Quantitative traits loci associated for biotic and abiotic resistance in maize (*Zea Mays* L.)

ABSTRACT

Maize is a essential food crop after rice and wheat, cultivated all over the world. Maize is consumed both by humans and animals and utilized as an industrial product viz., starch, pharmaceuticals, alcoholic beverages, oil, cosmetics, textiles, etc. In ancient times, landraces were more popular due to presence of more genetic variability, resistant to biotic and abiotic factors and have heterogeneous nature but it was replaced by improved and uniform cultivars with a higher yield. Modern maize has more homogeneity which is vulnerable to any dangerous pathogen strain. In the current era of molecular markers, DNA markers play an important role to identify diverse germplasm. To evaluate the diversity of maize, several mapping populations are developed and used for QTL mapping. Linkage mapping was first used in maize in the 1990s and is still common now along with genome-wide association mapping. Association mapping has been preferred due to the conserved historical linkage disequilibrium and elimination for the construction of a bi-parental mapping population. In this review, we focused, how much work on genome mapping has been done and what is the prospect of genome mapping.

Key words: Maize, mapping population and genome mapping

1. INTRODUCTION

Maize (*Zea maize* L.) is the essential cereal crop belonging to poaceae family and has been cultivated all over the world. It plays a vital source of income for the overwhelming population [1]. Maize is utilized in an industrial for the production of starch, pharmaceuticals, alcoholic beverages, oil, cosmetics, textiles, etc [2]. Due to the diverse uses of maize and its product, maize demand has increased continuously day by day all over the world [3].Recently, hybrid maize has been widely cultivated all over the world due to its higher yield as compared to that of landraces. Maize has been grown in tropical and sub-tropical climates [4]. In ancient time, landraces were more popular among the farmers as it is highly resistant to biotic and abiotic factor due to heterogeneous nature; even though the yield was low [5]. The present cultivated form of maize is originated from its wild relative teosinte (*Zea mays ssp. purviglumis*) but cultivated maize is quite distinguished from teosinte in terms of morphology and for several other characters [6].

The molecular markers used in several mapping populations like mortal and immortal to identify the quantitative traits loci (QTLs) [7]. The mortal population is a type of segregating, *viz.,* F_2 population and Advanced Backcross (ABC) population while in the immortal population which will not segregate, *viz.,* doubled haploid (DH), Recombinant inbred lines (RIL), F_2 derived lines and near isogenic lines (NIL) have been used for QTL identification [8]. The development of molecular markers plays an important role to map the QTLs. QTLs is a genomic region responsible for quantitative traits [9]. Numbers of QTLs were identified by the different researchers in maize for different traits using various molecular markers (Table 1).

2. MAPPING POPULATION

Mapping population consists of large segregating population that is derived from the sexual reproduction and used in development of linkage map. Mapping population needs diverse parents, polymorphism for one or two characteristics and should have high heritability for trait of interest [9]. The mapping population size should be approximately 250-500 for reliable construction of linkage map, in which it gives more appropriate result [10]. However, large population is necessary for high resolution of linkage map. For QTL analysis, mapping population should evaluate phenotypically before QTL study [9]. This applies for both monogenic and polygenic characters [11].

2.1. MORATAL POPULATION

2.1.1. F_2 Population

F_2 population is derived from the selfing of F_1 population or sib mating of F_1 population. F_1 population is heterozygous as their parents are differing from each other. So, in F_2 population one recombinants cycle occurred between two loci. Dominant and codominant ratio of phenotype is 3:1 and genotypic is 1:2:1 in F_2. F_2 population is mainly used for preliminary study and for oligogenes. F_2 population required less time and the procedure to develop F_2as compared to other mapping population is very easy as it required only two generation. It provides the effects of additive, dominance and epistatic variance. Xie et al., 2019 evaluated genetic map using 7613 SNPs in F_2 population and found 14 QTLs for tassel branch number (TBN), tassel weight(TW), central spike length (CSL), and meristem length (ML) [12].

2.1.2. Back Cross Population

Backcross population is developed by crossing between hybrids with either of their parents. Crossing between hybrids and recessive parent is known as testcross and have 1:1(dominant marker) and (codominant marker) 1:0 (codominant marker) ratio in coupling phase and repulsion phase respectively. The backcross population has advantage for marker assisted back crossing of interest trait as proposed in advance backcross quantitative trait loci method [13].

2.2. Immortal Population

2.2.1. Doubled Haploid

Double haploid is produced by the chromosome doubling of a haploid using the colchicine treatment. They are completely homozygous and have all identical sets of chromosomes. Only one gene is available for

all the genes. Haploid lines may develop spontaneously or produced artificially. Generally, haploid plants are sterile and have weak wealth, less vital. Choi et al., 2019 used DH lines that were developed from normal corn parents (HF1 and 11S6169) [14].

2.2.2. NIL Population

Near isogenic line (NILs) developed through backcrossing. Near isogenic lines are identical to recurrent parent except for one gene/locus. Practically, NILs is different for the single gene and genomic region of variable length flanking this locus. In addition, it also found different for some random genomic segments located elsewhere in the genome. Hence, a pair of NILs would most likely to differ for alleles from few to several loci which justifies the use of the term near isogenic lines for such lines. For instance, a line developed by the cross between a cultivated variety of tomato and a wild variety of tomato [13].

2.2.3. Recombinant Inbred Lines

Recombinant inbred lines (RILs) derived by the inter mating of F_2 plants or sib mating progeny of F_2 individuals' population. Linkage mapping concepts using RILs was first established in mice [11]. Single seed descent lines also called the RIL lines as RIL developed from each single seed of every line. RIL produced by the single seed descent method allow the self-pollination till 6-8 generations and hence, it become completely homozygous. In this method, there is no change in genetic makeup due to recombination in alternate parent at the same population. Thus, RILs create a permanent resource and have advantage to replicate indefinitely and could share by several groups in the research community. In studied, RILswere found better and gives more appropriate result than F_2 population [15].

3. QTL MAPPING

QTL mapping theory was described by Sax for the first time in 1923. He revealed that seed coat color (monogenic trait) decided the seed size in bean (a complex trait) [16]. He suggested that if segregation of oligogenic trait can detect the QTL that is linked with complex trait. This criterion is fulfilled by the modern QTL mapping technique [17]. The location of QTL on the whole genome gives the idea of polygenic characteristics that were involves in the expression of gene at particular time. A review is written by Tanksley [18]. QTL mapping involve the testing of whole genome with DNA markers to know likelihood chance present of QTLs. This technique reveals the significance QTL among individuals with trait of interest [19].

Table 1: List of QTLs detected using different molecular markers

S. No.	Marker	Trait	QTL	Chr. Location	Mapping Population	Reference
01	SSR	Phosphorus treatments	69	All chr.	210, F2:3 families	20
02	SSR	Kernel row number	13	1,2,3,4,5,6,7	500, F2 Individuals	21
03	SSR	grain oil and starch	21	1,5,6,7,4,8	265 F2:3 families	22
04	SSR	Test weight	5	1,2,.3,4,5,7,	225 F2:3	23
05	SSR	Resistance to Aflatoxin	40	1,3,4,5,9,10	250, F2:3 families	24
06	SSR	Root system	36	All Chr.	187 BC4F3	25

		architecture				
07	SSR	gray leaf spot		1,2,5,8	161 F2:3 families	26
08	SSR	plant architecture	18	1,2,3,7,9	239, RIL	27
09	SSR	kernel size and weight	55, 28	1,2,4,5,9,	270 F2:3 families	28
10	SSR	Gray leaf spot resistance	18	2, 3, 4, 5 & 8	478 F2:3 population	29
11	SSR	Ear Fasciation	65	All chr.	149 F2:3 families	30
12	SSR	protein, oil and starch contents	25, 13, 31&15	1, 2, 5, 6, 8, and 10.	498 RILs	31
13	SSR	Grain morphology traits	18, 26, 23&19	1,2,3,6,7,8,9	58, Ril	32
14	SSR	Inflorescence Architecture	19	1,2,3,4,5,6,7	202 and 218 F2:3 family	33
15	SSR	Agronomic traits	15	All chr.	121 Dh population	34
16	SSR	Maize kernel size And weight	52	1,2,3,4,5,7,8, 9,10	150 f7 rils	35
17	SSR	Forage agronomic traits	42, 41, 54, and 45	All chr.	250-720 DH and RILs	36
18	SSR	Nitrogen use efficiency (nue),	19	1,2,4,5,8,10	Recombinant inbred lines (181)	37
19	SSR	Agronomic traits	15	1, 2, 3, 4, 5, 7, 10	121 Double haploid	38
20	SNP	Northern leaf blight	29	All chr.	25,Nam, ril	39
21	SNP	Southern leaf blight	32	All chr.	5000 RIL	40
22	SNP	Plant height and biomass as secondary traits of drought tolerance	23	7,8,10,4	150 F2:3 line	41
23	SSR	Kernel related trait	7	1,4,6,7,9,10	F2:3 population	42
24	SNP	Kernel Weight	23,59	All chr.	408 RILs	43
25	SNP	Fusarium ear Rot resistance	15	2, 3, 4, 5, 9, 10	940 elite inbred lines	44
26	SNP	leaf morphology	111	All chr.	215, 223, 208 and 212 RILs	45
27	SNP	maize tassel	72	1,2,3,4,6,7,9	866 maize-teosinte BC2S3 RILs	46
28	SNP	ear leaf traits	23, 25, &17	1,2,3,4,6,7,8,	909 ril	47
29	SNP	Vitamin E	31	All chr.	213 F2:3	48
30	SNP	amylose biosynthesis	27	4,6,7,9	464 inbreds	49
31	SNP	Leaf Angle&Tassel Size	23	All chr.	213 F2:3 Population	50
32	SNP	Cob resistance, ear Rot resistance	28	1, 2, 3, 4,5, 6, 7, 9,10	258 Maize inbred	51
33	SNP	tassel-related traits	27	All chr.	266 F2:3 families ril	52
34	SNP	Leaf morphology traits	19,83	All chr.	866 maize-teosinte	53

			8		bc2s3 RILs	
35	SNP	Kernel size & weight	27	All except 6 and 10	204 ril lines	54
36	SNP	Salt tolerance	65	1, 3, 7, and 9,	209 DH	55
37	SNP	Delayed maize flowering in response to low Phosphate	41	2, 5, 6	262 Ril population	56
38	SNP	Water deficit-responsive	213	1,2,3,4,5,6,7, 8,9,10	267 Ril population	57
39	SNP	Dynamic plant height	68	1,2,3,4,5,6,7, 8,9,10	Inbred lines (117 temperate lines, 135 tropical lines	58
40	SNP	Tassel architecture	19	1, 2, 3, 4, 6, and 7	359 inbred lines and an ibm syn 10 population of 273 doubled haploid lines	59
41	SNP	Tassel-related traits	14	1, 2, 3, 5, 7, 8 and 10,	148 f2 population	60
42	SNP	Plant architecture	21	All chr.	301 RILs	61
43	SNP	Disease resistance (southern leaf blight (slb), northern leaf blight (nlb), and gray leaf spot)	17	1,2,3,4,5,6,7, 8,9,10	253 RIL	62
44	RFLP	Drought tolerance	22	1,3,6,5,7,9,10	105,F2:3 families	63
45	RFLP & SSR	Weevil resistance	17	1,2, 3, 5, 8, and 9,	Parental population, F2 individual	64
46	RFLP,SSR	gray leaf spot disease	30	1,3,4,6,7,9,10	145 ril	65
47	SSR, AFLP	Aluminum Tolerance	9	*2, 4, 5, 6, 7, 8, 9, 10*	350 *F2:3*	66

3.1. QTLs for Morphological and Agronomic Traits of Maize

The list of QTLs was identified by different researchers after 2010 mentioned in Table 1. The plant morphology and other characters based on genetics determine the grain yield [67]**. Several other quantitative trait loci were discovered for ear length, ear height ratio, ear height, plant height, cob color, kernel weight, set ear length and ear width etc.** in **double haploid population [14].** Wang et al 2019 study genome wide association mapping using 43,958 high-quality SNPs in 359 inbred lines and an IBM Syn 10 population of 273 doubled haploid under three environments (59).

3.2. QTLs mapping and plant disease resistance

Disease resistance has been detected with the help of genome wide association study associated with disease resistance, evaluated under 3 environments [44]. Many literatures have been described to kernel and cob including with ear rot resistance caused by *F. verticillioides* cob rot (FCR) [51]. Diverse lines with high

density markers have been conducted for common rust resistance under multiple environments and it was feasible to found QTL and several candidate genes. Zwonitzer et al 2010 investigated correlation among three diseases resistance and found highest association between SLB and GLS resistance. A significant association was found between resistance to each of the diseases and time to flowering. A total 9, 8, and 6 QTL were found for SLB, GLS, and NLB resistance respectively in maize[68].

4. Conclusion

Genomic approach is one of the most powerful tools for accelerating the knowledge of genome region. With the rapid increment of genomic technology all kinds of diversity in different environment can be assessed. Maize is one of the important cereal crops cultivated over worldwide. Multilocation data will help to determine yield and yield related traits. The Maize genome presents many technical challenges, to discover quantitative trait loci in maize is difficult task, in spite that, many QTLs have been discovered for agronomical traits and biochemical traits. In this review paper, we described the details of quantitative traits loci for agronomical traits.

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