OPEN ACCESS

Middle East Research Journal of Biological Sciences
ISSN 2789-7710 (Print & ISSN 2958-2091 (Online)
Frequency: Bi-Monthly
DOI: 10.36348/merjbs.2024.v04i02.001

KUWAIT SCHOLARS PUBLISHER
Website: http://www.kspublisher.com/
Email: office@kspublisher.com

Review on Molecular Marker Used in Barely Breeding

Fikir Desalew[1*]
[1]Seed Science and Technology, Holetta Agricultural Research Center, Holetta, Ethiopia

Abstract: Barley (*Hordeum vulgare*) is the largest cereal crop in the world, mostly used for animal feed, food, and industrial utilization. In its endosperm, the nutrients like starch and protein are stored and it determine the barely quality. Many barley-breeding programs around the world have used accessions from Ethiopia as parents in their crosses. Ethiopian landraces are known for several important traits, including resistance to powdery mildew. The NDSU breeding program mainly focuses on developing two-rowed and six-rowed malt barley cultivars adaptable to the northern Great Plains of the USA while the ICARDA breeding program develops cultivars for diverse agro-ecologies, including dry land and high rainfall regions.

Keywords: Marker, QTL Mapping, Marker Assisted Selection, Malt Barely, Linkage.

REVIEW PAPER

***Corresponding Author:**
Fikir Desalew
Seed Science and Technology, Holetta Agricultural Research Center, Holetta, Ethiopia

How to cite this paper:
Fikir Desalew (2024). Review on Molecular Marker Used in Barely Breeding. *Middle East Res J Biological Sci*, *4*(2): 30-34.

Article History:
| Submit: 14.02.2024 |
| Accepted: 15.03.2024 |
| Published: 20.03.2024 |

1. INTRODUCTION

Barley (*Hordeum vulgare*) is the largest cereal crop in the world, mostly used for animal feeding, food, and industrial utilization (Bond *et al*., 2015; FAOSTAT[1]).It is about 30% of the product is globally used for malting, breeding barley varieties with higher-quality of malt for processing is useful goal (Bond *et al*., 2015; Walker and Panozzo, 2016; Kochevenko *et al*., 2018).

Many barley-breeding programs around the world have used accessions from Ethiopia as parents in their crosses. Ethiopian landraces are known for several important traits, including resistance to powdery mildew (caused by *Erysiphe graminis* DC. f. sp. *hordei* Em. Marchal), leaf rust (caused by *Puccinia hordei* Otth), loose smut (caused by *Ustilago tritici* (Pers.) Rostr.), barley yellow dwarf virus (BYDV), and barley stripe mosaic virus (BSMV); and high lysine content (Adugna, 2011; Spies *et al*., 2012; Munoz *et al*., 2014). The Ethiopian Institute of Biodiversity Conservation (IBC) has conserved > 15,000 barley accessions, with nearly 67% being landraces collected in Ethiopia (Adugna, 2011). The diversity in Ethiopian barley landraces stems from the country's diverse agro-ecologies, diverse socio-cultural situations, and wide ranges of utilization of barley for food, feed, and alcoholic beverages.

Generally, the barley-breeding program utilizes landrace collections, exotic introductions, and lines from local crossing programs to develop cultivars for diverse production systems, including late, early, and 'Belg' (short growing season with planting in February to March). As a result, the Ethiopian barley-breeding program's germplasm has maintained high levels of genetic diversity. The barley-breeding programs of North Dakota State University (NDSU) and ICARDA have unique germplasm that reflects their breeding objectives.

Mapping of QTL for traits of breeding is an interesting precursor for MAS or molecular-marker based breeding. For showing malt quality QTL, different mapping approaches have been used, including bi-parental mapping populations (Emebiri *et al*., 2004; Zhou *et al*., 2012; Islamovic *et al*., 2014); association mapping (Cai *et al*., 2013; Matthies *et al*., 2014; Mohammadi *et al*., 2015); and fine mapping using chromosome substitution lines (Gao *et al*., 2004) and wild barley introgression lines (Schmalenbach and Pillen, 2009). Linkage and association mapping are the most commonly used QTL mapping approaches (Abdurakhmonov and Abdukarimov, 2008). There is an information gap to mapping using molecular markers. There for the objective of this paper is to review Molecular Marker used in barely breeding.

2. Molecular Marker System

A genetic marker is defined as a chromosomal landmark that allows tracing a specific region of DNA (Semagn *et al*., 2006). Genetic markers and the genes they mark are close together in the same chromosome that tends to stay together in each generation.

Several maps have been developed for barley using cytogenetic techniques (mainly using trisomy's), isozymes, morphological markers, and a range of DNA markers including SSR, DArT, and SNPs (Hussain, 2006; Wenzl *et al*., 2006; Varshney *et al*., 2007; Suzcs *et al*., 2009; Munoz *et al*., 2011). According to Gupta *et al*., (2001), SNPs are more abundant in plant systems compared to the human genome on which they were initially applied. Close *et al*., (2009) selected 3,072 SNPs to fill two 1,536-SNP "production" assays (BOPA1 and BOPA2). Examination of USA breeding materials with these SNP markers provided excellent coverage and sensitivity for detection of minor alleles (Close *et al*., 2009). Most importantly, SNPs provide the ultimate form of molecular markers because a nucleotide base is the smallest unit of inheritance (Edwards *et al*., 2007). Edwards *et al*., (2007) estimated the SNP frequency in barley to be one SNP every 27 to 240 bp. Even if SNPs at any particular site can in principle involve four different nucleotide variants, they are generally balletic in nature. Edwards *et al*., (2007) pointed out that SNP markers are abundant in the genome and low in mutation rate. However, the abundance of SNP markers in the genome compensates for their balletic nature. These features make SNPs excellent markers in studying genome evolution, map-based positional cloning, studying complex genetic traits, genetic mapping, detection of marker-trait associations, and assessment of genetic relationships between individuals (Edwards *et al*., 2007).

Elshire *et al*., (2011) developed a genotyping-by-sequencing (GBS) approach that is suitable for population studies, germplasm characterization, breeding, and trait mapping in diverse organisms. GBS is the latest application of next-generation sequencing protocols for the purposes of discovering SNPs in a variety of crop species and populations (Spindel *et al*., 2013). The GBS procedure reduces cost per sample by sequencing only subsets of genomic regions targeted by restriction enzymes (Elshire *et al*., 2011). The value of sequencing restriction site-associated genomic DNA (i.e., RAD tags) for high density SNP discovery and genotyping was first demonstrated by Baird and coworkers in 2008 (Elshire *et al*., 2011). Alternatively, a series of polymerase chain reactions (PCR) can also be used instead of restriction enzymes to sample specific regions of the genome to sequence.

Molecular markers serve a variety of purposes relevant to crop improvement and genetic study. The applications include QTL mapping (Jones *et al*., 1997; Gupta *et al*., 2001; Sreenivasulu *et al*., 2008; Edwards *et al*., 2007; Wang *et al*., 2012), genetic diversity analysis (Mohammadi and Prasanna, 2003), population structure studies (Wang *et al*., 2012), and phylogenetic and comparative genomics analyses (Whitkus *et al*., 1992). Molecular markers are also useful tools to overcome linkage drag and background genetic effect problems associated with utilization of landraces and wild types in crop improvement (Hussain, 2006). In crop breeding, molecular markers are useful in MAS methods, such as F2 enrichment, marker-assisted back crossing, marker-assisted recurrent selection (Bernardo and Charcosset, 2006), and genomic selection (Bernardo, 2009; Bernardo, 2010; Bernardo, 2013; Massman *et al*, 2012).

2.1 QTL Mapping

Two commonly used QTL mapping approaches are linkage mapping and association mapping (Abdurakhmonov and Abdukarimov, 2008; Cavanagh *et al*., 2008; Sreenivasulu *et al*., 2008). The linkage mapping approach utilizes a bi-parental mapping population segregating for the trait(s) of interest whereas association mapping utilizes a well-chosen natural population of lines, accessions, or cultivars referred to as the "mapping panel". Both linkage analysis and association mapping rely on co-inheritance of functional polymorphisms and neighboring DNA variants (Zhu *et al*., 2008), ultimately identifying genotype-phenotype associations that lead to discovery of QTL that are responsible for phenotypic variation (Abdurakhmonov and Abdukarimov, 2008; Zhu *et al*., 2008; Myles *et al*., 2009). The three basic requirements to map QTL are a genetic map of variable markers, a population with which to follow the segregation of these markers, and trait measurements on individuals of the population (Slate, 2005).

2.1.1 Linkage Disequilibrium (LD)

Linkage equilibrium (LE) and linkage disequilibrium (LD) are important terms to describe linkage relationships in population genetics (Abdurakhmonov and Abdukarimov, 2008). Linkage equilibrium is the random association of alleles at different loci in a population. On the contrary, LD is the non-random association of alleles at different loci in a population. Linkage disequilibrium does not necessarily imply genetic linkage, and it can occur between physically unlinked loci (Flint-Garcia, 2003; Mackay and Powell, 2006; Abdurakhmonov and Abdukarimov, 2008). Linkage refers to the correlated inheritance of loci due to their physical connection on a chromosome whereas LD refers to the correlation of alleles in a population (Flint-Garcia, 2003). In generally, LD creates the basis for the construction of genetic maps and the localization of genetic loci for a variety of charactors (Hussain, 2006). Association mapping particularly relies on LD decay (Mackay and Powell, 2006).

2.1.2 Linkage (Family) Mapping

Linkage mapping is a commonly employed QTL mapping method to explain phenotypic variation in terms of simple changes in DNA sequence in experimental populations created by bi-parental crosses (Myles *et al*., 2009). Linkage mapping involves six general steps (Abdurakhmonov and Abdukarimov, 2008): (1) developing an experimental population (F2 , doubled-haploid, backcross, near-isogenic lines, and recombinant-inbred lines), (2) phenotyping (collecting

data on traits) across environments, (3) genotyping using markers that identify polymorphisms in the parents, (4) constructing linkage maps using molecular markers, (5) statistically correlating phenotypic data with positioned markers, and (6) identifying QTL regions affecting a trait of interest. Some of the advantages of linkage mapping include identification of low frequency functional alleles and application when there is a strong relatedness problem (Myles *et al*., 2009).

2.1.3 Association (Population) Mapping in Barely

Association mapping involves searching for genotype-phenotype correlations (i.e. marker-trait associations) in unrelated individuals taken from a natural population (Myles *et al*., 2009). The method results in localization of QTL based on the strength of the correlation between mapped genetic markers and traits of interest (Mackay and Powell, 2006). Decay of LD is the basis for association mapping (Mackay and Powell, 2006). Association mapping can lead to the most effective utilization of ex-situ conserved natural genetic diversity (Abdurakhmonov and Abdukarimov, 2008).

The association mapping panel could be composed of three types of populations, namely; germplasm bank collections, elite breeding materials, and synthetic populations (Breseghello and Sorrells, 2006).

Family-based linkage (FBL) mapping is a special case of association mapping in which the mapping population is established from a small number of founders (Mackay and Powell, 2006). Cavanagh *et al*., (2008) also discussed the importance of Multi-parent Advanced Generation Inter-cross (MAGIC) populations derived from elite breeding germplasm for gene-trait analysis in crop species.

2.2 Yield and Yield-Related Traits

2.2.1 Mapped QTL for Different Traits in Barley

Grain yield improvement is the primary objective in many cereal-breeding programs (Welsh, 1981) and it can be defined in terms of the product of three yield components, i.e.; number of spikes per unit area, number of kernels per spike, and kernel weight (Nickell and Grafius, 1969). Currently, there is growing interest in the application of molecular marker information closely related to important traits in breeding programs. The first RFLP marker map for barley developed two decades ago was ultimately used to map agronomic, quality, and disease resistance traits (Sreenivasulu *et al*., 2008). Hussain (2006) reviewed several articles on QTL mapping in barley and discussed chromosomal location of 16 agronomic traits. According to review by Sreenivasulu *et al*., (2008), 1000-kernel weight and kernel number per spike were mapped to all chromosomes except 1H and 7H, respectively. The other yield component, spike number per unit area, was mapped to chromosome 3H. For plant height and days to heading, they reported several QTL in all seven chromosomes.

Xue *et al*., (2010) did linkage analysis for yield and yield components under waterlogged and well drained conditions using 156 doubled-haploid lines derived from the cross 'Yerong' (waterlogging-tolerant) x 'Franklin' (waterlogging-sensitive). Using a genetic linkage map of 496 DArT, 80 AFLP, and 28 microsatellite markers, they identified 31 QTL for kernel weight, grains per spike, spikes per plant, spike length, and grain yield, with individual QTL explaining 4.7% to 55.3% of the phenotypic variability. Interestingly, most of those QTL with larger effects were detected in the same region of chromosome 2H, indicating tight linkage or pleiotropic effects of the gene(s) controlling the traits. They also identified some unique QTL under waterlogging conditions, which implied that different markers might be used in selecting cultivars under such conditions.

2.2.2 Disease Resistance Traits in Barely

Selection for disease resistance has been equally important like improving crops for yield and yield components. Diseases can affect yield and quality of the product as well as leaving myco-toxins on the grain. Fusarium head blight (FHB; incited by *Fusarium graminearum* Schwabe), leaf scald (incited by *Rhynchosporium secalis* (Oudem.) J. J. Davis, the net form net blotch (incited by *Drechslera teres* (Sacc.) Shoemaker) and spot blotch (incited by *Cochliobolus sativus* (Ito & Kuribayashi) Drechs. ex Dastur) are among the major fungal diseases in barley (Hussain, 2006), with resistance to each by one to 14 genes.

Fusarium head blight is economically important disease that can cause yield and quality reduction in cereals, like in wheat and barley (Ma *et al*., 2000; Dahleen *et al*., 2003). The U.S. Government Accounting Office (GAO) estimated total losses due to FHB in the upper-Midwest USA exceeded $200 million from 1993-1997 (U.S. GAO, 1999). Nganje *et al*., (2001) estimated losses of $136 million in the same region from 1998-2000.

Leaf scald is one of the most severe diseases of barley in the highlands of Ethiopia where precipitation is high and temperature is low during the cropping season. Yield losses can range from 21% to 67%, and it also affects grain quality and ultimately the price paid for the grain (Kiros *et al*., 2004; Zhan *et al*., 2008).

3. CONCLUSION

Barley (*Hordeum vulgare*) is the most important cereal crop in the world, widely used for animal feeding feed, food, and industrial utilization. A genetic marker is a chromosomal landmark that allows tracing a specific region of DNA. Genetic markers and the genes they mark are close together in the same chromosome that tends to stay together in each

generation. Molecular markers serve a variety of purposes relevant to crop improvement and genetic study. Molecular markers are also useful tools to overcome linkage drag and background genetic effect problems associated with utilization of landraces and wild types in crop improvement. In crop breeding, molecular markers are useful in MAS methods, such as F2 enrichment, marker-assisted back crossing, and marker-assisted recurrent selection.

REFERENCES

- Abdurakhmonov, I. Y., & Abdukarimov, A. (2008). Application of association mapping to understanding the genetic diversity of plant germplasm resources. *International journal of plant genomics*, *2008*. doi: 10.1155/2008/574927.
- Adugna, A. (2011). Barley genetic resources collection and conservation in Ethiopia. In: Mulatu, B. and Grando, S. (eds).. Barley Research and Development in Ethiopia. Proceedings of the 2nd National Barley Research and Development Review Workshop. 28-30 November 2006, HARC, Holetta, Ethiopia. ICARDA, PO Box 5466, Aleppo, Syria. pp xiv + 391
- Bernardo, R. (2009). Genomewide selection for rapid introgression of exotic germplasm in maize. *Crop Science*, *49*(2), 419-425.
- Bernardo, R. (2010). Genomewide selection with minimal crossing in self-pollinated crops. *Crop Science*, *50*(2), 624-627.
- Bernardo, R. (2013). Genome-wide Selection when Major Genes Are Known. *Crop Sci*, *54*, 68–75.
- Bernardo, R., & Charcosset, A. (2006). Usefulness of gene information in marker-assisted recurrent selection: A simulation appraisal. *Crop Science*, *46*(2), 614-621.
- Bond, J., Capehart, T., Allen, E., & Kim, G. (2015). Boutique brews, barley, and the balance sheet: changes in malt barley industrial use require an updated forecasting approach. *Boutique brews, barley, and the balance sheet: changes in malt barley industrial use require an updated forecasting approach.*, (FDS-15a-SA), 18-23.
- Breseghello, F., & Sorrells, M. E. (2006). Association analysis as a strategy for improvement of quantitative traits in plants. *Crop Science*, *46*(3), 1323-1330.
- Cai, S., Yu, G., Chen, X., Huang, Y., Jiang, X., Zhang, G., & Jin, X. (2013). Grain protein content variation and its association analysis in barley. *BMC plant biology*, *13*, 1-11. doi:10.1186/1471-2229-13-35.
- Canci, P. C., Nduulu, L. M., Muehlbauer, G. J., Dill-Macky, R., Rasmusson, D. C., & Smith, K. P. (2004). Validation of quantitative trait loci for Fusarium head blight and kernel discoloration in barley. *Molecular Breeding*, *14*, 91-104.
- Close, T. J., Bhat, P. R., Lonardi, S., Wu, Y., Rostoks, N., Ramsay, L., ... & Waugh, R. (2009). Development and implementation of high-throughput SNP genotyping in barley. *BMC genomics*, *10*, 1-13. Doi: 10.1186/1471-2164-10-582.
- Dahleen, L. S., Agrama, H. A., Horsley, R. D., Steffenson, B. J., Schwarz, P. B., Mesfin, A., & Franckowiak, J. D. (2003). Identification of QTLs associated with Fusarium head blight resistance in Zhedar 2 barley. *Theoretical and applied genetics*, *108*, 95-104.
- Edwards, D., Forster, J. W., Chagné, D., & Batley. J. (2007). What Are SNPs? In N. C. Oraguzie, E.H.A.Rikkerink, S.E. Gardiner, & H. N. De Silva (Eds.). Association Mapping in Plants. Pp 41-52. Springer Science+Business Media, LLC. 233 Spring Street, New York, NY 10013, USA.
- Elshire, R. J., Glaubitz, J. C., Sun, Q., Poland, J. A., Kawamoto, K., Buckler, E. S., & Mitchell, S. E. (2011). A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. *PloS one*, *6*(5), e19379. doi: 10.1371/journal.pone.0019379.
- Emebiri, L., Michael, P., Moody, D. B., Ogbonnaya, F. C., & Black, C. (2009). Pyramiding QTLs to improve malting quality in barley: gains in phenotype and genetic diversity. *Molecular Breeding*, *23*(2), 219-228.
- Flint-Garcia, S. A. (2003). Structure of Linkage Disequilibrium in Plants. *Annu. Rev. Plant Biol*, *54*, 357-374.
- Fox, G. P., Panozzo, J. F., Li, C. D., Lance, R. C. M., Inkerman, P. A., & Henry, R. J. (2003). Molecular basis of barley quality. *Australian Journal of Agricultural Research*, *54*(12), 1081-1101.
- Gupta, P. K., Roy, J. K., & Prasad, M. (2001). Single nucleotide polymorphisms: a new paradigm for molecular marker technology and DNA polymorphism detection with emphasis on their use in plants. *Current science*, 524-535.
- Hori, K., Sato, K., Kobayashi, T., & Takeda, K. (2006). QTL analysis of Fusarium head blight severity in recombinant inbred population derived from a cross between two-rowed barley varieties. *Breeding Science*, *56*(1), 25-30.
- Hussain, S. S. (2006). Barley genetics and genomics: A review. Proc. *Pakistan Acad. Sci. 43*. 83-81.
- Islamovic, E., Obert, D. E., Budde, A. D., Schmitt, M., Brunick, R., Kilian, A., ... & Jackson, E. W. (2014). Quantitative trait loci of barley malting quality trait components in the Stellar/01Ab8219 mapping population. *Molecular breeding*, *34*, 59-73.
- Jones, N., Ougham, H., & Thomas, H. (1997). Markers and mapping: we are all geneticists now. *The New Phytologist*, *137*(1), 165-177.
- Kiros, M., Hulluka, M., & Abang, M. M. (2004). Phenotypic Diversity in Rehnchosporium seclis from Ethiopia and Host response to barley scald. *Plant Pathology Journal*, *3*(1), 26-34.
- Kochevenko, A., Jiang, Y., Seiler, C., Surdonja, K., Kollers, S., Reif, J. C., ... & Graner, A. (2018). Identification of QTL hot spots for malting quality in two elite breeding lines with distinct tolerance to

abiotic stress. *BMC plant biology*, *18*, 1-17. doi: 10.1186/s12870-018-1323-4

- Ma, Z., Steffenson, B. J., Prom, L. K., & Lapitan, N. L. (2000). Mapping of quantitative trait loci for Fusarium head blight resistance in barley. *Phytopathology*, *90*(10), 1079-1088.
- Mackay, I., & Powell, W. (2007). Methods for linkage disequilibrium mapping in crops. *Trends in plant science*, *12*(2), 57-63.
- Massman, J. M., Jung, H. J. G., & Bernardo, R. (2013). Genomewide selection versus marker-assisted recurrent selection to improve grain yield and stover-quality traits for cellulosic ethanol in maize. *Crop Science*, *53*(1), 58-66.
- Matthies, I. E., Malosetti, M., Röder, M. S., & van Eeuwijk, F. (2014). Genome-wide association mapping for kernel and malting quality traits using historical European barley records. *PloS one*, *9*(11), e110046.
- Mohammadi, M., Blake, T. K., Budde, A. D., Chao, S., Hayes, P. M., Horsley, R. D., ... & Smith, K. P. (2015). A genome-wide association study of malting quality across eight US barley breeding programs. *Theoretical and applied genetics*, *128*, 705-721. DOI 10.1007/s00122-015-2465-5.
- Muñoz-Amatriaín, M., Cuesta-Marcos, A., Hayes, P. M., & Muehlbauer, G. J. (2014). Barley genetic variation: implications for crop improvement. *Briefings in functional genomics*, *13*(4), 341-350. doi:10.1093/bfgp/elu006.
- Muñoz-Amatriaín, M., Moscou, M. J., Bhat, P. R., Svensson, J. T., Bartoš, J., Suchánková, P., ... & Close, T. J. (2011). An improved consensus linkage map of barley based on flow-sorted chromosomes and single nucleotide polymorphism markers. *The Plant Genome*, *4*(3).
- Myles, S., Peiffer, J., Brown, P. J., Ersoz, E. S., Zhang, Z., Costich, D. E., & Buckler, E. S. (2009). Association mapping: critical considerations shift from genotyping to experimental design. *The Plant Cell*, *21*(8), 2194-2202.
- Nickell, C. D., & Grafius, J. E. (1969). Analysis of a Negative Response to Selection for High Yield in Winter Barley, Hordeum vulgare L. 1. *Crop science*, *9*(4), 447-451.
- Schmalenbach, I., & Pillen, K. (2009). Detection and verification of malting quality QTLs using wild barley introgression lines. *Theoretical and applied genetics*, *118*, 1411-1427.
- Semagn, K., Bjørnstad, Å., & Ndjiondjop, M. N. (2006). An overview of molecular marker methods for plants. *African journal of biotechnology*, *5*(25).
- Slate, J. O. N. (2005). INVITED REVIEW: Quantitative trait locus mapping in natural populations: progress, caveats and future directions. *Molecular ecology*, *14*(2), 363-379.
- Spies, A., Korzun, V., Bayles, R., Rajaraman, J., Himmelbach, A., & Hedley, P. (2012). Allele mining in barley genetic resources reveals genes of race-non-specific powdery mildew resistance. *Frontiers in plant science*, *2*, 17212. Doi: 10.3389/fpls.2011.00113.
- Spindel, J., Wright, M., Chen, C., Cobb, J., Gage, J., Harrington, S., ... & McCouch, S. (2013). Bridging the genotyping gap: using genotyping by sequencing (GBS) to add high-density SNP markers and new value to traditional bi-parental mapping and breeding populations. *Theoretical and applied genetics*, *126*, 2699-2716.
- Sreenivasulu, N., Graner, A., & Wobus, U. (2008). Barley genomics: an overview. *International journal of plant genomics*, *2008*.
- Szűcs, P., Blake, V. C., Bhat, P. R., Chao, S., Close, T. J., Cuesta-Marcos, A., ... & Hayes, P. M. (2009). An integrated resource for barley linkage map and malting quality QTL alignment. *The Plant Genome*, *2*(2).
- U.S. General Accounting Office (GOA). 1999. Grain fungus creates financial distress for North. Dakota
- Walker, C. K., & Panozzo, J. F. (2016). Genetic characterisation, expression and association of quality traits and grain texture in barley (Hordeum vulgare L.). *Euphytica*, *212*(2), 157-171. doi: 10.1007/s10681-016-1767-2.
- Wang, M., Jiang, N., Jia, T., Leach, L., Cockram, J., Waugh, R., ... & Luo, Z. (2012). Genome-wide association mapping of agronomic and morphologic traits in highly structured populations of barley cultivars. *Theoretical and Applied Genetics*, *124*, 233-246.
- Welsh, J. R. (1981). *Fundamentals of plant genetics and breeding*. John Wiley & Sons.
- Wenzl, P., Li, H., Carling, J., Zhou, M., Raman, H., Paul, E., ... & Kilian, A. (2006). A high-density consensus map of barley linking DArT markers to SSR, RFLP and STS loci and agricultural traits. *Bmc Genomics*, *7*, 1-22. doi: 10.1186/1471-2164-7-206.
- Whitkus, R., Doebley, J., & Lee, M. (1992). Comparative genome mapping of Sorghum and maize. *Genetics*, *132*(4), 1119-1130.
- Yu, G. T., Franckowiak, J. D., Neate, S. M., Zhang, B., & Horsley, R. D. (2010). A native QTL for Fusarium head blight resistance in North American barley (Hordeum vulgare L.) independent of height, maturity, and spike type loci. *Genome*, *53*(2), 111-118.
- Zhang, Z., Ersoz, E., Lai, C. Q., Todhunter, R. J., Tiwari, H. K., Gore, M. A., ... & Buckler, E. S. (2010). Mixed linear model approach adapted for genome-wide association studies. *Nature genetics*, *42*(4), 355-360.
- Zhou, T., Takashi, I., Ryouichi, K., Naohiko, H., Makpot, K., Takechiro, H., & Kazuhiro. S. (2012). Malting Quality Quantitative Trait Loci on a High-density Mikamo gelden x Harrington Cross in Barley (Hordeum vulgare L.). *Mol. Breeding*, *30*, 103-112.