The Pharma Innovation Journal 2023; 12(8): 2270-2284

www.ThePharmaJournal.com

The Pharma Innovation

ISSN (E): 2277-7695
ISSN (P): 2349-8242
NAAS Rating: 5.23
TPI 2023; 12(8): 2270-2284

www.thepharmajournal.com
Received: 09-05-2023
Accepted: 12-06-2023

All Author's names given below the References

A review: Application of GWAS technology for the improvement in wheat for hybrid development

Asha Kushwah, Sanjay Singh, RS Sikarwar, Uttam Kumar, Sakshi Sharma, Sushma Tiwari, Manish Vishwakarma, Pradeep Kumar Yadav, Mahvash Khaleel, Sarika Mahor, Poonam, Kiran Makwana, Abhishek Singh Kushwah, Ramcharan Ahirwar, M Yasin and Ravi Kumar Kushwah

Abstract
With the progression in next-generation sequencing technology, leading to millions of single nucleotide polymorphisms in all crop species as well as wheat, genome-wide association study (GWAS) has become a leading approach for characteristic categorization. Development of hybrid wheat is based on scoring relative importance globally because it assures increased and more sustainable yield than other varieties. Extrusion of anther is a characteristic which can be determined optically valuing the intensity of conferred anthers exterior to the glumes of the florets. Genetic compositions were optically evaluated for extrusion of anthers by making use of scale from 1-9 with 1 indicating minute or only the tip of anther can be seen and 9 indicating large numbers of anther completely present outside of the floret. Association mapping have three major advantages as compared to genetic mapping based on bi-parent population crosses. These are; - 1) larger & high pool of various representative genes can be surveyed. 2) It by passes the expenditure and time of mapping population studies which otherwise required in making the cross and generation advancement. 3) Mapping of maximum parameters in one set. In addition to this the other benefits is the finer mapping focus as compared to conventional breeding through mapping. Adoption of genome-wide association studies was united with gene regulatory set of connections and pathway analyses or epistatic interactions analyses; all these have taken the relationship mapping move toward to new heights in improvement of wheat production.

Keywords: Phytotoxic, cleistogamous, GWAS, hybridizing agents, heterosis, sterile, etc

Introduction
Development of hybrid wheat is scoring relative importance globally because it assures increased and more sustainable yield than other varieties. The cleistogamous floral nature of wheat (*Triticum aestivum* L.) is main bottleneck in cross-pollination of wheat that leads anthers inside the flower, enable it strictly self-fertilizer. Hence, high anther extrusion is required to promote allogamy and to satisfy with high level of pollen presence for the female plant for hybrid seed production.

Historical aspect of hybrids in Wheat
Edwards *et al.* (2001) [105] reported that the Wheat is a highly autogamous crop; hence, development of hybrids in wheat is very difficult. Kihara in 1951 firstly reported the discovery of use of CMS and FR (fertility restoration) in wheat which gave a hope for commercial hybrid seed production in wheat. From here onwards the production of hybrid wheat on commercial basis was started from several countries like USA, France, Australia and South Africa (Singh *et al*., 2010) [151].
Singh *et al.* (2010) [151] were started the hybrid seed production in wheat following approaches of male sterility have been used; 1) cytoplasmic male sterility 2) Genetic male sterility 3) artificial induction through chemical hybridizing agents (CHA) and 4) chromosome sterility. In India wheat breeding program has been started in 2009 by Indian Council of Agricultural Research (ICAR) using Cytoplasmic Male Sterility (CMS) but no hybrid was produced. But in the middle of few private organizations in India such as, Mahyco developed two hybrids of wheat (Pratham 7070 and Pratham 7272) in 2002 using cytoplasmic male sterility method for the production under less conditions and these two hybrids occupied 60,000 acres in six different states by 2004.

Corresponding Author:
Sanjay Singh
Researcher, Department of Horticulture, SHUATS, Prayagraj, Uttar Pradesh, India

Later several researches have been reported for hybrid development in wheat through A-B-R line system Singh *et al*., 2015) [152].

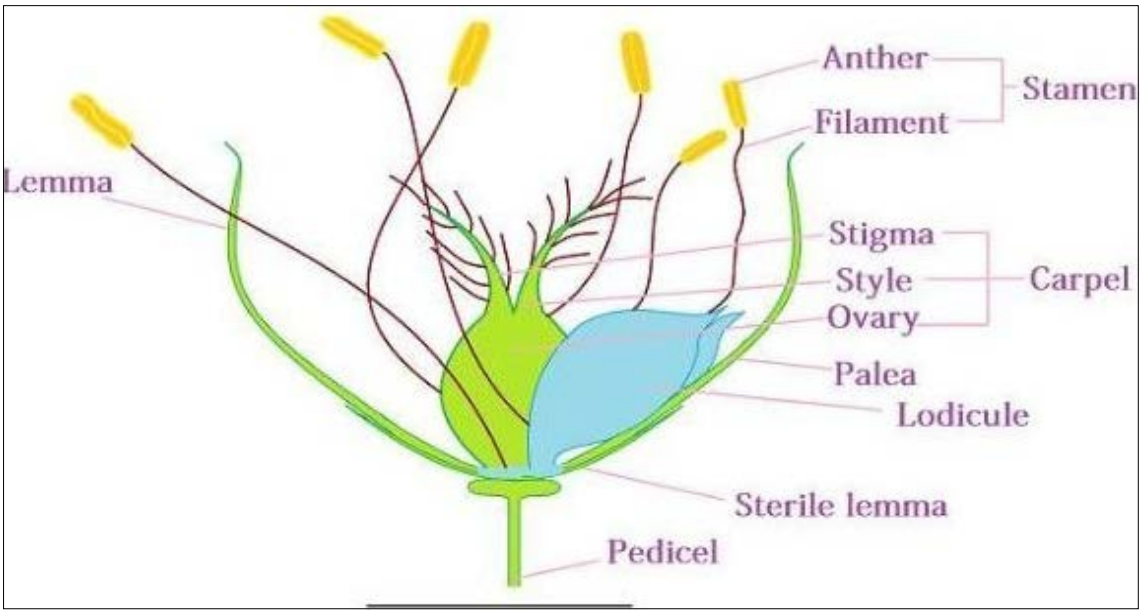
Parodi *et al.* (2009) [114] suggested the use of CHA's and Cytoplasmic genetic male sterility was also used in wheat (Asfaw, 2005) [2]. He found the difficulty in the setting of seed on the male sterile parent in seed production. The first finding on the impact of maleic hydrazide on wheat was given by Hoagland *et al*., 1953 [54]. Most of the CHAs have been used like gibberellins and ethylene but they were phytotoxic at the doses required to produce sterility in female. Some CHA's (WL 84811, Shell; clofencet (Genesis), Monsanto) have been suggested by Parodi *et al*., 2009 [114] who are pollen suppressors which are safer, having low phytotoxic effects and lowering improved quality of seeds. The chemicals suggested by him was efficient and can be used against large number of genotypes. Out of above-mentioned CHA's proposed by Parodi *et al*., in 2009 [114].

The extent of heterosis is also the basic requirement of hybrid development in wheat. Heterosis was first reported in wheat by Freeman (1919) [38] and can be explained by: (i) partial or complete dominance (Keeble and Pellew, 1910) [70], (ii) Over dominance, (iii) Epistasis (Richey, 1942) [127]. The expression of any potential heterosis for a component is likely to be strongly influenced by the environmental factors which may affect genotypes differently. However, many researchers have attempted to determine the component of yield responsible for heterosis in hybrid wheat. The principal studies of the source of grain heterosis indicated the tillers, grain number and grain weight as major components for realizing high yield potential. The results indicate that a single component is not the sole source of heterosis. This is not surprising since it is well known that there is considerable variation between line varieties of wheat in the performance of individual components (Singh *et al*., 2010) [151]. For this grouping of the lines into different pools have been tried to develop more utilization of heterosis (Xia *et al*., 2005) [176] but these are not having exception to genetically diverse in a particular environment. Therefore, uses of groups from different environments have been suggested to promote maximum genetic diversity among gene pools (Koekemoer *et al*., 2011) [73]. Several attempts were also made in the different research done by (Zhao *et al*., 2013, 2015; Boeven *et al*., 2016) [176, 175 13]. As per the finding done by Zhao *et al*., 2015 [175] on 135 promising wheat lines from Europe, for making 1604 single cross hybrids. He concluded that, yield of grains is the most promising parameter and additive effect is more effective than dominance effect. Various studies have also been done on Spelt wheat (*Triticum aestivum ssp. Spelta*) to utilize separate heterotic group in wheat hybrid breeding (Akel *et al*., 2018; Nielsen *et al*., 2014; Würschum *et al*., 2018; Boeven *et al*., 2016) [3, 110, 165, 13]. The outcomes of these studies showed lower yield heterosis and negative heterosis for grain quality. Therefore, it has been concluded that wheat is also not potentially strong so that it can utilize as separate group for heterosis in hybrid cultivation of wheat.

Overall, presence of non-functional pollens in the form of cytoplasmic, genetic & with the help of CHA's will be the most efficient method to ensure cross fertilization in wheat (Muqaddasi *et al*., 2017) [101]. However, now a day, the most popular method for hybrid cultivation in wheat is induction of male sterility through CHA's (Longin *et al*., 2012) [82]. Nevertheless, for the successful development of wheat hybrid, it is important to modify floral architecture of wheat to ensure cross-pollination (Whitford *et al*., 2013) [164]. This can be purely guaranteed by enough anther extrusion and shedding of viable pollen outside the flowers (Muqaddasi *et al*., 2017) [101].

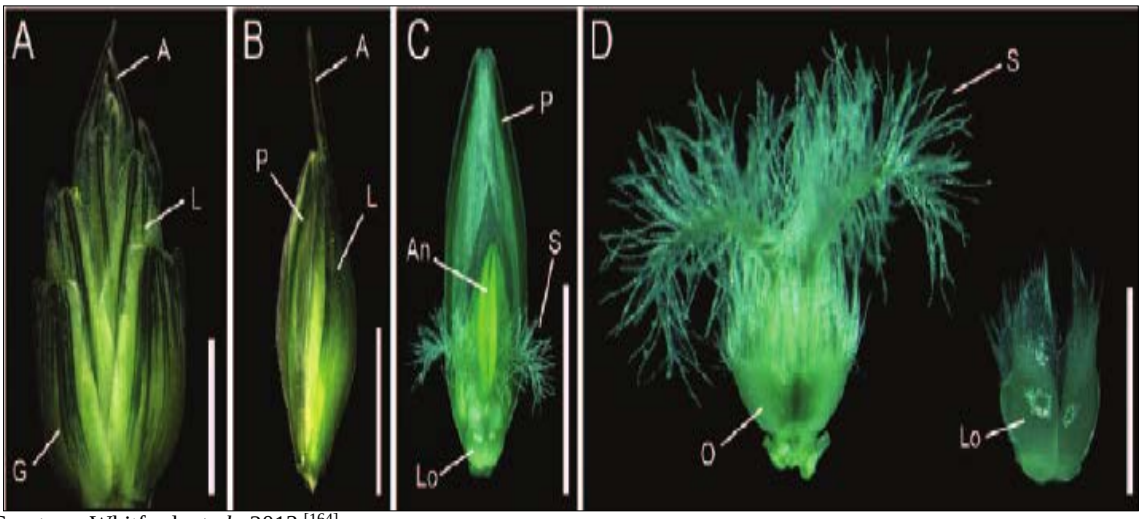
Role of floral architecture in wheat

Floral structure: The inflorescence of wheat is known as spike or composite ear. It is highly self-pollinated and is not having any petals or sepals. There is a presence of two styles in the female emerging with 2 feathers like stigmas and an ovary. On the opposite male flowers generally having three to five stamens made up of anther and filament as shown in Fig 1. The wheat flower is covered with two types of glumes; outer glume is known as lemma and an inner glume is called as palea.



Courtesy: https://scienceaid.net/Economic_Botany

Fig 1: Floral Structure of wheat

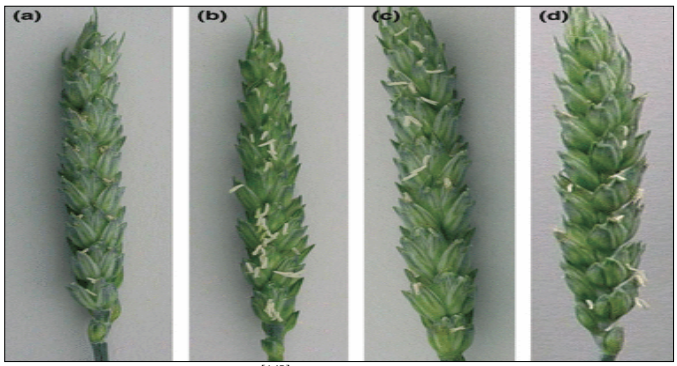


Courtesy: Whitford, *et al*., 2013 [164]

Fig 2: Detailed structure of wheat flowers and spikes.

Importance of Anther Extrusion (AE) in wheat

Muqaddasi *et al.* (2017) [101] reported that Anther Extrusion (AE) is the major hybrid contributing trait in wheat. It is the process where anthers come out from the spikelets at the time of anthesis. These anthers ensure cross pollination outside the spikelets after bursting in the air. Formerly it is spotted that the extrusion of anther hinge on the slitting of the floret. Keeping in expectation, the experiment highlights depends on 'the opening of glumes'.



Courtesy: Skiness *et al*., 2010 [142]

Fig 3: Anther extrusion in different genotypes a) Very poor anther extrusion b) High anther extrusion c) & d) Intermediate anther extrusion

Specifically, on the opening of glumes open or not (were also known as qualitative aspects of open flowering) and time period are of consequence turning on to the time of opening of glumes, opens for short duration due to which the pollens are not getting adequate time to come out or to get remain in between the glumes; such arrangements hold back the ability of movement of anthers in air itself. e.g in 3rd or 4th spikelet (Obermayer, 1916) [111]. However, it doesn't define that the opening of glumes is directly engaged with the extrusion of anthers. It is spotted that 1-2 anthers of floret are hanged on within the folded perimeter of palea or away, despite of the opening of the flower and the extending of the filaments (Percival, 1921) [118]. Zukov, 1969 [179] established a tie-up coefficient of 0.93 in hexaploid wheats (interpolating the percentage of unopened floret and the percentage of anther extrusion); whereas in diploid and tetraploid it was found to be 0.86 and 0.90 commonly. Taking into consideration the slitting of the floret for a short run during anthesis, it appears as a supremacy for cross-pollination in such a way that at this stage anthers are shoved out. With contrasting weather in triennial the percentage of extruding anther varied from 61.6-89.2% and 67.7-93.0% in common, including the driest year only few anthers were extruded (Rajki, 1962) [126]. This concedes through inspection of Livers, 1964; he stepped in renewing the minimum setting of seed by open fertilization on non-functional male parents in such sites which lacks water; this will be beneficial for indigent extrusion of anthers for the areas and also results in increasing of closed flowering in drought situations (cf. section 'Opening of the glumes'). Nettevic, 1966 took the numbers of anther extrusion as a principle for enhanced flowering pattern- this spotting can result in error and committed to an extent of flower to be opened amid 30 wheat varieties from 12% (Zavolskaja, 938) to 99% (durum wheat Hordeiforme 1404). The percentage of spikelet belonging to the extruding anthers of 1st three florets in 8 hard red wheat varieties varies from 25% (Centana) to 72% (Thatcher) (Joppa *et al*., 1968) [58]; whereas in 2 durum wheat varieties less percentage were determined, *viz* 22% and 32% differences were noted in segment of florets with extruded anther in 3 Russian varieties (Nikulina, 1969) [102]. In the varieties of durum Micurinka and Novomicurinka the extruding anthers of floret percentage during flowering was about 48% and 85% in 1966 (Kiricenko and Rodionova, 1969) [66]; according to these outcomes it sounds as prominent difference can arise depending on year to year. Reznikova (1969) [180] initiated the difference in percentage of florets with anther extrusion during contrasting years amid varieties, however the characteristics of varieties were under control. As per the findings of D' souza, (1970) the trial of 3 years results with appreciable difference in varieties; including the percentage of ranged anthers (less than 3% to more than 8%) in the midst of wheat varieties.

AE is a parameter which may be calculated visually by checking to what level anthers are coming outside glumes of the different florets. It is calculated using a scale from zero to nine with zero indicating the poor anther extrusion and nine indicating the excellent anther extrusion. The visual estimation of AE using a linear scale zero to nine was also given by Skinnes *et al*., (2010) [142]. He represented AE on the basis of low, intermediate and high as shown in Figure 3.

Extrusion of anther is a characteristic which can be determined optically valuing the intensity of conferred anthers exterior to the glumes of the florets. Genetic compositions were optically evaluated for extrusion of anthers by making use of scale from 1-9 with 1 reflecting minute or only the tip of anther can be seen and 9 reflecting large numbers of anther completely present outside of the floret. The reason for choosing visual assessment completely over more depth is because it increases the number of genetic compositions which can be obtained within minimal time. Extrusion of anther was done when the 50% of spikes exhibited their anthers and started shedding their pollen, which is also known as anthesis date. The obligation was held to systematize the schedule of evaluation to reduce prejudice in the field. The evaluation of genetic composition was affected by factors such as the spike of wheat, the amount of anthers spotted in accordance with each spikelet (Maximal the 9 is commonly feasible on the presumption the primary, secondary and tertiary florets having identical dates.

Role of genomics in history of wheat breeding

Earlier wheat improvement program was done by hybridization and very less mutation breeding and these methods played an important role in wheat breeding (Rasheed & Xia, 2019) [130]. This slow but successful progress of wheat breeding leads improvement in yield, abiotic and biotic stress (Mujeeb-kazi *et al*., 2013) [99]. Overall developments of wheat breeding from markers to genome based have been given in Fig: 4.

Early generation molecular markers

Traditional markers

Morphological markers

Karakoy *et al.* (2014) [64] studied that these are physical markers having distinguished qualities like various morphological and agronomic parameters like structure of seed, colour of seeds and many other important parameters. These are very handy to use and does not require any instruments. Some of the disadvantages of these markers are: they are not in huge quantity, very much influenced by the stages of crop growth and are having various issues related to environments (Eagles *et al*., 2001) [30]. Earlier, researchers and humans used these marker successfully for the identification of variation for improved plant breeding.

Cytological markers

Jiang (2013) [60] were detects that the variations parameters like size, shape, banding pattern and many more traits which are important. These are known as cytological markers because in this the variations tell the subtraction in the distributions of euchromatin and heterochromatin. These markers are utilized in the finding of linkage groups and in mapping which is physical.

Biochemical markers

Bailey (1983) [7] found that these are also called as isozymes which are available in various forms of molecular enzymes which are coded by several genes, but are having same work. They are co-dominant in nature, very easy to utilize and very cost-efficient. However, a very less number of these markers are available; also having the problem for detecting very less polymorphism and is having long extraction procedure of plant parts and different growth stages of various plants (Mondini *et al*., 2009) [91].

Molecular markers/DNA markers

Mondini *et al.* (2009) [91] were studied that these are the sequences of nucleotides which can make to distinction of dissimilar individuals. An ultimate marker should be co-dominant in nature, distribution should be even throughout the genome, reproducibility arte will be high and is having the ability to identify polymorphic loci in higher rate.

Table 1: Comparative list of the important characteristics of most commonly used molecular markers

Characteristics	RFLP	RAPD	AFLP	ISSR	SSR	SNP	DArT	Retrotransposons
CD/D	CD	D	D	D	CD	CD	D	D
Reproducibility in Results	H	H	I	M&H	H	H	H	H
Polymorphic condition	M	VH	H	H	H	H	H	H
DNA quality	H	H	H	L	L	H	H	H
DNA quantity	H	M	L	L	L	L	L	L
Marker index	L	H	M	M	M	H	H	H
Genome abundance	H	VH	VH	M	M	VH	VH	H
Cost	H	L	H	H	H	Variable	Cheapest	Cheapest
Sequencing	Yes	No	No	No	Yes	Yes	Yes	No
Status	Past	Past	Past	Present	Present	Present	Present	Present
PCR requirement	No	Yes	Yes	Yes	Yes	Yes	No	Yes

Courtesy: Nadeem *et al*., 2018 [106]

CD: Co-dominant, D: Dominant, H: High, M&H: Medium & High, L: Low, M: Medium, VH: Very High, I: Intermediate

Several molecular markers have been practiced and utilized successfully in breeding and plant genetics studies in different agricultural and horticultural crops. On their method of detection some brief information about molecular markers are explained below. Comparative list of the promising characteristics of most of the molecular markers utilized are given in Table 1.

Markers Based on Hybridization

Restriction Fragment Length Polymorphism (RFLP)

It is the first molecular marker technique and is the single marker system on the basis of hybridization. In this, the restriction enzymes are utilized to cut down the DNA at specific loci which is known as recognition sites resulting higher number of fragments with various lengths at different positions. This separation can be seen in the form of band scan via Agarose or PAGE (Polyacrylamide Gel

Electrophoresis). In this the restriction enzymes is not having the ability to cut the fragment if single base-pair variation occurs in at specific loci. However, the heterozygous condition will occur only if this point mutation occurs in one chromosome but not in the other, as both bands are present (Madhumati, 2014) [88].

Markers Based on PCR (Polymerase Chain Reaction)

This technique was first invented by Kary Mullis in 1983. In this technique a small quantity of DNA can amplify without the involvement of any organisms which is living (Mullis *et al*.,1986) [100]. The main steps involved in PCR reaction is Denaturation, annealing and extension.

Randomly Amplified Polymorphic DNA (RAPD)

Williams *et al.* (1990) [163] was developed this method and Solely. In this, 10 nucleotides and random primer is used for the amplification of DNA. During the PCR reaction, amplification will only takes place when two for hybridization show similarity to each other and their direction will be opposite. For exact visualization of different bands, ETBR stained agarose gel is used (Jones *et al*., 1997) [57]. The level of polymorphism detected either between the sites which are bind and can be seen in the electrophoresis's with the presence or absence of specific bands (Jiang, 2013) [60].

Amplified Fragment Length Polymorphism (AFLP)

Lynch and Walsh, (1998) [84] reported that the markers which combine the RFLP marker and PCR method is known as AFLP. In this DNA digestion is done and after that performance of PCR takes place. These are easy and economical and information of sequence is not required priorly. In AFLP, for the cutting of DNA two restriction enzymes are used. For the working, each corner of the fragments is ligated with the oligonucleotides. The fragment of short nucleic acid are utilized for the ligation in PCR is known as oligonucleotides (Madhumati, 2014) [88]. In this the visualization of bands takes place by using agarose gel or PAGE stained with $AgNO_3$ or by autoradiography (Madhumati, 2014) [88].

Microsatellites or Single Sequence Repeats (SSR's)

SSRs (Litt and Luty, 1989; Tautz, 1989) [80, 155], short tandem repeats and simple sequence length polymorphisms (Schlotteroer *et al*., 1991) [139]. These are the tandem repeat of 1-6 nucleotides that exist omni present in genome of various species (Beckmann & Weber, 1992) [8]. Microsatellites can be mono-nucleotide, di-nucleotide, tri-nucleotide, tetra-nucleotide, penta-nucleotide and hexa-nucleotide (Weber, 1990) [161]. They are present in the genome, chloroplast (Provan *et al*., 2001) [119] and mitochondria (Rajendra Kumar *et al*., 2007) [125]. In protein-coding genes, the availability of SSR's is called as expressed sequence tags (ESTs) (Morgante *et al*., 2002) [94]. The main function of this marker is high polymorphism with less repeats per locus (Zane *et al*., 2002) [172]. The formation of SSR markers is based on the production of a SSR library and then identification of specific microsatellites. After the completion of this procedure, the identification of regions which are favourable for designing of primer is done and then running of PCR takes place. Evaluation & Interpretation of banding patterns are performed and assessment has been done on the basis of polymorphism (Roder *et al*., 1988) [128]. SSR markers show good reproducibility level. It is co-dominant and has a greater abundance of genome. They are widely used for the mapping studies in plants (Schlotteroer *et al*., 1991; Kalia *et al*., 2011) [139, 68].

Chloroplast Microsatellites (cpSSRs)

These markers are popular for population genetics studies (Provan *et al*., 2001) [119]. They contain mono-nucleotide motif regions which are repeated at least 8-15 times. They show high polymorphic value and it varies across species and loci. The two main features who distinguish the cpSSRs from nuclear microsatellites are (i) Inheritance of chloroplasts uniparentlly (ii) the chloroplast chromosome is a non-recombinant molecule due to which all cpSSRs loci are linked (Navasceus & Emerson, 2005) [103]. These are applied successfully in agriculture and basic plant sciences (Ebert & Peakall, 2009) [31].

Sequence-related Amplified Polymorphism (SRAP)

Such marker is formed by Li and Quiros in 2001. The main function is the enlargement of open reading frames (ORFs). In this system the enlargement is done using two primers (forward and reverse). The primers used for this marker system are 17–18 nucleotides long. For forward primer they use CCGG and AATT used as a reverse primer and the setting of 35 °C temperature of annealing in the first 5 cycles during PCR reaction will be done. The reaming cycles (35) are run at 50 °C temperature of annealing. The enlarged regions are visualized in the agarose gel with the help of autoradiography. SRAP markers are dominant in nature &scoring of DNA fragments are done by calculating the band in the form of 0 (absence) or 1 (presence). This is widely used in various sectors like construction mapping, genomic mapping and cDNA fingerprinting (Salazar *et al*., 2014) [146].

Inter simple sequence repeat (ISSR)

This marker was first produced by Zietkiewicz *et al*., 1994 [178]. In this the primers having a size of 15–30 bases and these are utilized in this technique. This allow us the usage of high temperature of annealing of about 45-60 °C; the length of the enlarged products are 200-2000 base pairs and these can be seen through agarose gel or PAGE (Fang & Roose, 1997) [35]. These are also dominant markers like SRAP (Zietkiewicz *et al*., 1994) [178]; but its usage is for the production of co-dominant markers also. This is very simple marker and easily handled as compared to other markers like RAPD and the prior knowledge of DNA sequences are also not required in this marker (Chatterjee *et al*., 2004) [18].

Cleaved amplified polymorphic sequences (CAPS)

Originally CAPS are also known as PCR–RFLP markers due to combination of RFLP and PCR (Maeda *et al*., 1990) [92]. Two gels; Agarose gel and acrylamide gel is utilized for the appearance of CAPS markers. These are co-dominant in nature and are very much used in genotyping, cloning and identification of molecular studies (Spaniolas *et al*., 2006; Weiland & Yu, 2003) [143].

Sequence-characterized amplified regions (SCAR)

SCAR technique was initially produced in 1993 by Paran and Michelmore in lettuce for disease resistance genes against downy mildew (Paran & Michelmore, 1993) [115]. These are confined markers and its reproducible rate is high in

comparison with RAPD (Yang *et al*., 2013) [102]. The nature of these markers is co-dominant and mono-locus, which are very much used in mapping population physically (Yang *et al*., 2013) [102]. These are developed through purification of fragments of PCR after by formation of primers (SCAR) (Paran & Michelmore, 1993; Kiran *et al*., 2010) [115, 65]. The Polymorphism level is identified by utilizing agarose and after that investigation of sequence nucleotide of DNA fragments takes place.

Table 2: Advantages and disadvantages of different molecular markers

Markers	Advantages	Disadvantages	References
MM	Financially economical and ease in handling	Having low polymorphism	[1]
BM	Specific instruments not required Co-dominant Ease in handling	Having low polymorphism Influenced by climatic factors	[2]
RFLPs	Prior sequencing is not necessary Co-dominant	Time Taking. Need pure DNA in huge quantity	[3]
RAPD	Polymorphic & ease in handling Need DNA in less quantity	More purified DNA is required Dominant Reproducibility in results is poor	[4-3]
AFLP	Reproducibility rate of results is high Reliable marker	More purified DNA is required Dominant Need pure DNA in huge quantity	[3, 5, 6]
SSRs	Reproducibility rate of results is high Required less quantity of DNA Co-dominant	Cost is high There is a presence of null alleles	[7, 8, 9]
ISSR	Strong in polymorphism Safe, simple & easy to handle	Requires pure DNA Low reproducibility rate Different sized fragment	[10, 11, 12]
SRAP	Handy Reliable Safe and ease in isolation of bands	Dominant marker with moderate &high throughput ratio	[13, 14]
Retrotransposons	Safe, simple and ease in usage Reproducibility rate is high	Dominant marker	[15, 16, 17]
SNP	Efficient Wide adaptation in genome Prior sequencing information not required Results reproducibility rate is high Co-dominant marker	Developmental cost is high	[4, 3]
DArT	Efficient Polymorphism level high Prior sequencing information not required Results reproducibility rate is high	Dominant marker Developmental cost is high	[18, 19]

Courtesy: Nadeem *et al*., 2018 [106]: Eagles *et al*., 2001; [30]: Mondini *et al*., 2009; [91]: Madhumati, 2014; [88]: Jiang, 2013; [60]:, Provan *et al*., 2001; [119]: Zane *et al*., 2002; [172]: Kalia *et al*., 2011; [68]: Zietkiewicz *et al*., 1994; [178]: Ng & Tan, 2015; [38]: Uzun *et al*., 2009; [158]: Roy *et al*., 2015; [136]: Kalendar *et al*., 2011; [62]: Kalendar *et al*., 1999; [63]: Jaccoud *et al*., 2001; [56]: Huttner *et al*., 2004 [55]; MM: Molecular Markers; BM: Biochemical Markers

Next generation molecular markers

Sequence-based markers

These are those markers in which bases of nucleotides and order, both is detected along with the strand of DNA (Franca *et al*., 2002) [37]. This technology have been developed from the reality that markers based on hybridization method are not very much reliable and their level of polymorphism is also not high. The beginning technologies based on sequencing method like next-generation sequencing and genotyping by sequencing transformed the breeding strategies via formation of SNPs gives level of polymorphism high (Davey *et al*., 2011) [19]. Some recent sequencing methods are as follows:

Next-generation sequencing (NGS)

NGS technique has the great ability to form various hundreds of millions to several hundreds of billions bases of DNA per run (Shendure & Ji, 2008) [104]. Now many organizations have this technique and they are able to show their commercial availability, such as Illumina MiSeq and HiSeq 2500 (Bentely *et al*., 2008) [9], Roche 454 FLX Titanium (Thudi *et al*., 2012) [156] and Ion Torrent PGM (Rothberg *et al*., 2011) [135]. These NGSs gives in economical and keenly covering the whole genome (Deschamps *et al*., 2012) [28]. The benefits of NGS are (1) Its accuracy. (2) It gives high output in less cost. (3) Recently this technique is very much used in the construction of linkage/halophyte maps and in genome-wide association studies (GWAS) (Elshire *et al*., 2011) [23]. (4) NGS marker also enables us to sequence the older DNA samples and this method has given strength in the area of meta-genomics (Mardis, 2008) [90].

Genotyping by sequencing (GBS)

Now a days, this technique is very much used due to its use in simple way. This method of sequencing was formed in the Buckler lab under the Illumina, next generation sequencing platform. Based on ion PGM use system, GBS techniques are of two types: (1) restriction enzyme digestion: this method is for the use in marker assisted selection (MAS). In this method, prior to the ligation of adapters, DNA is digested with one or two specific restriction enzymes. (2) Enrichment of multiplex PCR: This technique provides opportunity to the

specific PCR primers which are selected for the amplification of point of view. The method of digestion in the restriction enzyme, a complete set of SNPs is identified for a genome section.

Following are the sequence based markers developed on the basis of sequencing methods which are discussed above.

Single-nucleotide polymorphism (SNP)

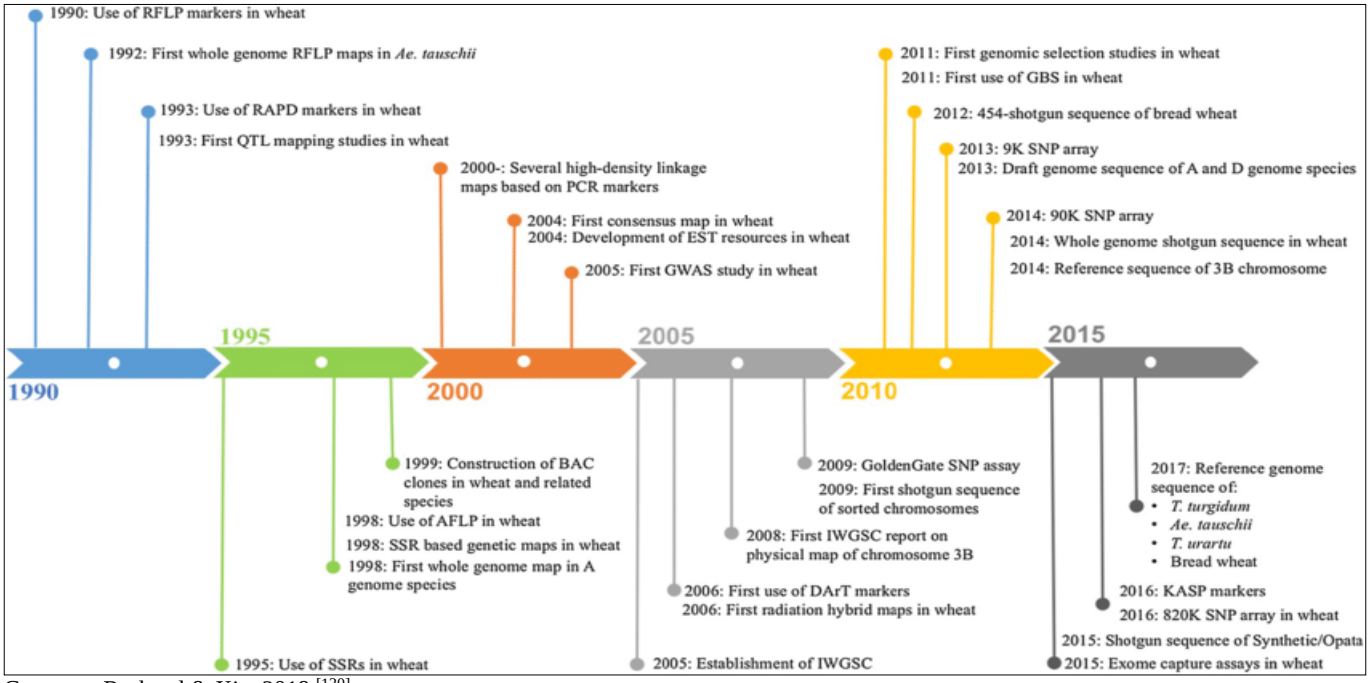
These are the markers that perform single base-pair changes which are exist in the sequence of genome to an individual. They may be transitions or transversions based on the substitution of nucleotides. A huge number of methods available for the genotyping of SNP markers which are based on various methods of platform identification and discrimination of alleles. Identification of SNP markers have been done via sequence data analysis preserved in various databases.

Diversity Array Technology (DArTSeq)

This technique provides great option for the genotyping, which are evenly allocated on the whole genome. This technique is having high reproducibility rate and is used in the micro-array hybridization technology. No earlier sequencing is required for the identification of loci for interested traits (Jaccoud *et al*., 2001; Huttner *et al*., 2004) [56, 55]. The essential fact about this method is that it gives high output and is very financially economical in use. Its only one reaction can genotype various thousands of genomic loci and also able to discover the polymorphism in the locus. An identical channel is used for the scoring and development of marker. Once the marker have been developed specific assays is not required for genotyping. Such types of markers are successfully used for genotyping (Huttner *et al*., 2004) [55]. The main benefits and losses of several genetic markers are described in Table 2.

Gene/DNAChip based markers

An Affymetrix wheat GeneChip oligonucleotide array has been developed with over 61127 probe sets representing 55052 transcripts (http://www.affymetrix.com), and this has enabled the generation of numerous high-quality gene expression data sets (Coram *et al*., 2008) [19]. With this chip assay of transcriptome of the developing grains have been developed (Wan *et al*., 2008) [19] and it is also used to detect the genes which are concerned for the formation of low heat resistant (Laudencia-Chingcuanco *et al*., 2011). This Chip have future applications like to profile with *Puccinia striiformis* by confirming the changes occurred after inoculation in wheat parental lines that distinguished for the availability of the Yr5 gene (Coram, Wang, and Chen, 2008) [19].



Courtesy: Rasheed & Xia, 2019 [130]

Fig 4: Overall markers evolutions in wheat breeding

Genome wide association analysis for anther extrusion trait in wheat

GWAS is a very important tool for the identification of phenotypic variation. It is a new tool which involves rapid scanning of thousands of markers across the set of DNA. In the past few years, GWAS & QTL were the two promising methods for the identification gene function; these approaches were also used for the identification of genes which were responsible for segregation and are accountable for the variation (phenotypic) (Chan *et al*., 2011; Ogura and Busch,2015; Burghardt *et al*., 2017) [17, 112, 16]. GWAS have different approach then QTL in 2 main significant points. (1) Earlier mapping of QTL is totally dependent on only two parents for mapping; therefore, breeder can use limited amount of genetic variation for the improvement of any crop. (2) Relatively very less recombination's originated during the creation of a biparental mapping population. Using biparental mapping population various researchers have developed QTL's in different crops. The detail of various QTL's identified by Bi-parental mapping and GWAS was given by Colasuonno *et al*., 2021[20] and are shown in Table 3.

There are some factors which affect the performance of GWAS. The main prospect of association studied from wide genome is concerned to the number and size of the genes

which are responsible for different variation. The genes which are responsible for variation in highly difficult multi genic quantitative parameters such as plant height; GWAS will not be the strong tool for variation as suggested by several findings (Yang *et al*., 2013; Peiffer *et al*., 2014; Burghardt *et al*., 2017) [170, 116, 16]

Table 3: Summary of quantitative trait loci (QTL) identified using Bi-parental mapping and GWAS.

Crosses	Type	No. of Genotypes	No. of QTL's Identified	Traits	References
Abiotic Stress					
Langdin X G18-16	RIL	156	31	CIR, OP, CC, FLRI	[1]
Kofa X svevo	RIL	247	12	PDL, SPAD, NDVI	[2]
Omrabi5 X Belikh2	RIL	114	6	CL, RRT	[3]
Colosseo X Lloyd	RIL	176	28	RRT	[4]
Meridiano X Caludio	RIL	181	32	RRT	[4]
Simeto X Mollise Colli	RIL	136	18	RRT	[5]
Elite Cultivars	Genome Wide Studies	57	4	RRT	[6]
Elite Cultivars	Genome Wide Studies	183	2	RRT	[7]
Elite Cultivars	Genome Wide Studies	183	31	RRT	[4]
UNIBO-DP	Genome Wide Studies	248	73	DB, NDVI, SPAD	[8]
Biotic Stress					
Strongfield X Blackbird	DH	85	2	FHB	[9]
LDN X LDN-Dic7A	RIL	118	1	FHB	[10]
Colosseo X Lloyd	RIL	176	1	LR	[11]
Meridiano X Caludio	RIL	181	1	SBCMV	[12]
DS X Td161	BC	134	1	FHB	[13]
Floradur X Td161	BC	129	3	FHB	[13]
Helidur X Td161	BC	126	1	FHB	[13]
Kristal X Sebatel	RIL	85	7	SR	[14]
Simeto X Levante	RIL	180	7	SBCMV	[15]
Karur X DBC-480	RIL	111	1	FHB	[16]
Strongfield X Blackbird	DH	90	2	LS	[17]
Kofa X W9262-260D3	DH	155	1	YR	[18]
Joppa X 10Ae564	RIL	205	3	FHB	[19]
Rusty X PI 192051-1	RIL	180	5	LR	[20]
Ben X Tunisian 108	BIL	171	3	FHB	[21]
Greenshank X AC Avonlea	DH	132	4	CP	[22]
Different Sources	Genome Wide Studies	323	3	FHB	[23]
Worldwide collection	Genome Wide Studies	496	50	LR	[24]
Elite Cultivars	Genome Wide Studies	183	8	SR	[25]
Ethopian lanraces	Genome Wide Studies	318	20	STB	[26]
Elite Cultivars	Genome Wide Studies	250	16	YR	[27]
Elite Cultivars	Genome Wide Studies	92	1	YR	[28]
Tetraploid panel	Genome Wide Studies	230	37	SR	[29]
Spring lines	Genome Wide Studies	228	7	FHB	[30]
Quality					
Colosseo X Lloyd	BP	176	12	YPC	[31]
Kofa X svevo	BP	249	4	YPC	[31]
Meridiano X Caludio	BP	181	6	YPC	[31]
Svevo X Y12-3	RIL	208	9	GPC	[32]
Saragolla X 02-5B-318	RIL	135	9	GPC	[33]
Pelissier X Strongfield	DH	162	6	SV	[34]
Worldwide collection	Genome Wide Studies	93	20	YPC	[35]
Agrogen	Genome Wide Studies	104	19	AX	[36]
Agrogen	Genome Wide Studies	230	7	BG	[37]
Durum Collection	Genome Wide Studies	124	6	YPC	[38]
Canadian Durum Wheats	Genome Wide Studies	169	6	YPC	[39]
Canadian durum lines	Genome Wide Studies	192	28	YPC	[40]
Mediterranean landraces	Genome Wide Studies	172	14	GPC, GS, TW, YPC	[41]
European Varieties	Genome Wide Studies	514	10	AE	[42]
NASMA X IAS20*5/H567.71	RIL	197	7	FHB	[43]
NASMA X RPB709.71/COC	RIL	185	6	FHB	[43]
Advanced parental lines	Genome Wide Studies	663	5	AE	[44]
Advanced breeding lines	Genome Wide Studies	139	8	SBD	[45]

AE: Anther Extrusion; YPC: yellow pigment content; TW: test weight; SV: SDS-sedimentation volume; PGC: phosphorus grain concentration; PM: powdery mildew; Chlorophyll concentration measure; GSeY: grain selenium yield; GZnC: grain zinc concentration; LR: leaf rust; CC: Chlorophyll content; DB: dry biomass; NDVI: normalized difference vegetation index; GSC: grain sulfur concentration; GPC: grain protein content; soil-borne cereal mosaic virus; YR: yellow rust; AX: Arabinoxylan; GS: gluten strength; STB: *Zymoseptoria tritici* blotch; BG:-glucan; FHB: Fusarium head blight; SBCMV:SR: stem rust; RRT: root-related trait; CP: *Claviceps purpurea*; CIR: carbon isotope ratio; CL: coleoptile length; FLRI: flag leaf rolling index; OP: osmotic potential; SPAD:LS: loose smut; GSeC: grain selenium concentration; Fb: flour yellow color; PDL: length of the ear peduncle[1]: Peleg *et al*., 2009; [117]: Graziani *et al*., 2014; [48]: Nagel *et al*., 2014; [107]: Iannucci *et al*., 2017; [59]: Condorelli *et al*., 2018; [18]: Somers *et al*., 2006; [153]: Kumar *et al*., 2007; [67]: Haile *et al*., 2012; [49]: Prat *et al*., 2017; [78]: Kumar *et al*., 2018; [75]: Lin *et al*., 2018; [79]: Zhao *et al*., 2018; [104]: Aoun *et al*., 2019; [4]: Pirseyedi *et al*., 2019; [72]: Gordon *et al*., 2020; [29]: Ghavami *et al*., 2011; [24]: Aoun *et al*., 2016; [5]: Letta *et al*., 2014; [77]: Kidane *et al*., 2017; [72]: Liu *et al*., 2017; [81]: Saccomanno *et al*., 2018;[145]: Steiner *et al*., 2018; [144]: Colasuonno *et al*., 2017; [20]: Fatiukha *et al*., 2020; [41]: Giancaspro *et al*., 2019; [45]: Ruan *et al*., 2020; [137]: Marcotuli *et al*., 2015; [37]: Marcotuli *et al*., 2016; [96]: Colasuonno *et al*., 2017; [20]: N'Diaye *et al*., 2017; [104]: N'Diaye *et al*., 2018; [015]: Rosello *et al*., 2018; [134]: Muqaddasi *et al*.,2017; [101]: Xu *et al*., 2019; [167]: Adhikari *et al*., 2020; [1]: Tomar *et al*., 2021[157]

A big challenge in GWAS is the so-called 'missing heritability', which refers to the observation that only a small proportion of phenotypic variation can be accounted for by all associated SNPs. This concept has been thoroughly discussed in the context of human diseases (Manolio *et al*., 2009) [89]. Partial explanations for the missing heritability problem have been proposed. First, rare variants (Eichler *et al*., 2010, Manolio *et al*., 2009) [33, 89]. Second, many loci have small effects on the traits of interest, especially when these traits are quantitative, and therefore hard to statistically identify due to low power (Brachi *et al*., 2011) [14]. Third, multiple functional alleles of the same gene could be associated with different phenotypes, which would be difficult to identify by using univariate models (Korte *et al*., 2013, Zhou and Stephens, 2014) [74, 174]. Fourth, there are several interacting loci whose effects have not been discovered by additive-based GWAS (Seymour *et al*., 2016) [149]. Fifth, epistatic interactions between genes might also contribute to genetic variation (Wei *et al*., 2014) [160]. Finally, another potential source of the missing heritability is epigenetic variation, but this requires more sophisticated genotyping methods to be detected (Rakyan *et al*., 2011) [129]. Following the hypotheses described above, many studies focus on improving the methodological aspects of GWAS to provide more accurate associations. For example, multi-trait and multi-SNPs models to be created for the increase of detecting associations and to jointly analyze the polygenic gene-context interactions (Casale *et al*., 2017, Resende *et al*., 2017) [22, 133]. Other studies have focused on dominance and epistatic effects, especially in hybrid species (Seymour *et al*., 2016) [149].

GWAS (Genome Wide Association Studies) was estimated to observe and identify loci associated traits with agronomic, morphology of seeds (Shape & dimpling), and quality of seeds (protein, starch, and fiber concentrations) parameters. It is a reliable method for the identification of the genetic basis of difficult parameters utilizing the gene diversity which is naturally occurred (Korte and Farlow, 2013) [74]. This analysis also provides advanced resolution of mapping population than conventional bi-parent population studies to find out associations between various markers and different parameters of interest. This is utilized for the investigation of markers which are associated with promising characters in broad area of different crops (Zhang *et al*., 2017) [171]. The requirement for this analysis is evaluation of the population structure to identify the genetic similarity of individuals and reduce the finding of wrong associations (Korte and Farlow, 2013; Hormozdiari *et al*., 2016) [74, 50], and is reliable for the utility of huge markers. Now a days, recent trends in the platform of NGS and genotyping of SNP's will give some additional things for the characterization of diversity at a high focus and permit breeders for the identification and choosing the diversity which is useful to form new cultivars. In the current scenario, the presence of promising and good performance genotyping methods via SNP, Genome Wide Association Studies has been utilized as promising way for the identification of alleles linked with various parameters in large number of crops (Desgroux *et al*., 2016; Zhou *et al*., 2017; Mourad *et al*., 2018) [29, 174, 98].

Association mapping have three major advantages as compared to genetic mapping based on bi-parent population crosses. These are; - 1) larger & high pool of various representative genes can be surveyed. 2) It by passes the expenditure and time of mapping population studies which otherwise required in making the cross and generation advancement. 3) Mapping of maximum parameters in one set. In addition to this the other benefits is the finer mapping focus as compared to conventional breeding through mapping, where the investigated loci need to finely-mapping before using in marker assisted breeding (Remington *et al*., 2001) [132]. Though, statistical tools needed for the estimation are complex, since false associations which is positive in between the marker and a parameter can be occurred with the presence of structure of population causing linkage disequilibrium in between various loci that are not having any linkage or only for free linkage. To deal with this unknown population structure, some analytical tools have prepared (Falush *et al*., 2003) [36]. A condition may come in the selection procedure, genetic drift and system of mating (Flint-Garcia *et al*., 2003) [43]. In several plants, the domestication and process of breeding can be caused such Linkage Disequilibrium. Some Methods to fulfill with population structure analysis ranged from the quantitative transmission disequilibrium test through genomic control to structured association (Yu and Buckler 2006) [169]. Lastly, there is a set of random markers utilized to identify the population structure and will do its analysis, which is applied in a linear model for the checking of associations. Therefore, this will show a wider adaptability to MLM, kinship relations of the lines are incorporated, and show modified version of both type I and type II error rates as described by Yu *et al*., (2006) [168-169]. Less is called for the direct similarity of such approaches in estimating loci with genuine experimental dataset.

Conclusion and Suggestions

The incorporation of GWAS associations with cell type-

specific functional data has notably furthered our understanding of how genetic variation leads to disease. On the one aspects, SNP enrichment approaches have enabled the prioritization of cell types and tissues based on their disease-relevance. These methods work by testing for the gathering of variants in regulatory elements particular to a given cell type. They can either be constrained to genome-wide noteworthy variants or estimates, enrichments based on the assistance of all common SNPs. On the other aspects, co-localization analysis integrates eQTL and GWAS associations to identify the target genes of GWAS loci, leveraging LD information and association patterns.

References

1 Adhikari A, Basnet BR, Crossa J, Dreisigacker S, Camarillo F, Bhati PK, *et al*. Genome-wide association mapping and genomic prediction of anther extrusion in CIMMYT hybrid wheat breeding program via modeling pedigree, genomic relationship, and interaction with the environment. Frontiers in Genetics, 2020;11:1384.
2 Asfaw A. Behavior of bread wheat (*Triticum aestivum* L.) Male sterilized with cytoplasmic-genetic and chemical systems and their impact in hybrid seed production. Asian J Plant Sci. 2005;4:316-322.
3 Akel W, Thorwarth P, Mirdita V, Weissman EA, Liu G, Würschum T, *et al*. Can spelt wheat be used as heterotic group for hybrid wheat breeding?. Theoretical and applied genetics. 2018;131(4):973-984.
4 Akhtar N, Nazir MF, Rabnawaz A, Mahmood T, Safdar ME, Asif M, *et al*. Estimation of heritability, correlation and path coefficient analysis in fine grain rice (*Oryza sativa* L.). Journal of Animal and Plant Sciences; c2011, 21(4).
5 Aoun M, Breiland M, Kathryn Turner M, Loladze A, Chao S, Xu SS, *et al*. Genome-wide association mapping of leaf rust response in a durum wheat worldwide germplasm collection. Plant Genome, 2016;9:3.
6 Aoun M, Kolmer JA, Rouse MN, Elias EM, Breiland M, Bulbula WD, *et al*. Mapping of novel leaf rust and stem rust resistance genes in the Portuguese durum wheat landrace PI 192051. G3.2019;9:2535-2547.
7 Bailey DC. Isozymic variation and plant breeders' rights. In Developments in Plant Genetics and Breeding. *Elsevier*, 1983;1:425-440.
8 Beckmann JS, Weber JL. Survey of human and rat microsatellites. Genomics. 1992;12(4):627-631.
9 Bentley DR, Balasubramanian S, Swerdlow HP, *et al*. Accurate whole human genome sequencing using reversible terminator chemistry. Nature. 2008;456 (7218):53-59.
10 Baloch FS, Alsaleh A, de Miera LE, *et al*. DNA based iPB Sretrotransposon markers for investigating the population structure of pea (*Pisum sativum*) germplasm from Turkey. Biochem Syst Ecol. 2015;61:244-252.
11 Beissinger TM, Hirsch CN, Sekhon RS, *et al*. Marker density and read depth for genotyping populations using genotyping-by-sequencing. Genetics. 2013;193(4):1073-1081.
12 Bhagyawant SS. RAPD-SCAR markers: an interface tool for authentication of traits. J Biosci Med. 2016;4:1-9.
13 Boeven PH, Longin CFH, Würschum T. A unified framework for hybrid breeding and the establishment of heterotic groups in wheat. Theoretical and applied genetics. 2016;129(6):1231-1245.
14 Brachi B, Morris GP, Borevitz JO. Genome-wide association studies in plants: the missing heritability is in the field. Genome biology. 2011;12(10):1-8.
15 Buerstmayr M, Buerstmayr H. Comparative mapping of quantitative trait loci for Fusarium head blight resistance and anther retention in the winter wheat population Capo× Arina. Theoretical and Applied Genetics. 2015;128(8):1519-1530.
16 Burghardt LT, Young ND, Tiffin P. A guide to genome-wide association mapping in plants. Current protocols in plant biology. 2017;2(1):22-38.
17 Chan C, Qi X, Li MW, Wong FL, Lam HM. Recent developments of genomic research in soybean. J Genet. Genomics. 2011;39(7):317-324.
18 Chatterjee SN, Vijayan K, Roy GC. ISSR profiling of genetic variability in the ecotypes of Antheraea mylitta Drury, the tropical tasar silkworm. Russ J Genet. 2004;40(2):152-159.
19 Coram TE, Settles ML, Wang M, Chen X. Surveying expression level polymorphism and single-feature polymorphism in near-isogenic wheat lines differing for the Yr5 stripe rust resistance locus. Theoretical and Applied Genetics. 2008;117(3),401-411.
20 Colasuonno P, Lozito ML, Marcotuli I, Nigro D, Giancaspro A, Mangini G, *et al*. The carotenoid biosynthetic and catabolic genes in wheat and their association with yellow pigments. BMC Genom. 2017;18:122.
21 Canè MA, Maccaferri M, Nazemi G, Salvi S, Francia R, Colalongo C, *et al*. Association mapping for root architectural traits in durum wheat seedlings as related to agronomic performance. Mol. Breed. 2014;34:1629-1645.
22 Casale FP, Horta D, Rakitsch B, Stegle O. Joint genetic analysis using variant sets reveals polygenic gene-context interactions. PLoS genetics; c2017, 13(4).
23 CEC IBPGR. Descriptors for wheat (Revised). International Board for Plant Genetic Resources, Rome; Programme Committee on Disease Resistance Breeding and Use of Gene Banks, Brussels, Belgium; c1985.
24 Cisar G, DB Cooper. Hybrid wheat. In: Curtis, B.C., S. Rajaram, and H. Gómez Macpherson (eds.). Bread Wheat Improvement and Production.FAO Plant Production and Protection Series, No 30. FAO, Roma, Italia.
25 Colasuonno P, Marcotuli I, Gadaleta A, Soriano JM. From genetic maps to QTL cloning: An overview for durum wheat. Plants. 2021;10(2):35.
26 Condorelli GE, Maccaferri M, Newcomb M, Andrade-Sanchez P, White JW, French AN, *et al*. Comparative aerial and ground based high throughput phenotyping for the genetic dissection of NDVI as a proxy for drought adaptive traits in durum wheat. Front. Plant Sci. 2018;9:893.
27 Davey JW, Hohenlohe PA, Etter PD, *et al*. Genome-wide genetic marker discovery and genotyping using next generation sequencing. Nat Rev Genet. 2011;12(7):499-510.
28 Deschamps S, Llaca V, May GD. Genotyping-by-sequencing in plants. Biology. 2012;1(3):460-483.
29 Desgroux A, L'anthoëne V, Roux-Duparque M, Rivière JP, Aubert G, Tayeh N, *et al*. Genome-wide association mapping of partial resistance to Aphanomyces euteiches in pea. BMC genomics. 2016;17(1):1-21.

30 Eagles HA, Bariana HS, Ogbonnaya FC, Rebetzke GJ, Hollamby GJ, Henry RJ, *et al*. Implementation of markers in Australian wheat breeding. Australian Journal of Agricultural Research. 2001;52(12):1349-1356.
31 Ebert D, Peakall ROD. Chloroplast simple sequence repeats (cpSSRs): technical resources and recommendations for expanding cpSSR discovery and applications to a wide array of plant species. Molecular Ecology Resources. 2009;9(3):673-690.
32 El Hanafi S, Bendaou N, Kehel Z, Sanchez-Garcia M, Tadesse W. Phenotypic evaluation of elite spring bread wheat genotypes for hybrid potential traits. Euphytica. 2020;216(11):1-16.
33 Eichler EE, Flint J, Gibson G, Kong A, Leal SM, Moore JH, *et al*. Missing heritability and strategies for finding the underlying causes of complex disease. Nature reviews genetics. 2010;11(6):446-450.
34 Elshire RJ, Glaubitz JC, Sun Q, *et al*. A robust, simple genotyping-by-sequencing (GBS) approach for high diversity species. PloS one. 2011;6(5):e19379.
35 Fang DQ, Roose ML. Identification of closely related citrus cultivars with inter-simple sequence repeat markers. Theor Appl Genet. 1997;95(3):408-417.
36 Falush D, Stephens M, Pritchard JK. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. Genetics. 2003;164(4):1567-1587.
37 Franca LT, Carrilho E, Kist TB. A review of DNA sequencing techniques. Q Rev Biophys. 2002;35(2):169-200.
38 Freeman GF. Heredity of quantitative characters in wheat. Genetics. 1919;4:1-93.
39 Fan F, Cui B, Zhang T, *et al*. LTR-retrotransposon activation, IRAP marker development and its potential in 280 M. A. Nadeem *et al*. genetic diversity assessment of masson pine (*Pinus massoniana*). Tree Genet Genomes. 2014;10(1):213-222.
40 Farahani S, Maleki M, Mehrabi R, Kanouni H, Scheben A, Batley J, *et al*. Whole genome diversity, population structure, and linkage disequilibrium analysis of chickpea (*Cicer arietinum* L.) genotypes using genome-wide DArTseq-based SNP markers.Genes. 2019;10(9):676.
41 Fatiukha A, Filler N, Lupo I, Lidzbarsky G, Klymiuk V, Korol AB, *et al*. Grain protein content and thousand kernel weight QTLs identified in a durum_wild emmer wheat mapping population tested in five environments. Theor. Appl. Genet. 2020;133:119-131.
42 Feldman M, Levy AA. Origin and evolution of wheat and related Triticeae species. In Alien introgression in Wheat, Springer, Cham; c2015. p. 21-76.
43 Flint-Garcia SA, Darrah LL, McMullen MD, Hibbard BE. Phenotypic versus marker-assisted selection for stalk strength and second-generation European corn borer resistance in maize. Theoretical and Applied Genetics. 2003;107:1331-1336.
44 Ghavami F, Elias EM, Mamidi S, Ansari O, Sargolzaei M, Adhikari T, *et al*. Mixed model association mapping for fusarium head blight resistance in Tunisian-derived durum wheat populations. G3. 2011;1:209-218.
45 Giancaspro A, Give SL, Zacheo SA, Blanco A, Gadaleta A. Genetic Variation for Protein Content and Yield-Related Traits in a Durum Population Derived from an Inter-Specific Cross Between Hexaploid and Tetraploid Wheat Cultivars. Front. Plant Sci. 2019;10:1509.
46 Gordon A, McCartney C, Knox RE, Ereful N, Hiebert CW, Konkin DJ, *et al*. Genetic and transcriptional dissection of resistance to *Claviceps purpurea* in the durum wheat cultivar Greenshank. Theor. Appl. Genet. 2020;133:1873-1886.
47 Grattapaglia D. Status and perspectives of genomic selection in forest tree breeding. Genomic selection for crop improvement. Springer, Cham; c2017. p. 199-249.
48 Graziani M, Maccaferri M, Royo C, Salvatorelli F, Tuberosa R. QTL dissection of yield components and morpho-physiological traits in a durum wheat elite population tested in contrasting thermo-pluviometric conditions. Crop Pasture Sci. 2014;65:80-95.
49 Haile JK, Nachit MM, Hammer K, Badebo A, Röder MS. QTL mapping of resistance to race Ug99 of *Puccinia graminis* f.sp. tritici in durum wheat (*Triticum durum* Desf.). Mol. Breed; c2012.
50 Hormozdiari F, Van De Bunt M, Segre AV, Li X, Joo JWJ, Bilow M, *et al*. Colocalization of GWAS and eQTL signals detects target genes. The American Journal of Human Genetics. 2016;99(6):1245-1260.
51 https://eands.dacnet.nic.in/
52 https://iiwbr.icar.gov.in/2020/08/27/59th-aicrp-on-wheat-and-barley-workers-virtual-meeting/
53 https://www.vsni.co.uk/
54 Hoagland AR, Elliott FC, Rasmussen LW. Some Histological and Morphological Effects of Maleic Hydrazide on a Spring Wheat 1. Agronomy Journal. 1953;45(10):468-472.
55 Huttner E, Wenzl P, Akbari M, *et al*. Diversity arrays technology: a novel tool for harnessing the genetic potential of orphan crops. Serageldin I, Persley GJ, editors. Discovery to delivery: Bio Vision Alexandria 2004; Proceedings of the 2004 Conference of the World Biological Biotechnology & Biotechnological Equipment 281 Forum; 2004 Apr 3-6; Alexandria, Egypt. Wallingford: CABI; c2004. p.145-155.
56 Jaccoud D, Peng K, Feinstein D, *et al*. Diversity arrays: a solid state technology for sequence information independent genotyping. Nucleic Acids Res. 2001;29(4):E25.
57 Jones CJ, Edwards KJ, Castaglione S, Winfield MO, Sala F, Van de Wiel C, *et al*. Reproducibility testing of RAPD, AFLP and SSR markers in plants by a network of European laboratories. Molecular breeding. 1997;3(5):381-390.
58 Joppa LR, Mcneal FH, Berg MA. Pollen production and pollen shedding of hard red spring (*Triticum aestivum* L. em.Thell.) and durum (*T.durum* Desf.) wheats. Crop Sci. 1968;8:487-490.
59 Iannucci A, Marone D, Russo MA, De Vita P, Miullo V, Ferragonio P, Blanco A, *et al*. Mapping QTL for Root and shoot morphological traits in a durum wheat _ *T dicoccum* segregating population at seedling stage. Int. J Genom; c2017.
60 Jiang GL. Molecular markers and marker-assisted breeding in plants. Plant breeding from laboratories to fields; c2013. p. 45-83.
61 Jing R, Bolshakov V, Flavell AJ. The tagged microarray marker (TAM) method for high-throughput detection of single nucleotide and indel polymorphisms. Nat Protoc. 2007;2(1):168-177.

62 Kalendar R, Flavell AJ, Ellis TH, *et al*. Analysis of plant diversity with retrotransposon-based molecular markers. Heredity. 2011;106(4):520-530.
63 Kalendar R, Grob T, Regina M, *et al*. IRAP and REMAP: two new retrotransposon-based DNA fingerprinting techniques. Theor Appl Genet. 1999;98(5):704-711.
64 Karaköy T, Baloch FS, Toklu F, Özkan H. Variation for selected morphological and quality-related traits among 178 faba bean landraces collected from Turkey. Plant Genetic Resources. 2014;12(1):5-13.
65 Kiran U, Khan S, Mirza KJ, *et al*. SCAR markers: a potential tool for authentication of herbal drugs. Fitoterapia. 2010;81(8):969-976.
66 Kiricenko FG, Rodionova VA. Study of biology of flowering in winter durum wheat).Vest.sel.'-khoz. Nauki. Mosk. 6:7-10 Pl. Breed. 1969;40:1970:529.
67 Kumar S, Stack RW, Friesen TL, Faris JD. Identification of a novel fusarium head blight resistance quantitative trait locus on chromosome 7A in tetraploid wheat. Phytopathol. 2007;97:592-597.
68 Kalia RK, Rai MK, Kalia S, *et al*. Microsatellite markers: an overview of the recent progress in plants. Euphytica. 2011;177(3):309-334.
69 Karaköy T, Baloch FS, Toklu F, Özkan H. Variation for selected morphological and quality-related traits among 178 faba bean landraces collected from Turkey. Plant Genetic Resources. 2014;12(1):5-13.
70 Keeble F, Pellew C. The mode of inheritance of stature and of time of flowering in peas (*Pisum sativum*). J Genet. I; c1910. p. 47-56.
71 Kempe K, Rubtsova M, Gils M. Split-gene system for hybrid wheat seed production. Proceedings of the National Academy of Sciences. 2014;111(25):9097-9102.
72 Kidane YG, Hailemariam BN, Mengistu DK, Fadda C, Pè ME, Dell'Acqua M. Genome-Wide Association Study of *Septoria tritici* Blotch Resistance in Ethiopian Durum Wheat Landraces. Front. Plant Sci. 2017;8:1586.
73 Koekemoer FP, Van Eeden E, Bonjean AP. An overview of hybrid wheat production in South Africa and review of current worldwide wheat hybrid developments. Bonjean AP, Angus WJ (eds) The world wheat book- a history of wheat breeding, vol 2. Lavoisier publishing, Paris; c2011. p. 907-950.
74 Korte A, Farlow A. The advantages and limitations of trait analysis with GWAS: a review. Plant methods. 2013;9(1):1-9.
75 Kumar S, Knox RE, Singh AK, DePaw RM, Campbell HR, Isidro-Sanchez J, *et al*. High-density genetic mapping of a major QTL for resistance to multiple races of loose smut in a tetraploid wheat cross. PLoS ONE; c2018, 13.
76 Laudencia-Chingcuanco, Debbie, Ganeshan, Seedhabadee, Frank, Fowler, *et al*. Genome-wide gene expression analysis supports a developmental model of low temperature tolerance gene regulation in wheat (*Triticum aestivum* L.). BMC genomics. 2011;12:299. 10.1186/1471-2164-12-299.
77 Letta T, Olivera P, Maccaferri M, Jin Y, Ammar K, Badebo A, *et al*. Association mapping reveals novel stem rust resistance loci in Durum wheat at the seedling stage. Plant Genome. 2014;7:1-13.
78 Li C, Qian W, Maclean CJ, Zhang J. The fitness landscape of a tRNA gene. Science. 2016;352(6287):837-840.
79 Lin X, N'Diaye A, Walkowiak S, Nilsen KT, Cory AT, Haile J, *et al*. Genetic analysis of resistance to stripe rust in durum wheat (*Triticum turgidum* L. var. durum). PLoS ONE; c2018, 13.
80 Litt M, Luty JA. A hypervariable microsatellite revealed by *in vitro* amplification of adinucleotide repeat within the cardiac muscle actin gene. Am J Hum Genet. 1989;44(3):397-401.
81 Liu W, Maccaferri M, Bulli P, Rynearson S, Tuberosa R, Chen X, *et al*. Genome-wide association mapping for seedling and field resistance to *Puccinia striiformis* f. sp. tritici in elite durum wheat. Theor. Appl. Genet. 2017;130:649-667.
82 Longin CFH, Mühleisen J, Maurer HP, Zhang HL, Gowda M, Reif JC. Hybrid breeding in autogamous cereals. Theory of Applied Genetics. 2012;125:1087-1096.
83 Lu Q, Lillemo M, Skinnes H, He X, Shi J, Ji F, *et al*. Anther extrusion and plant height are associated with Type I resistance to Fusarium head blight in bread wheat line 'Shanghai-3/Catbird'. Theoretical and applied genetics. 2013;126(2):317-334.
84 Lynch M, Walsh B. Genetics and analysis of quantitative traits. Sunderland (MA): Sinauer; c1998.
85 Maccaferri M, Francia R, Ratti C, Rubies-Autonell C, Colalongo C, Ferrazzano G, *et al*. Genetic analysis of Soil-Borne Cereal Mosaic Virus response in durum wheat: Evidence for the role of the major quantitative trait locus QSbm.ubo-2BS and of minor quantitative trait loci. Mol. Breed. 2012;29:973-988.
86 Maccaferri M, Sanguineti MC, Demontis A, El-Ahmed A, Garcia Del Moral L, Maalouf F, *et al*. Association mapping in durum wheat grown across a broad range of water regimes. J Exp. Bot. 2011;62:409-438.
87 Marcotuli I, Houston K, Waugh R, Fincher GB, Burton RA, Blanco A, *et al*. Genome wide association mapping for arabinoxylan content in a collection of tetraploid wheats. PLOS One. 2015;10:e0132787.
88 Madhumati B. Potential and application of molecular markers techniques for plant genome analysis. Int. J Pure App Biosci. 2014;2(1):169-88.
89 Manolio TA, Collins FS, Cox NJ, Goldstein DB, Hindorff LA, Hunter DJ, *et al*. Finding the missing heritability of complex diseases. Nature. 2009;461(7265):747-753.
90 Mardis ER. Next-generation DNA sequencing methods. Annu Rev Genomics Hum Genet. 2008;9:387-402.
91 Mondini L, Noorani A, Pagnotta MA. Assessing plant genetic diversity by molecular tools. Diversity. 2009;1(1):19-35.
92 Maeda M, Uryu N, Murayama N, *et al*. A simple and rapid method for HLA-DP genotyping by digestion of PCRamplified DNA with allele-specific restriction endonucleases. Hum Immunol. 1990;27(2):111-121.
93 Mondini L, Noorani A, Pagnotta MA. Assessing plant genetic diversity by molecular tools. Diversity. 2009;1(1):19-35.
94 Morgante M, Hanafey M, Powell W. Microsatellites are preferentially associated with nonrepetitive DNA in plant genomes. Nat Genet. 2002;30(2):194-200.
95 Maccaferri M, El-Feki W, Nazemi G, Salvi S, Cané MA, Colalongo C, *et al*. Prioritizing quantitative trait loci for root system architecture in tetraploid wheat. J Exp. Bot. 2016;67:1161-1178.

96 Marcotuli I, Houston K, Schwerdt JG, Waugh R, Fincher GB, Burton RA, *et al*. Genetic diversity and genome wide association study of _-glucan content in tetraploid wheat grains. PLoS ONE. 2016;11:e0152590.
97 Mengistu DK, Kidane YG, Fadda C, Pè ME. Genetic diversity in Ethiopian durum wheat (*Triticum turgidum* var durum) inferred from phenotypic variations. Plant Genet Resour Charact Util. 2018;16:39-49.
98 Mourad AM, Sallam A, Belamkar V, Wegulo S, Bowden R, Jin Y, *et al*. Genome-wide association study for identification and validation of novel SNP markers for Sr6 stem rust resistance gene in bread wheat. Frontiers in plant science. 2018;9:380.
99 Mujeeb-Kazi A, Kazi AG, Dundas I, Rasheed A, Ogbonnaya F, Kishii M, *et al*. Genetic diversity for wheat improvement as a conduit to food security. Advances in Agronomy. 2013;122:179-257.
100 Mullis K, Faloona F, Scharf S, Saiki R, Horn G, Erlich H. Specific enzymatic amplification of DNA *in vitro*: the polymerase chain reaction. In Cold Spring Harbor symposia on quantitative biology. 1986;51:263-273.
101 Muqaddasi QH, Brassac J, Börner A, Pillen K, Röder MS. Genetic architecture of anther extrusion in spring and winter wheat. Frontiers in plant science. 2017;8:754.
102 Nikulina ND. (Anthesis in winter bread wheat). Selekts. Semenov. 1969;(6):46. (PI. Breed. Abstr. 40, 1970:4725).
103 Navascués M, Emerson BC. Chloroplast microsatellites: Measures of genetic diversity and the effect of homoplasy. Molecular Ecology. 2005;14:1333-1341.
104 N'Diaye A, Haile JK, Cory AT, Clarke FR, Clarke JM, Knox RE, *et al*. Single marker and haplotype-based association analysis of semolina and pasta colour in elite durum wheat breeding lines using a high-density consensus map. PLoS ONE. c2017, 12.
105 N'Diaye A, Haile JK, Nilsen KT, Walkowiak S, Ruan Y, Singh AK, *et al*. Haplotype loci under selection in Canadian durum wheat germplasm over 60 years of breeding: Association with grain yield, quality traits, protein loss, and plant height. Front. Plant Sci. 2018;9:1-19.
106 Nadeem MA, Nawaz MA, Shahid MQ, Doğan Y, Comertpay G, Yıldız M, *et al*. DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. Biotechnology & Biotechnological Equipment. 2018;32(2):261-285.
107 Nagel M, Navakode S, Scheibal V, Baum M, Nachit M, Röder MS, *et al*. The genetic basis of durum wheat germination and seedling growth under osmotic stress. Biol. Plant. 2014;58:681-688.
108 Nakaya A, Isobe SN. Will genomic selection be a practical method for plant breeding?. Annals of botany. 2012;110(6):1303-1316.
109 Ng WL, Tan SG. Inter-simple sequence repeat (ISSR) markers: are we doing it right. ASM Sci J. 2015;9(1):30-39.
110 Nielsen NH, Backes G, Stougaard J, Andersen SU, Jahoor A. Genetic diversity and population structure analysis of European hexaploid bread wheat (*Triticum aestivum* L.) varieties. PLoS One; c2014.
111 Obermayer E. Untersuchungen fiber das Bluhen and die Befruchtung von Winterroggen and Winterweizen. Z. PflZucht. 1916;4:347-403.
112 Ogura T, Busch W. From phenotypes to causal sequences: using genome wide association studies to dissect the sequence basis for variation of plant development. Current opinion in plant biology. 2015;23:98-108.
113 Prat N, Guilbert C, Prah U, Wachter E, Steiner B, Langin T, *et al*. QTL mapping of Fusarium head blight resistance in three related durum wheat populations. Theor. Appl. Genet. 2017;130:13-27.
114 Parodi PC, Gaju MDLA. Male sterility induced by the chemical hybridizing agent clofencet on wheat, *Triticum aestivum* and *T. turgidum* var. durum. Ciencia e investigación agrarian. 2009;36(2):267-276.
115 Paran I, Michelmore RW. Development of reliable PCR based markers linked to downy mildew resistance genes in lettuce. Theor Appl Genet. 1993;85(8):985-993.
116 Peiffer JA, Romay MC, Gore MA, Flint-Garcia SA, Zhang Z, Millard MJ, *et al*. The genetic architecture of maize height. Genetics. 2014;196(4):1337-1356.
117 Peleg Z, Saranga Y, Suprunova T, Ronin Y, Röder M, Kilian A, *et al*. High-density genetic map of durum wheat X wild emmer wheat based on SSR and DArT markers. Theor. Appl. Genet. 2008;117:103-115.
118 Percival J. The wheat plant - A monograph. Duchworth & Co, London; c1921, 463.
119 Provan J, Powell W, Hollingsworth PM. Chloroplast microsatellites: new tools for studies in plant ecology and evolution. Trends Ecol Evol. 2001;16(3):142-147.
120 Peterson G, Dong Y, Horbach C, Fu YB. Genotyping-by-sequencing for plant genetic diversity analysis: a lab guide for SNP genotyping. Diversity. 2014;6:665-80.
121 Pirseyedi SM, Kumar A, Ghavami F, Hegstad JB, Mergoum M, Mazaheri M, *et al*. Mapping QTL for Fusarium head blight resistance in a Tunisian-derived durum wheat population. Cereal Res. Commun. 2019;47:78-87
122 Poczai P, Varga I, Laos M, *et al*. Advances in plant genetargeted and functional markers: a review. Plant Methods. 2013;9(1):6.
123 Poland JA, Rife TW. Genotyping-by-sequencing for plant breeding and genetics. Plant Genome. 2012;5(3):92-102.
124 Prat N, Guilbert C, Prah U, Wachter E, Steiner B, Langin T, *et al*. QTL mapping of Fusarium head blight resistance in three related durum wheat populations. Theor. Appl. Genet. 2017;130:13-27.
125 Rajendra Kumar P, Biswal AK, Balachandran SM, *et al*. Simple sequence repeats in organellar genomes of rice: frequency and distribution in genic and intergenic regions. Bioinformatics. 2007;23(1):1-4.
126 Rajki E. Some problems of the biology of flowering in wheat. Proc. Symp. Genet. and Wheat Breed., Martonvasar; c1962. p. 41-62.
127 Richey FD. Mock-dominance and hybrid vigor. Science (Washington, DC). 1942;96:280-281.
128 Roder MS, Korzun V, Wendehake K, *et al*. A microsatellite € map of wheat. Genetics. 1998;149(4):2007-2023.
129 Rakyan VK, Down TA, Balding DJ, Beck S. Epigenome-wide association studies for common human diseases. Nat. Rev. 2011;12:529-541.
130 Rasheed A, Xia X. From markers to genome-based breeding in wheat. Theoretical and Applied Genetics. 2019;132(3):767-784.
131 Rembe M, Zhao Y, Jiang Y, Reif JC. Reciprocal recurrent genomic selection: an attractive tool to leverage

hybrid wheat breeding. Theor. Appl. Genet. 2019;132:687-698.
132 Remington DL, Thornsberry JM, Matsuoka Y, Wilson LM, Whitt SR, Doebley J, *et al*. Structure of linkage disequilibrium and phenotypic associations in the maize genome. Proc Natl Acad Sci USA. 2001;98:11479-11484.
133 Resende RT. Regional heritability mapping and gwas for molecular breeding in eucalyptus hybrids; c2017.
134 Rosello M, Royo C, Alvaro F, Villegas D, Nazco R, Soriano JM. Pasta-making quality QTLome from Mediterranean durum wheat landraces. Front. Plant Sci. 2018;9:1512.
135 Rothberg JM, Hinz W, Rearick TM, *et al*. An integrated semiconductor device enabling non-optical genome sequencing. Nature. 2011;475(7356):348-352.
136 Roy NS, Choi JY, Lee SI, *et al*. Marker utility of transposable elements for plant genetics, breeding, and ecology: a review. Genes Genom. 2015;37(2):141-151.
137 Ruan Y, Yu B, Knox RE, Singh AK, DePauw R, Cuthbert R, *et al*. High density mapping of quantitative trait loci conferring gluten strength in canadian durum wheat. Front. Plant Sci. 2020;11:170.
138 Sanguineti MC, Li S, Maccaferri M, Corneti S, Rotondo F, Chiari T, *et al*. Genetic dissection of seminal root architecture in elite durum wheat germplasm. Annals of Applied Biology. 2007;151:291-305.
139 Schlotteroer C, Amos B, Tautz D. Conservation of poly-€ morphic simple sequence loci in cetacean species. Nature. 1991;354(6348):63-65.
140 Shendure J, Ji H. Next-generation DNA sequencing. Nat Biotechnol. 2008;26(10):1135-1145.
141 Singh SP, Srivastava R, Kumar J. Male sterility systems in wheat and opportunities for hybrid wheat development. Acta Physiologiae Plantarum. 2015;37(1):1713.
142 Skinnes H, Semagn K, Tarkegne Y, Marøy AG, Bjørnstad Å. The inheritance of anther extrusion in hexaploid wheat and its relationship to Fusarium head blight resistance and deoxynivalenol content. Plant Breeding. 2010;129(2):149-155.
143 Spaniolas S, May ST, Bennett MJ, *et al*. Authentication of coffee by means of PCR-RFLP analysis and lab-on-a-chip capillary electrophoresis. J Agric Food Chem. 2006;54(20):7466-7470.
144 Steiner B, Buerstmayr M, Wagner C, Danler A, Eshonkulov B, Ehn M, Buerstmayr H. Fine-mapping of the Fusarium head blight resistance QTL Qfhs.ifa-5A identifies two resistance QTL associated with anther extrusion. Theor. Appl. Genet. 2019;132:2039-2053.
145 Saccomanno A, Matny O, Marone D, Laidò G, Petruzzino G, Mazzucotelli E, *et al*. Genetic mapping of loci for resistance to stem rust in a tetraploid wheat collection. Int. J Mol. Sci. 2018;19:3907.
146 Salazar JA, Rasouli M, Moghaddam RF, *et al*. Low-cost strategies for development of molecular markers linked to agronomic traits in Prunus. Agric Sci. 2014;5(05):430-439.
147 Schnable PS, Springer NM. Progress toward understanding heterosis in crop plants. Annual Review Plant Biology. 2013;64:71-88.
148 Schulman AH, Wicker T. A field guide to transposable elements. In: Fedoroff NV, editor. Vol. 2, Plant transposons and genome dynamics in evolution. Oxford, Wiley Blackwell; c2013. p. 15-40.
149 Seymour DK, Chae E, Grimm DG, Pizarro CM, Habring-Müller A, Vasseur F, *et al*. Genetic architecture of nonadditive inheritance in Arabidopsis thaliana hybrids. Proceedings of the National Academy of Sciences; c2016, 113(46).
150 Shewry PR, Hey SJ. The contribution of wheat to human diet and health. Food and energy security. 2015;4(3):178-202.
151 Singh SK, Chatrath R, Mishra B. Perspective of hybrid wheat research: A review. Indian Journal of Agricultural Sciences. 2010;80(12):1013-27.
152 Singh SP, Srivastava R, Kumar J. Male sterility systems in wheat and opportunities for hybrid wheat development. Acta Physiologiae Plantarum. 2015;37(1):1713.
153 Somers JM, Goldner EM, Waraich P, Hsu L. Prevalence and incidence studies of anxiety disorders: a systematic review of the literature. The Canadian Journal of Psychiatry. 2006;51(2):100-113.
154 Tang Y, Liu X, Wang J, Li M, Wang Q, Tian F, *et al*. GAPIT version 2: an enhanced integrated tool for genomic association and prediction. The plant genome, plantgenome. 2016;9(2):2015-11.
155 Tautz D. Hypervariability of simple sequences as a general source for polymorphic DNA markers. Nucleic Acids Res. 1989 Aug 25;17(16):6463-71.
156 Thudi M, Li Y, Jackson SA, *et al*. Current state-of-art of sequencing technologies for plant genomics research. Brief Funct Genomics. 2012;11(1):3-11.
157 Tomar V, Singh D, Dhillon GS, Singh RP, Poland J, Joshi AK, *et al*. New QTLs for spot blotch disease resistance in wheat (*Triticum aestivum* L.) using genome-wide association mapping. Frontiers in genetics. 2021;11:1740.
158 Uzun A, Yesiloglu T, Aka-Kacar Y, *et al*. Genetic diversity and relationships within citrus and related genera based on sequence related amplified polymorphism markers (SRAPs). Sci Hort. 2009;121(3):306-312.
159 Wang S, Wong D, Forrest K, Allen A, Chao S, Huang BE, *et al*. Characterization of polyploid wheat genomic diversity using a high-density 90 000 single nucleotide polymorphism array. Plant biotechnology Journal. 2014;12(6):787-796.
160 Wei WH, Hemani G, Haley CS. Detecting epistasis in human complex traits. Nature Reviews Genetics. 2014;15(11):722-733.
161 Weber JL. Informativeness of human (dC-dA) n¢(dG-dT) n polymorphisms. Genomics. 1990;7(4):524-530.
162 Weiland JJ, Yu MH. A cleaved amplified polymorphic sequence (CAPS) marker associated with root-knot nematode resistance in sugarbeet. Crop Sci. 2003;43(5):1814-188.
163 Williams JGK, Kubelik AR, Livak KJ, Rafalski JA, Tingey SV. DNA polymorphisms amplified by arbitrary primers are useful as genetic markers. Nucleic Ads Rpsearch. 1990;18:6531-6535.
164 Whitford R, Fleury D, Reif JC, *et al* Hybrid breeding in wheat: Technologies to improve hybrid wheat seed production. J Exp Bot. 2013;645411-5428.
165 Würschum T, Leiser WL, Langer SM, Tucker MR, Longin CFH. Phenotypic and genetic analysis of spike and kernel characteristics in wheat reveals long-term

genetic trends of grain yield components. Theoretical and Applied Genetics. 2018;131(10):2071-2084.
166 Xia XC, Reif JC, Melchinger AE, Frisch M, Hoisington DA, Beck D, *et al*. Genetic diversity among CIMMYT maize inbred lines investigated with SSR markers: II. Subtropical, tropical midaltitude, and highland maize inbred lines and their relationships with elite US and European maize. Crop Science. 2005;45(6):2573-2582.
167 Xu K, He X, Dreisigacker S, He Z, Singh PK. Anther extrusion and its association with Fusarium head blight in CIMMYT wheat germplasm. Agronomy. 2019;10(1):47.
168 Yu PS, Chen ST, Chang IF. Support vector regression for real-time flood stage forecasting. Journal of hydrology. 2006;328(3-4):704-716.
169 Yu J, Buckler ES. Genetic association mapping and genome organization of maize. Current opinion in biotechnology. 2006;17(2):155-160.
170 Yang L, Fu S, Khan A, *et al*. Molecular cloning and development of RAPD-SCAR markers for Dimocarpus longan variety authentication. Springer Plus. 2013;2:501.
171 Zhang P, He Z, Tian X, Gao F, Xu D, Liu J, *et al*. Cloning of TaTPP-6AL1 associated with grain weight in bread wheat and development of functional marker. Molecular Breeding. 2017;37(6):1-8.
172 Zane L, Bargelloni L, Patarnello T. Strategies for microsatellite isolation: a review. Mol Ecol. 2002;11(1):1-16.
173 Zhao M, Leng Y, Chao S, Xu SS, Zhong S. Molecular mapping of QTL for Fusarium head blight resistance introgressed into durum wheat. Theor. Appl. Genet. 2018;131:1939-1951.
174 Zhou X, Stephens M. Efficient multivariate linear mixed model algorithms for genome-wide association studies. Nat Methods. 2014;11:407-409.
175 Zhao Y, Li Z, Liu G, Jiang Y, Maurer HP, Würschum T, *et al*. Genome-based establishment of a high-yielding heterotic pattern for hybrid wheat breeding. Proceedings of the National Academy of Sciences. 2015;112(51):15624-15629.
176 Zhao H, Wang B, He J, Yang J, Pan L, Sun D, *et al*. Genetic diversity and population structure of Miscanthus sinensis germplasm in China. PLoS One. 2013;8(10):e75672.
177 Zhou J, Edgar BA, Boutros M. ATF3 acts as a rheostat to control JNK signalling during intestinal regeneration. Nat. Commun. 2017;8:14289.
178 Zietkiewicz E, Rafalski A, Labuda D. Genome fingerprinting by simple sequence repeat (SSR)-anchored polymerase chain reaction amplification. Genomics. 1994;20(2):176-183.
179 Zukov VI. Method of determining open flowering in wheat). Selekts. Semenov. (Pl.Breed.Abstr.40, 1970:4700). 1969;(6):73.
180 Rukavishnikova VM, Reznikova LS. Titration of com plement by 50% haemolysis in patients with generalized rubrophytosis. Vestnik Dermatologii i Venerologii. 1969;43(7):45-8.

All Author's names

Asha Kushwah
Department of Genetics and Plant Breeding, R.A.K. College of Agriculture, Sehore, RVSKVV, Gwalior, Madhya Pradesh, India

Sanjay Singh
Researcher, Department of Horticulture, SHUATS, Prayagraj, Uttar Pradesh, India

RS Sikarwar
Professor, Department of Genetics and Plant Breeding, RVSKVV, Madhya Pradesh, India

Uttam Kumar
Wheat Breeder, Department of Genetics and Plant Breeding, BISA, Ludhiana, CIMMYT, Punjab, India

Sakshi Sharma
Research Scholar, Department of Genetics and Plant Breeding, RVSKVV, Gwalior, Madhya Pradesh, India

Sushma Tiwari
Scientist, Department of Molecular Breeding and Plant Btechnology, RVSKVV, Gwalior, Madhya Pradesh, India

Manish Vishwakarma
Scientist, Department of Genetics and Plant Breeding, BISA, Jabalpur CIMMYT, Madhya Pradesh, India

Pradeep Kumar Yadav
Research Scholar, Department of Genetics and Plant Breeding, RVSKVV, Gwalior, Madhya Pradesh, India

Mahvash Khaleel
Research Assistant, Department of Genetics and Plant Breeding, RAK Agriculture College, Sehore, Madhya Pradesh, India

Sarika Mahor
Research Scholar, Department of Agronomy RVSKVV, Gwalior, Madhya Pradesh, India

Poonam
Research Scholar, Department of Horticulture, RVSKVV, Gwalior, Madhya Pradesh, India

Kiran Makwanad
Research Scholar, Department of Genetics and Plant Breeding, RVSKVV, Gwalior, Madhya Pradesh, India

Abhishek Singh Kushwah
Research Scholar, Department of Horticulture, ITM, School of Agriculture, Gwalior, Madhya Pradesh, India

M Yasin
Scientist, Department of Genetics and Plant Breeding, RAK. Agriculture College, Sehore, Madhya Pradesh, India

Ramcharan Ahirwar
Research Scholar, Department of Genetics and Plant Breeding, RVSKVV, Gwalior, Madhya Pradesh, India

Ravi Kumar Kushwah
Research Scholar, Department of Horticulture, JNKVV, Jabalpur, Madhya Pradesh, India