effect' genes and often polygenic in nature. Because specific genes that provide high levels of resistance are easy to detect and manipulate, most barley breeders have used them in their breeding programs. However, these genes deployment is vulnerable to the changes in the pathogen following boom-bust cycle. Therefore, gene pyramiding involving deployment of multiple seedling resistance genes has been highly effective and widely adopted.

Murty (1942) conducted the first study on the genetics of barley stripe rust resistance in India who reported that stripe rust resistance in the American cultivar "Alpha" was conditioned by two dominant genes. During 1960's a number of studies on the genetics of stripe rust resistance in barley genotypes were done in India and abroad (Bakshi and Bahl, 1965; Luthra, 1966; Nover and Scholz, 1969). In barley, both dominant and recessive genes are reported for stripe rust resistance by different workers (Table 1). Verma *et al.* (2016) reported adult plant and seedling resistance to stripe rust from ICARDA high-input barley breeding programme and identified 12 sources against five *Psh* races in India. Patial *et al.* (2016, 2018) studied the gene action studies for grain yield and its component traits in yellow rust advanced breeding lines and reported the potential yield traits and genotypes for yield enhancement.

Table 1: Genetics of stripe rust resistance in barley

S. No.	Reference	Reported work on genetics of stripe rust resistance
1.	Johnson (1968)	Single dominant gene in 'Cambrinus' cultivar.
2.	Nover and Scholz (1969)	Single recessive gene to European race *24* in 'BBA 2890'
3.	Upadhyay and Prakash (1977)	Susceptibility of 'Bigo' to an Indian race *24* and resistance in 'Abyssinian 14' controlled by one or more genes.
4.	Dayani and Bakshi (1978)	Resistance to field infection (predominate races *24* and *G*) in 'EB1556' controlled by two recessive genes.
5.	Luthra and Chopra (1990)	Cultivar 'Himani' carries the dominant gene *Rps*1 giving resistance to race *G*.
6.	Chen and Line (1999)	Genotypes BBA 809, Bigo, BBA 2890, Hiproly, and Grannelose Zweizeilige have one recessive gene; Emir, PI I5, PI 548734, 548708, PI 548747, Varunda have two recessive genes; Stauffers Obersulzer and Abyssinian 14 have one dominant gene and one recessive gene against *Psh*-1.
7.	Chen and Line (2003)	Reported 26 different genes for stripe rust resistance.
8.	Pahalawatta and Chen (2005)	One dominant (*RpstS1)* and one recessive (r*pstS2)* gene in cultivar 'Steptoe' for resistance to races *PST*-41 and *PST*-45.
9.	Yan and Chen (2007)	In BA 2890 F_8 RILs confirmed the presence of a single recessive gene for resistance.
10.	Prakash and Verma (2009)	The inheritance pattern of yellow rust resistance in four lines (RD 2552, RD 2503, RD 2508 and RD 2634) indicating that resistance was governed by single dominant gene.
11.	Derevnina *et al.* (2015)	Single resistant gene in 16 Australian and three exotic barley lines.

Although a fairly small number of resistance genes have been formally assigned for barley stripe rust compared to other barley rusts, reports of both qualitative and quantitative resistance to *Psh* have well documented (Nover and Scholz, 1969; Chen and Line, 1999; Dracatos *et al.*, 2019). In the past 40 years, different genes, either catalogued or transiently, have been identified as dominant (*Rps*) and recessive (*rps*) (Clare *et al.*, 2016). However, with the appearance of new races of pathogen, many of these genes have lost the resistance.

Initially, during 1960s, Johnson (1968) and Nover and Scholz (1969) reported *rps1 (yr*1), *rps2 (yr*2), *rps3 (yr*3) and *Rps4 (Yr4)* genes in differential barley sets used in India. In addition to this Luthra *et al.* (1991) reported *Rps4 (Yr*4) in EB410; *rps5 (yr*5) in EB438 and EB 1556; *rps6 (yr*6) in EB 1556; *rps7 (yr*7), *rps8 (yr*8) and *rps9 (yr*9) in EB1626; *rps1 (yr*1), *Rps10 (Yr*10) and *Rps11 (Yr*11) in Abyssinian 14; and *rps3 (yr*3), *Rps12 (Yr*12) and *Rps13 (Yr*13) in I5 for effective resistance against Indian *Psh* races. Johnson (1968) reported a gene in cultivars 'Europa', 'Cambrinus', and 'Deba Abed' that were designated as R*ps4 (Yr*4). Chen and Line (1999) described three recessive genes (*rps1*, *rps*2 and *rps*3) providing resistance to the stripe rust pathogen. Later, they described a fourth gene, *rps*4 in their studies. Kumar *et al.* (2012), did not observe virulence on genotypes 'Helis Franken' (with resistance genes *Rps*4 (*Yr*4 and, *rpsHF*), 'Emir' (*rpsEm1* and *rpsEm2*) and 'Asterix' (*Rps4* (*Yr4*), rpsAst) and reported these genes to be effective for providing resistance to yellow rust. Safavi *et al.* (2013) in Iran reported no virulence on 12 barley differential sets with race-specific resistance genes *rpsEm1*, *rpsEm2*, *rpsHF*, *Rps4*, *rpsVa1*, *rpsVa2* and *rpsAst* and considered these genes as effective genes which can be used in pyramiding with race-non-specific resistance genes to attaining durable and highly effective resistance to stripe rust. The resistance genes *rps2*, *Rps1b*, *Rps3*, and *rpsI5* were deemed ineffective as these genes demonstrated susceptible reaction and virulence. Clare *et al.* (2016) isolated the *RpsHOR1428-5H* locus present in cultivar 'HOR1428' in a 'Manchuria' genetic background and designate the locus as *Rps9*. The additive nature of *Rps9* suggests that the locus is a semi-dominant resistance gene, which contrasts with the observed recessive nature of *rpsHOR1428-1* and *rpsHOR1428-2* by Chen and Line (1999).

Several QTLs conferring resistance to stripe rust have been found. The first genetic study of barley stripe rust resistance was conducted in the United States by Chen *et al.* (1994) using a doubled haploid population that was developed by crossing a susceptible line (a backcross derivative of 'Bowman') with a resistant breeding line (LB1ran/ UNA8271/'Glora'/'Come'). Using molecular markers, they mapped two resistant QTL on chromosomes 5H and 4H. Castro *et al.* (2002) in 'Shyri × Galena' double haploid population reported two QTLs on chromosomes 4 and 5H conferring resistance to three *Psh* isolates (*Psh*-1, *Psh*-13 and *Psh*-14). In the doubled haploid population arising from a cross between 'Franklin' and 'Yerong'. Derevnina *et al.* (2015) reported genes that contribute to seedling resistance and mapped them to the long arms of chromosomes 5H and 7H, respectively. The temporary designations *Rpsp-hFranklin* and *Rpsp-hYerong* were applied to these genes. At the adult plant stage, three QTLs were identified in the same population; two were located in the same positions as *Rpsp-hYerong* and *Rpsp-hFranklin*, while the third was mapped to 5HS. Klos *et al.* (2016) highlighted QTL in 'Lenetah × Grannelose Zweizeilige' recombinant inbred line cross and reported a major seedling resistance QTL on chromosome 4H in cultivar 'Grannelose Zweizeilige'. Using *Psh* races from North America and Europe, Klos *et al.* (2016) and Dracatos *et al.* (2016) respectively reported QTL mapping of resistance at the seedling stage. Visioni *et al.* (2018) observed 18 QTL for resistance to barley stripe rust in adult plant stages and 45 QTL distributed over the seven barley chromosomes for seedlings resistance to five races. Vatter *et al.* (2018) used 5,715 informative SNPs to explore SNP-based nested association mapping in HEB-25. Twelve robust QTL were found to be associated with resistant and eight of these were deemed novel.

Table 2: QTLs conferring resistance to yellow rust in barley

QTLs	**Chromosome Location**	**Markers**	**Method**	**References**
QYr1H, QYr3H	1H, 3H	RFLP markers	Linkage Mapping	Toojinda *et al.*, 2000
QYr2H, QYr7H	2H, 7H	AFLP markers	Linkage Mapping	Castro *et al.*, 2003
QYr5H, QYr6H	5H, 6H	SSR markers	Linkage Mapping	Derevnina *et al.*, 2015
QYr1H, QYr3H, QYr7H	1H, 3H, 7H	SNP markers	GWAS	Vatter *et al.*, 2018
QYr2H, QYr5H	2H, 5H	SSR markers	GWAS	Verma *et al.*, 2018
QYr4H, QYr6H	4H, 6H	SNP markers	GWAS	Visioni *et al.*, 2018

Till date, seven *Rps* (Resistance to *Puccinia striiformis*) loci have undergone genetic mapping- *Rps*1 on chromosome 3H (Yan and Chen, 2007), *Rps*4 on chromosome 1H (Johnson 1968), *rps5 (rpsGZ)* on chromosome 4H (Klos *et al.*, 2016), *Rps*6 on chromosome 7HL, *Rps7* and *Rps8* on 1H and 4H, respectively (Bettgenhaeuser *et al.*, 2021); and *Rps9* on 5H (Clare *et al.*, 2016). Chen *et al.* (1994) identified two genes conferring resistance to the barley stripe rust in Mexico and South America germplasm against race *24*. These genes were mapped to the M arms of barley chromosomes 7 and 4 in a doubled haploid population using molecular markers and QTL mapping approach. Two additive effect QTL loci that confer resistance to *P. striiformis* f. sp. *hordei* in 'HOR1428' were mapped by Clare *et al.* (2016) which were located on chromosomes 3H and 5H. Li *et al.* (2016) using a high-density mapping population (>10,000 gametes) precisely mapped *Rps6* within a 0.14 cM region (~500 kb contig). An intermediate host resistance gene in barley, also thought to provide resistance against wheat stripe rust, '*Rps6*', was isolated, fine-mapped, and positioned to chromosome 7H by Dawson *et al.* (2016).

Breeding yellow rust resistant barley varieties

Sustainable control of pathogens is possible through the manipulation and deployment of resistance genes in cultivars, thereby providing in-built resistance with no extra cost and avoids the harmful effects of chemicals on environment. The development of high yielding cultivar with enhanced disease resistance is quite challenging which involves identification of resistant sources, understanding of the mode of genetic inheritance of the character, followed by hybridization and selection approach. Different breeding strategies have resulted in the development of several yellow-resistant barley varieties (Kumar *et al.*, 2012, Bishnoi *et al.*, 2022; Kumar *et al.*, 2020). A multitude of varieties, including BHS169, BH393, DL88, NDB1173, and VLB56 have been developed through hybridization and selection methods (Singh *et al.*, 2016). However, sometimes, exotic germplasm are also used for direct release of varieties, for example barley lines LSB2, Dolma, HBL113, BHS400, VLB118, and BHS380 received from ICARDA have been released directly for cultivation in Northern Hill Zone of India (Gangwar *et al.*, 2018). Pyramiding multiple disease resistance genes into high yielding germplasm remains a major challenge in barley breeding. Singh (2008) reported barley cultivars RD2508, RD2035, DWRUB52, RD2552 and RD2624 with multiple disease resistance in India and accessions BCU167 from the indigenous and BCU51, 26 and BCU127 from the exotic collection having multiple resistance (Yadav and Kumar, 1999). The previous, laborious, and time-consuming classical approaches were primarily used by barley breeders which involved simple genetics, selection, mutation breeding, and hybridization. Therefore, barley breeders turned to the more advanced and integrated molecular approaches in order to expedite resistant breeding (Harwood, 2019).

Doubled haploid breeding in barley for yellow rust resistance

Cultivated barley is an inbreeding species so superior lines which are homozygous and true breeding needs to be developed. This when achieved through conventional plant breeding techniques is time consuming (approximately 10 + years) (Patial *et al*, 2015; Patial *et al.,* 2021; Patial *et al.*, 2022). Therefore, the importance of haploid and doubled haploid (DH) techniques to speed the genetic gain in breeding programs as well as in basic and applied research cannot be overstated. For cultivated barley improvement programme, plant breeders have used *H. spontaneum* (Thomas *et al.*, 1987) and other wild species as a novel gene source but, the resultant hybrids are sterile or non-viable. Hence, transfer of important and novel traits through conventional approach becomes unrealistic. By applying DH technique, successful hybrid can be rescued and from the early breeding generations, genotypes carrying the trait to be introgressed (Patial *et al.*, 2023; Patial and Verma 2023), as well as having the highest possible proportion of the elite genome, can be selected quickly (Patial *et al.*, 2016; 2017; 2019; 2023b; Patial and Pal 2017).

Clapham (1973) developed first haploid in barley and haploid production mechanism in the crop was investigated by Sunderland (1974). A plethora of *in-vivo* and *in-vitro* protocols exists to accommodate the widely varying degrees of response between species to DH induction in barley (Patial *et al.*, 2022). Initially wide hybridization technique between *H. vulgare* with *H. bulbosum* was available and resulted in development of DH in most genotypes of barley (Kasha and Kao, 1970) and this technique have become routine tools in barley for direct release of cultivars. Later improvement in anther culture (Kao, 1981) and isolated microspore culture (Kasha, 1990) were perfected for barley breeding programmes. However, due to genotypic non-specificity, the *bulbosum* method is the most commonly used to produce barley haploids (Choo *et al.*, 1985). Barley has over 100 direct DH cultivars (Forster and Thomas, 2005; Weyen, 2009) released in Canada (Mingo, Rodeo), New Zealand (Gwylan), the U.K. (Doublet) and other countries. Using anther culture technique, barley cultivars 'Anthere' (D, 1995), 'Henni' (D, 1995), 'Sarah' (D, 1997), 'Uschi' (D, 1997), 'Carola', 'Nelly' (D, 1998) and "Ya/LM94-PC27" resistant to stripe rust (Gomez-Pondo *et al.*, 2009) were released. Gomez-Pondo *et al.* (2009) produced DH barley lines with higher yield, grain quality and resistance to stripe rust from anther culture technique. Due to DH advances, barley is considered the cereal model crop species for haploid production and research.

A number of DH lines have been developed and used for inheritance and breeding studies against different biotic stresses. For triple disease resistance (stem rust, leaf rust and powdery mildew), Steffenson *et al.* (1995) developed anther culture F_1 population from a cross of accession 'Q21861' and the susceptible line 'SM89010' with reported inheritance of one gene and two genes.

In addition to variety development, DH populations are a significant research tool for mapping single locus genes and QTL controlling traits of interest (Patial *et al.*, 2019; Gandi *et al.,* 2023). Today DH populations are used routinely in mapping. Toojinda *et al.* (2000) outlined the number, location, and function of genes that confer resistance to BYDV, leaf rust, and stripe rust diseases using 94 DH lines. In the same population, they also mapped Resistance Gene Analog Polymorphism loci based on degenerate motifs of cloned disease resistance genes. The DH population has served as a major study material for breeders and geneticist. The technique offers an opportunity to speed up traditional breeding methods, can be applied at any generation thereby allows greater flexibility and allowing rapid response to changing market demands.

Innovative barley breeding approaches: Molecular and Genomics tools for yellow rust resistance

With the development of the modern molecular breeding tools, plant breeding is becoming ever more precise, easier, and faster and offers the opportunity to increase the speed and efficiency. Many barley breeding programs now routinely use molecular technologies, such as marker assisted selection (MAS), virus-induced gene silencing (VIGS), targeted induced local lesions in genome (TILLING), genomics, recombinant DNA technology, and gene cloning to identify major loci controlling disease resistance. The potential applications of molecular breeding in crop plants for developing disease resilience have been well discussed by many researchers (Diab, 2006; Kota *et al.,* 2001; Varshney *et al.,* 2007).

Marker technology for yellow rust resistance breeding

The use of molecular markers in barley improvement is routinely applied in many breeding programs for major loci controlling disease resistance. Markers have been primarily used in backcross breeding to select lines with a genome composition similar to the recurrent parent and to introgress recessive traits. Markers have shown to be useful in progeny breeding for developing valuable parents and enriching F_1s with intricate crosses. Earlier, RFLP markers were employed to develop the first comprehensive molecular marker maps in barley (Graner *et al.*, 1991) which led to the mapping of a series of agronomic, quality and disease resistance traits (Friedt and Ordon , 2008). Subsequently, a number of barley genetic maps based on different DNA markers (such as AFLPs, RAPD, RFLPs, STSs, and SSRs) were published (Varshney *et al.*, 2007). Now, SNP markers are rapidly replacing SSRs or Diversity Arrays Technology (DArT) markers because they are more abundant, reproducible, amenable to automation and increasingly cost-effective (Diab, 2006). The shift from RFLP to SSR and SNP markers has been important in facilitating the tracking of resistant genes in

Table 3: Introgression of disease resistance in barley through MAS

Gene (s)/QTLs	**Recurrent Line (s)**	**Donor Line (s)**	**Marker type (name)**	**Reference**
QTLs on chromosomes 4 (4H) and 7 (5H),	Steptoe	BSR41	106 AFLPs, and eight RAPDs	Toojinda *et al.* (1998)
QTLs 4, 7 QTL 5	Galena	Accession CI10587 (PI 243183)	SSRs	Castro *et al.* (2003)
QTL on 1H, 4H, 5H	BCD47 and BCD12	Baronesse	SSR (GMSO21, kO6267, Bmac0213, EBmac0679, HvMLO3, Bmag0337)	Richardson *et al.* (2006)
QTLs on 1H, 2H, 3H, 5H	Harrington	CIho 3515	SNP (9K iSelect)	Wellings *et al.* (2011)
QTLs on 1H, 3H, 7H	Chevron	CIho 3515	SSR (HvMLO3, Bmag0337)	Smith *et al.* (2015)
QTLs on 4H, 5H, 6H	Barke	CIho 3515	SNP (9K iSelect)	Visioni *et al.* (2018)
QTLs on 2H, 3H, 6H	Morex	CIho 3515	SNP (9K iSelect)	Gyawali *et al.* (2021)

barley. This systematic development of functional markers was facilitated with Expressed sequence tags (ESTs) using appropriate software tools (Thiel *et al.*, 2004). The ESTs helps to identifying sequence polymorphism (mainly single-nucleotide and small InDels) in the corresponding EST alignments from multiple-genotypes of barley, which have been exploited for the development of markers. A computer algorithm SNiPping for discovery of functional markers (Kota *et al.,* 2001), SNP2CAPS for computational conversion of SNP markers into CAPS markers (Thiel *et al.*, 2003) and consensus maps (Diab, 2006; Varshney *et al.,* 2007) has been developed for barley. Barley's qualitative resistance mechanisms have been thoroughly investigated in terms of genomic location and specificity (Thomas *et al.*, 1995; Giese *et al.*, 1993; Graner and Tekauz, 1996), and in scenarios where a genetic map is unavailable, researchers occasionally employ Bulk Segregant Analysis (BSA) to map resistant genes.

Gene cloning in barley

To provide much needed protection against virulent pathogen strains, cloning of resistance (R) genes from wild or sexually incompatible species is required. Also, when *R* genes are bred one at a time into crop lines, the protection that they confer is often overcome within a few seasons by pathogen evolution. However, if several cloned R genes were available, it would be possible to pyramid R genes in a crop, which might provide more durable resistance. Dracatos *et al.* (2019) used "MutChromSeq" a recently developed molecular genomics tool for the rapid cloning of genes in plants, to clone the first leaf rust resistance gene, *Rph1 (Rph1.a),* from cultivated barley.

Next-generation sequencing (NGS) in barley

In barley, NGS methods- reduced-representation libraries (RRLs) (You, 2011; Gompert *et al.*, 2010), complexity reduction of polymorphic sequences (CRoPS) (Mammadov *et al.*, 2010), restriction-site-associated DNA sequencing (RAD-seq) (Baxter, 2011) and low-coverage sequencing for genotyping (Andolfatto *et al.*, 2011; Elshire *et al.*, 2011) are valuable for genome-wide marker development, genotyping and targeted sequencing across the genomes. Recent rapid advances of NGS facilitate the identification of novel rust resistant genes in barley.

Future priorities

Barley, a crop of rainfed agriculture, can serve as an important crop for supplementing the forage and grain demand of the farmers. Apart from developing better varieties for biotic stresses, the variety suitable for brewery, dual purpose and resistant to abiotic stresses will add to the value of the crop. Over the decades, tireless efforts of barley breeders to transfer adaptive traits/genes from landraces to elite genotypes and modern cultivars have met with little success; apparently, due to problems of linkage drag, more residual heterozygosity and complex adaptive gene cassettes involved in metabolic pathways. Emphasis should be placed on increasing the yield potential of barley landraces without altering their adaptation: landraces need to be invariably used as recipient rather than as donor parents. With the advent of marker-assisted and omics-based tools a great opportunity is available to barley breeders for transferring gene(s)/QTLs from landraces to popular cultivars while minimizing problems like linkage drag. Breeding strategy to introgress noble genes from wild genetic resources to the cultivated barley through pre-breeding aided with markers technique is required. The breeding for yellow rust resistance should focus on pyramiding of genes having seedling and adult plant resistance

Barley being highly adaptable can be an excellent source of genes for stress tolerance. An increased adoption of MAS in barley rust resistance breeding programs requires a rapid genomics research, new high-throughput marker genotyping platforms, a large number of markers and parallel development of user friendly software and databases and complete barley genome annotation which will raise the likelihood of finding potential resistance genes underlying various illnesses.

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Author contributions

The review was written and enriched by MP and SKB. All authors read, edited, and approved the final manuscript.

Conflict of interest

No

Declaration

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References

1. Andolfatto P, D Davison, D Erezyilmaz, TT Hu, J Mast, TS Morita and DL Stern. Multiplexed shotgun genotyping for rapid and efficient genetic mapping. *Genome Res*. 2011. ***21***:610-617.

2. Baba WN, I Rashid, A Shah, M Ahmad, A Gani and FA Masoodi. Effect of microwave roasting on antioxidant and anti-cancerous activities of barley flour. *Journal Saudi Society of Agricultural Sciences* 2014; ***27***:143-154.

3. Bakshi JS and PN Bahl. Inheritance of resistance to four races of yellow rust in two varieties of barley. *Indian J. Genet. Plant Breed*. 1965; ***25***:239-242.

4. Baxter SW, JW Davey, JS Johnston, AM Shelton, DG Heckel, CD Jiggins and ML Blaxter. Linkage mapping and comparative genomics using next-generation RAD sequencing of a non-model organism. *PLoS One*. 2011; ***6***(4):e19315.

5. Bettgenhaeuser J, I Hernandez-PinzOn, AM Dawson, M Gardiner, P Green, J Taylor, J., et al. The barley immune receptor *Mla* recognizes multiple pathogens and contributes to host range dynamics. *Nat. Commun*. 2021; ***25:***6915. doi: 10.1038/s41467-021-27288-3

6. Bishnoi SK, M Patial, C Lal and RPS Verma. Barley breeding. *In*: Fundamentals of field crop breeding. eds. D. K. Yadava, H. K. Dikshit, G. P., Mishra, S., Tripathi. Singapore: Springer. 2022; 259-308.

7. Castro A, PM Hayes, T Fillichkin and C Rossi. Update of barley stripe rust resistance QTL in the Calicuchima-sib x Bowman mapping population. *Barley genetics Newsletter* 2002; ***32***:1-12.

8. Castro AJ, F Capettini, AE Corey, T Filichkina, PM Hayes, A Kleinhofs, D Kudrna, K Richardson, S Sandoval-Islas, C Rossi and H Vivar. Mapping and pyramiding of qualitative and quantitative resistance to stripe rust in barley. *Theoretical and Applied Genetics* 2003; ***107***:922-930.

9. Castro AJ, F Capettini, AE Corey, T Filichkina, PM Hayes, A Kleinhofs, D Kudrna, K Richardson, S Sandoval-Islas, C Rossi and H Vivar. Mapping and pyramiding of qualitative and quantitative resistance to stripe rust in barley. *Theoretical and Applied Genetics* 2003; ***107***:922-930.

10. Castro AJ, F Capettini, AE Corey, T Filichkina, PM Hayes, A Kleinhofs, D Kudrna, K Richardson, S Sandoval-Islas, C Rossi and H Vivar. Mapping and pyramiding of qualitative and quantitative resistance to stripe rust in barley. *Theoretical and Applied Genetics* 2003; ***107***:922-930.

11. Chen FQ, D Prehn, PM Hayes, D Mulrooney, A Corey and H Vivar. Mapping genes for resistance to barley stripe rust (*Puccinia striiformis* f. sp. *hordei*). *Theoret. Appl. Genetics* 1994; ***88:***215-219.

12. Chen X and RF Line. Recessive genes for resistance to *Puccinia striiformis* f. sp. *hordei* in barley. *Phytopathology* 1999; ***89***:226-232.

13. Chen X and RF Line. Recessive genes for resistance to *Puccinia striiformis* f. sp. *hordei* in barley. *Phytopathology* 1999; ***89***:226-232.

14. Chen XM and RF Line. Identification of genes for resistance to *Puccinia striiformis* f. sp. *hordei* in 18 barley genotypes. *Euphytica* 2003; ***129***:127-145.

15. Chen XM, RF Line and H Leung. Virulence and polymorphic DNA relationships of *Puccinia striiformis* f. sp. *hordei* to other rusts. *Phytopathology* 1995; ***85***:1335-1342.

16. Choo TM, E Reinbergs and KJ Kasha. Use of haploids in breeding barley. *Plant Breeding Reviews* 1985; ***3***:219-252.

17. Clapham D. Haploid *Hordeum* plants from anthers *in vitro. Z Pflanzenzücht* 1973; ***69***:142-155.

18. Clare S, W Kitcher, M Gardiner, P Green, A Hubbard and MJ Moscou. 2016.bioRxiv 093773; doi: https://doi.org/10.1101/093773

19. Clare S, W Kitcher, M Gardiner, P Green, A Hubbard and MJ. Moscou. 2016. *ioRxiv* 093773; doi: https://doi. rg/10.1101/093773

20. Dawson AM, JN Ferguson, M Gardiner, P Green, A Hubbard and MJ Moscou. Isolation and fine mapping of *Rps6*: an intermediate host resistance gene in barley to wheat stripe rust. *Theor Appl Genet.* 2016; ***129***(4):831-843.

21. Dayani TR and JS Bakshi. Inheritance of resistance to stripe rust in barley. *Indian J. Genet.* 1978; ***38***:281-283.
22. Derevnina L, M Zhou, D Singh, CR Wellings and RF Park. 2015. The genetic basis of resistance to barley grass yellow rust (*Puccinia striiformis* f. sp. *pseudo-hordei*) in Australian barley cultivars. *Theor Appl Genet.* 2015; ***128***(2):187-97.
23. Derevnina L, M Zhou, D Singh , CR Wellings and RF Park. The genetic basis of resistance to barley grass yellow rust (*Puccinia striiformis* f. sp. *pseudo-hordei*) in Australian barley cultivars. *Theor Appl Genet.* 2015; ***128***(2):187-97.
24. Derevnina L, M Zhou, D Singh, CR Wellings and RF Park. The genetic basis of resistance to barley grass yellow rust (*Puccinia striiformis* f. sp. *pseudo-hordei*) in Australian barley cultivars.*Theor Appl Genet.* 2015; ***128***(2):187-97.
25. Diab AA. Construction of barley consensus map showing chromosomal regions associated with economically important traits. *African Journal of Biotechnology* 2006; ***5***(3):235-248.
26. Dracatos PM, J BartoS, H Elmansour, D Singh, M KarafiatovA, P Zhang, B Steuernagel, R Svacina, JCA Cobbin, B Clark, S Hoxha, MS Khatkar, J Dolezel, BB Wulff and RF Park *Plant Physiology* 2019; ***179***(4):1362-1372.
27. Dracatos PM, MS Khatkar, D Singh, F Stefanato, RF Park and LA Boyd. Resistance in Australian barley (*Hordeum vulgare*) germplasm to the exotic pathogen *Puccinia striiformis* f. sp. *hordei*, causal agent of stripe rust. *Plant Pathol.* 2016; ***65***;734-743.
28. Dubin HJ and RW Stubbs. Epidemic spread of barley stripe rust in South America. *Plant Disease.* 1986; ***70***(2):141-4.
29. Elshire RJ, JC Glaubitz, Q Sun, JA Poland, K Kawamoto, ES Buckler and SE Mitchell. A robust, simple Genotyping-by-Sequencing (GBS) approach for high diversity species. *Plos one.* 2011; ***6***(5):e19379.
30. Forster BP and WT Thomas. Doubled haploids in genetics and plant breeding. *In*: Janick J. (Ed.). *Plant Breeding Reviews.* Vol. 25. John Wiley Sons, 2005; ***25***;57-88.
31. Friedt W and F Ordon. Molecular markers for gene pyramiding and resistance breeding in barley. In: *Genomics-Assisted Crop Improvement, Vol 2: Genomics Applications in Crops*, Varshney R and R.Tuberosa, Eds., p. 498, Springer, Berlin, Germany, 2008.
32. Gandhi S, HK Chaudhary, D Pal, S Kumar, C Singh, SK Bishnoi and M Patial. *Imperata cylindrica* mediated doubled haploidy in wheat (*Triticum aestivum* L.): quittances and breakthrough. *Journal of Cereal Research* 2023; ***15*** (1):31-40.
33. Gangwar OP, SC Bhardwaj, GP Singh, P Prasad and S Kumar. Barley diseases and their management: an Indian perspective. *Wheat Barley Res.* 2018; ***10***(3):138-150.
34. Giese H, AG Holm-Jensen, HE Jensen and J Jensen. Localization of the Laevigatum powdery mildew resistance gene to barley chromosome 2 by the use of RFLP markers. *Theor Appl. Genet.* 1993; ***85:***897-900.
35. Gomez-Pando LR, J Jimenez-Davalos, A Eguiluz-de la Barra, EA Castellanos, JF Palomino, MI Tremolada, M Varela, JC Lorenzo. Field performance of new *in vitro* androgenesis-derived double haploids of barley. *Euphytica* 2009; ***166:***269-276.
36. Gompert Z, ML Forister, JA Fordyce, CC Nice, RJ Williamson, CA Buerkle. Bayesian analysis of molecular variance in pyrosequences quantifies population genetic structure across the genome of Lycaeides butterflies. *Mol Ecol* 2010; ***19***(12): 2455 -73.
37. Graner A and A Tekauz. RFLP mapping in barley of a dominant gene conferring resistance to scald (*Rhynchosporium secalis*). *Theor. Appl. Genet.* 1996; ***93:***421-425.
38. Graner A, A Jahoor, J Schondelmaier, H Siedler, K Pillen, G Fischbek, G Wenzel and RG Herrmann. Construction of an RFLP map of barley. *Theoretical and Applied Genetics* 1991; ***83***(2); 250-256.
39. Graner A, A Jahoor, J Schondelmaier, H Siedler, K Pillen, G Fischbeck, G Wenzel and RG Herrmann. Construction of an RFLP map of barley. *Theor Appl Genet.* 1991; ***83***:250-256.
40. Gyawali S, S Chao, S Vaish, SP Singh, S Rehman, SR Vishwakarma, RPS Verma. Genome wide association studies (GWAS) of spot blotch resistance

at the seedling and the adult plant stages in a collection of spring barley. *Mol Breeding* 2018; ***38*:**62.

41. Gyawali S, S Mamidi, S Chao,SC Bhardwaj, PS Shekhawat, R Selvakumar, OP Gangwar and RPS Verma. Genome-wide association studies revealed novel stripe rust resistance QTL in barley at seedling and adult-plant stages. *Euphytica* 2021; ***217*:**3. https://doi.org/10.1007/s10681-020-02728-1

42. Harwood WA. An introduction to barley: the crop and the model. Springer. 2019 pp 1-5.

43. Holtekjolen AK, AB Baevere, M Rodbotten, H Berg and SH Knutsen. Antioxidant properties and sensory profiles of breads containing barley flour. *Food Chemistry* 2008; ***110***(2):414-421.

44. Johnson R. 1968. Genetics of resistance of barley to stripe rust. In: 1st International Congress of Plant Pathology, R. K. S. Woods, ed. University of California Press, London, England

45. Johnson R. Genetics of resistance of barley to stripe rust. In: 1st International Congress of Plant Pathology, R. K. S. Woods, ed. University of California Press, London, England. 1968.

46. Kao KN. Plant formation from barley anther culture with Ficoll media. *Z. Pflanzenphysiol.* 1981; ***103***:437-443.

47. Kasha KJ and KN Kao. High frequency haploid production in barley (*Hordeum vulgare* L.). *Nature* 1970; ***225***:874-876.

48. Kasha KJ, A Ziauddin and UH Cho. Haploids in cereal improvement: anther and microspore culture. In: Gene manipulation in plant improvement II., ed. by J.P. Gustafson, Plenum Press. New York: 1990; 213-235. https://doi.org/10.1007/978-1-4684-7047-5_11.

49. Kilian B, H Ozkan, J Kohl, AV Haeseler, F Barale, O Deusch, A Brandolini, C Yucel, W Martin and F Salamini. Haplotype structure at seven barley genes: relevance to gene pool bottlenecks, phylogeny of ear type and site of barley domestication. *Mol Genet Genomics* 2006; ***276*:** 230-241.

50. Kleinhofs A, A Kilian, MAS Maroof, RM Biyashev, P Hayes, FQ Chen, N Lapitan, A Fenwick, TK Blake, V Kanazin, E Ananiev, L Dahleen, D Kudrna, J Bollinger, SJ Knapp, B Liu, M Sorrells, M Heun, JD Franckowiak, D Hoffman, R Skadsen, and BJ Steffenson. A molecular, isozyme and morphological map of the barley (*Hordeum vulgare*) genome. *Theor. Appl. Genet.* 1993; ***86*:**705-712.

51. Klos EK, T Gordon, P Bregitzer, P Hayes, X Chen, I del Blanco, S Fisk and JM Bonman. Barley stripe rust resistance QTL: Development and validation of SNP markers for resistance to *Puccinia striiformis* f. sp. *hordei. Phytopathology* 2016; ***106***:1344-1351.

52. Kota R, M Wolf, W Michalek and A Graner. Application of denaturing high-performance liquid chromatography for mapping of single nucleotide polymorphisms in barley (Hordeum vulgare L.). Genome 2001; ***44***(4):523-528.

53. Kumar K, MD Holtz, K Xi and TK Turkington. Virulence of Puccinia striiformis on wheat and barley in central Alberta. Can J Plant Pathol. 2012; ***34***:551-561.

54. Kumar K, MD Holtz, K Xi, and TK Turkington. Virulence of Puccinia striiformis on wheat and barley in central Alberta. Canadian Journal of Plant Pathology 2012; ***34***(4), 551-561.

55. Kumar S, M Patial, R Sharma. Efficient barley breeding. *In*: Gosal, S., Wani, S. (eds) Accelerated Plant Breeding, Volume 1. Springer, Cham. 2020. https://doi.org/10.1007/978-3-030-41866-3_13

56. Li K, J Hegarty, C Zhang, A Wan, J Wu, GB Guedira, X Chen, M Munoz-Amatriain, D Fu and J Dubcovsky. Fine mapping of barley locus Rps6 conferring resistance to wheat stripe rust. Theor Appl Genet. 2016; ***129***(4):845-859.

57. Luthra JK and VL Chopra. Genetics of stripe rust resistance in barley. Indian Journal of Genetics and Plant Breeding 1990; ***50*:**390-395.

58. Luthra JK, RPS Verma and KV Prabhu. Development of isogenic lines in barley with reference to *Puccinia striiformis* West. In: Barley Genetics VI. Proceedings of the Sixth International Barley Genetics Symposium, July 22-27, 1991. Helsingborg, Sweden. PP. 622-625.

59. Luthra JK. Inheritance of seedling resistance to races 57 and G of yellow rust in barley. Indian J. Genet. Plant Breed. 1966; ***26***:356-359.

60. Mammadov JA, W Chen, R Ren, R Pai, W Marchione, F Yalcin, H Witsenboer, TW Greene, SA Thompson and SP Kumpatla. Development of highly polymorphic SNP markers from the complexity reduced portion of maize [Zea mays L.] genome for use in marker-assisted breeding. Theor Appl Genet 2010; ***121:***577-588.

61. Martin JM, TK Blake and EA Hocket. Diversity among North America spring cultivar based on coefficients of parentage. Crop Science 1991; ***31***:113-1137.

62. Mathur AK and BS Siradhana. Screening of indigenous and exotic barley germplasm against Indian races of yellow rust. Indian Journal of Mycology and Plant Pathology 1990; ***20***(2):182.

63. Murty SS. Segregation and correlated inheritance of rust-resistance and epidermal characters in a barley cross. Indian J. Genet. 1942; ***2***:73-75

64. Nelson R, T Wiesner-Hanks, R Wisser and P Balint-Kurti. Navigating complexity to breeddisease-resistant crops. Nat Rev Genet. 2018; ***19***:21.

65. Nover I and F Scholz. Genetic studies on the resistance of barley to yellow rust. *Theor. Appl. Genet.* 1969; **39**:150-5.

66. Nover I and F Scholz. Genetic studies on the resistance of barley to yellow rust (Puccinia striiformis West.). Theor. Appl. Genet. 1969; ***39***:150-155.

67. Nover I and F Scholz. Genetic studies on the resistance of barley to yellow rust (Puccinia striiformis West.). Theor. Appl. Genet. 1969; ***39***:150-155.

68. Oerke EC. Crop losses to pests. *Journal of Agricultural Science* 2006; 144:31-43.

69. Pahalawatta V and X Chen. Inheritance and molecular mapping of barley genes conferring resistance to wheat stripe rust. Phytopathology 2005; ***95***(8):884-9.

70. Patial M and D Pal. Wheat improvement *via* doubled haploidy breeding. *In*: Wheat a premier food crop. Edt by Kumar,A., Kumar, A. and Prasad, B. Kalyani Publisher, 2017. pp 67–76.

71. Patial M, and R Verma. Developing wheat lines for rust resistance through Imperata cylindrica mediated chromosome elimination doubled haploidy technique: A Review. Journal of Cereal Research 2023; ***5***(3):309-319.

72. Patial M, D Pal, A Thakur, RS Bana and S Patial. Doubled haploidy techniques in wheat (Triticum aestivum L.): an overview. Proceedings of the National Academy of Sciences, India Section B: Biological Sciences. 2019; ***89***:27-41.

73. Patial M, D Pal, A Thakur, RS Bana and S Patial. Doubled haploidy techniques in wheat (Triticum aestivum L.): An Overview. Proc. Natl. Acad. Sci., India, Sect. B Biol. Sci. 2019; ***89***:27-41.

74. Patial M, D Pal, HK Chaudhary, J Kumar and A Thakur. Exploring the potential of Imperata cylindrica, a wild grass for development of doubled haploids in wheat. Int. J. Trop. Agric. 2016; ***34***:1211-1213.

75. Patial M, D Pal, HK Chaudhary, J Kumar and KV Prabhu. Exploration of wild grass Imperata cylindrica for development of doubled haploids in winter x spring wheat (Triticum aestivum L.) hybrids accompanied with combining ability and hybrid potential estimation. Indian J. Genet. Plant Breed. 2017; ***77***:316-320.

76. Patial M, D Pal, J Kumar and H Chaudhary. Doubled haploids production in wheat (Triticum aestivum L.) via Imperata cylindrica mediated chromosome elimination approach. Int. J. Trop. Agric. 2015; ***33***:3333-3335.

77. Patial M, D Pal, J Kumar. Combining ability and gene action studies for grain yield and its component traits in barley (Hordeum vulgare L.). SABRAO J. Breed. Genet. 2016; ***48***:90-96.

78. Patial M, D Pal, KK Pramanick, OP Gangwar, N Kishore. BHS 474 (BBM 777) (IC0635023; INGR20018), a Barley (Hordeum vulgare) germplasm with resistance to all pathotypes of yellow rust and brown rust in seedling and adult plant stage. seedling resistance against all pathotypes of black rust except for pathotype 11. Indian Journal of Plant Genetic Resources 2021; ***34***(2): 321.

79. Patial M, D Pal, R Kapoor and KK Pramanick. Inheritance and combining ability of grain yield in half diallel barley population. Wheat and Barley Research 2018; ***10***(3):173-178.

80. Patial M, D Pal, SC Bhardwaj, KK Pramanick, OP Gangwar, BHS 481 (BBM 815) (IC640685; INGR21125), a barley (Hordeum vulgare L.) germplasm with resistance to seedling resistance to leaf and stripe black rust as well as adult plant resistance to yellow rust. Indian Journal of Plant Genetic Resources 2023; ***36***(3):471.

81. Patial M, HK Chaudhary, D Pal, SC Bhardwaj, OP Gangwar, KK Pramanick. DH-1 (IC640653; INGR21119), a wheat (Triticum aestivum L.) germplasm with resistance to yellow and brown rust in seedling stage adult plant stage. Indian Journal of Plant Genetic Resources 2023a; ***36***(3):463.

82. Patial M, HK Chaudhary, N Sharma, OP Gangwar, N Kishore, D Pal, KK Pramanick, SC Bhardwaj and R Chauhan. Developing genetic stock for yellow and brown rust resistance in Triticum aestivum L. via Imperata cylindrica-mediated doubled haploidy technique. Cereal Res. Commun. 2022; ***50***:439-48.

83. Patial M, HK Chaudhary, N Sharma, S Sundaresha, R Kapoor, D Pal, KK Pramanick, AK Shukla and J Kumar. Effect of different in-vitro and in-vivo variables on the efficiency of doubled haploid production in Triticum aestivum L. using Imperata cylindrica-mediated chromosome elimination technique. Cereal Res. Commun. 2021; ***49***:133-40.

84. Patial M, R Chauhan, HK Chaudhary, KK Pramanick, AK Shukla, V Kumar and RPS Verma. Au-courant and novel technologies for efficient doubled haploid development in barley (Hordeum vulgare L.). Critical Reviews in Biotechnology 2023b; ***4***(3):575-593.

85. Patial M, R Chauhan, HK Chaudhary, KK Pramanick, AK Shukla, V Kumar and RPS Verma. Au-courant and novel technologies for efficient doubled haploid development in barley (*Hordeum vulgare* L.). Critical Reviews in Biotechnology 2022; 43(4):575-593.

86. Patial, M, M Kumar, SK Bishnoi, D Pal, KK Pramanick, AK Shukla and S Gandhi. Genetic variability and trait association for grain yield in barley (Hordeum vulgare L.). Journal of Cereal Research 2023; ***15***(2): 2582-2675.

87. Prakash V and RPS Verma. Inheritance of yellow rust resistance in barley (Hordeum vulgare L.). Indian Journal of Genetics and Plant Breeding 2009; ***69***(2):99-101.

88. Richardson KL, MI Vales, JG Kling, CC Mundt and PM Hayes. Pyramiding and dissecting disease resistance QTL to barley stripe rust. Theor Appl Genet. 2006; ***113***(3):485-95.

89. Safavi SA, Y Jahani-Jelodar and S Ebrahimnejad. Virulence patterns of barley yellow rust and effective resistance genes to Puccinia striiformis in three parts of Iran. Archives of Phytopathology and Plant Protection 2013; ***46***(8):903-910.

90. Singh DP. Evaluation of barley genotypes against multiple diseases. SAARC J Agric. 2008; ***6***:117-120.

91. Singh J, C Lal, D Kumar, A Khippal, L Kumar, V Kumar, R Malik, S Kumar, AS Kharub, RPS Verma and I Sharma. Widening the genetic base of Indian barley through the use of exotics. Int J Trop Agric. 2016; ***34***(1):1-10.

92. Sjakste TG, I Rashal and MS Roder. Inheritance of microsatellites alleles in pedigrees of Latvian barley and related European ancestors. Theoretical and Applied Genetics 2003; ***106***(3):539-49

93. Smith O, G Momber, R Bates, P Garwood, S Fitch, M Pallen, V Gaffney and RG Allaby. Sedimentary DNA from a submerged site reveals wheat in the British Isles 8000 years ago. *Science* 2015; 347:998-1001.

94. Steffenson BJ., Y Jin, BG Rossnagel, J Rasmussen and KN Kao. Genetics of multiple disease resistance in a doubled haploid population of barley. Plant Breed. 1995; ***114***:50-54.

95. Sunderland N. Anther culture as a means of haploid induction. *In*: Kasha KJ (ed) Haploids in higher plants – advances and potential, Univ of Guelph. 1974. pp 91-122.

96. Thiel T, R Kota, I Grosse, N Stein and A Graner. SNP2CAPS: a SNP and INDEL analysis tool for

CAPS marker development. Nucleic Acids Research 2004; ***32***(1):e5.

97. Thiel T, W Michalek, RK Varshney and A Graner. Exploiting EST databases for the development and characterization of gene-derived SSR-markers in barley (Hordeum vulgare L.). Theoretical and Applied Genetics 2003; ***106***(3):411-422.

98. Thomas CE, T Inaba and Y Cohen. Physiological specialization in Pseudoperonospora cubensis. Phytopathology. 1987; ***77***:1621-1624.

99. Thomas WT, W Powell, R Waugh, KJ Chalmers, UM Barua, P Jack, V Lea, BP Forster, JS Swanston, RP Ellis, PR Hanson and RC Lance. Detection of quantitative trait loci for agronomic, yield, grain and disease characters in spring barley (Hordeum vulgare L.). Theor. Appl. Genet. 1995; ***91***(6-7):1037-1104.

100. Toojinda T, E Baird, A Booth, L Broers, P Hayes, W Powell, WTB Thomas, H Vivar and G Young. Introgression of quantitative trait loci (QTLs) determining stripe rust resistance in barley: an example of marker –assisted line development. Theoretical and Applied Genetics 1998; ***96:***123-131.

101. Toojinda T, LH Broers, XM Chen, PM Hayes, A Kleinhofs, J Korte, D Kudrna, H Leung, R Line, W Powell, L Ramsay, HE Vivar and R Waugh. Mapping quantitative and qualitative disease genes in a double haploid population of barley (Hordeum vulgare). Theor. Appl. Genet. 2000; ***101***:580-589.

102. Upadhyay MK and S Prakash. Identification of diverse genes conferring resistance to Indian races of stripe rust of barley. Indian J Genet & Plant Breed. 1977; ***37***:68-72.

103. Varshney RK, TC Marcel, L Ramsay, J Russell, MS Roder, N Stein, R Waugh, P Langridge, R E Niks and A Graner. A high density barley microsatellite consensus map with 775 SSR loci. Theoretical and Applied Genetics, 2007; ***114***(6):1091-1103.

104. Vatter T, A Maurer, D Perovic, D Kopahnke, K Pillen and F Ordon. Identification of QTL conferring resistance to stripe rust (Puccinia striiformis f. sp. hordei) and leaf rust (Puccinia hordei) in barley using nested association mapping (NAM). PLoS ONE 2018; ***13***(1): e0191666.

105. Vatter T, A Maurer, D Perovic, D Kopahnke, K Pillen and F Ordon. Identification of QTL conferring resistance to stripe rust (Puccinia striiformis f. sp. hordei) and leaf rust (Puccinia hordei) in barley using nested association mapping (NAM). PLoS ONE 2018; ***13***(1): e0191666. https://doi.org/10.1371/journal.pone.0191666

106. Verma RPS, B Sarkar, AS Kharub and R Selvakumar. Challenges for barley production in India. Indian Farming. 2010; 41-48. Science 144, 31-43.

107. Verma RPS, R Selvakumar, OP Gangwar, PS Shekhawat, SC Bhardwaj, S Rehman, DS Poudyal and S Gyawali. Identification of additional sources of resistance to Puccinia striiformis f. sp. hordei (Psh) in a collection of barley genotypes adapted to the high input condition. Journal of phytopathology 2018; ***166(***5):355-364.

108. Verma RPS, R Selvakumar, OP Gangwar, PS Shekhawat, SC Bhardwaj, S Rehman, DS Poudyal and S Gyawali. Identification of additional sources of resistance to Puccinia striiformis f. sp. hordei (Psh) in a collection of barley genotypes adapted to the high input condition. Journal of phytopathoogy 2018; ***166***(5): 355-364.

109. Visioni A, S Gyawali, R Selvakumar, OP Gangwar, PS Shekhawat, SC Bhardwaj, AM Al-Abdallat, Z Kehel and RPS Verma. Genome wide association mapping of seedling and adult plant resistance to barley stripe rust (Puccinia striiformis f. sp. hordei) in India. Front Plant Sci. 2018; ***9***:520.

110. Visioni A, S Gyawali, R Selvakumar, OP Gangwar, PS Shekhawat, SC Bhardwaj, AM Al-Abdallat, Z Kehel and RPS Verma. Genome wide association mapping of seedling and adult plant resistance to barley stripe rust (Puccinia striiformis f. sp. hordei) in India. Front. Plant Sci. 2018; ***9***:520.

111. Wellings CR. Global status of stripe rust: a review of historical and current threats. Euphytica 2011; ***179:***129-141.

112. Weyen J. Barley and wheat doubled haploids in breeding. *In*: Touraev, A Forster, BP Jain, S.M. (eds) Advances in haploid production in higher plants. Springer, Dordrecht. (2009). https://doi.org/10.1007/978-1-4020-8854-4_15.

113. Wych RD and DC Rasmasson. Genetic improvement in malting barley cultivar since 1920. Crop science 1983; ***23***:1037-1040.

114. Yadav JR and J Kumar. Evaluation of exotic and indigenous barley accessions for resistance against Indian pathotypes of Puccinia triiformis hordei. Rachis 1999; ***18***(2):60-63.

115. Yan G and X Chen. Molecular Mapping of the rps1.A Recessive Gene for Resistance to Stripe Rust in BBA 2890 Barley. Phytopathology 2007; ***97***(6):668-673.

116. Yan G and X Chen. Molecular mapping of the rps1.A recessive gene for resistance to stripe rust in BBA 2890 Barley. Phytopathology 2007; ***97***(6):668-673.

117. You FM, N Huo, KR Deal, YQ Gu, MC Luo, PE McGuire, J Dvorak and OD Anderson. Annotation-based genome-wide SNP discovery in the large and complex Aegilops tauschii genome using next-generation sequencing without a reference genome sequence. BMC Genomics 2011; ***12***:59.