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Genome mapping: Utilization of molecular markers in genome mapping

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Abstract
Maize is one of the cereals crops grown under world wide area. now days ranking of maize is third in among cereals. It's main utilization as a form of food and fodder in all over world. Maize consumed by the human and it is also income source of majority overwhelming population. It is used by the industrial product such as corn starch and other things. Maize contains good properties for food calorie 30-60 % and dietary protein, that is very easy digestible for human. cultivated maize is developed from the teosinte maize, teosinte maize contains good resistance for biotic and abiotic factor, but new cultivated species has been deteriorate due to modernization of cultivation. Complex characters governed by the polygenic genes, polygenic genes may be influenced by environment resulting losses in yield. We need to study to identify the genes that contribute the specific characters. we need to analysis of genome mapping. Genome mapping analyzed with the help of markers such as marker system. Genome mapping is a method to identify the allele of a gene that is present in which one position and what is distance between them. Molecular marker has scattered all over population to know genome mapping in among variety, such as SSR, SNPs and RFLP etc. (Govindaraj *et al.,* 2015). But in this review paper three marker has been more utilized.

Keywords: Maize, Genome mapping, molecular marker, SSR, SNPs and RFLP

Introduction

Maize (*Zea maize* L.) belongs to poaceae family and it is cultivated all over world. Global rank of maize is third in among cereals in all over worldwide their own productivity and significance utilization as a food and fodder (first and second is rice and wheat respectively). Maize used by human, and it is income source of majority overwhelming population (EARO 2000) [17]. It used as a industrial product such as starch based product, corn starch and other things. Heavy use of maize and maize product, maize demanding increased continue in all over world (Wada *et al.,* 2008) [71]. Maize have good properties for food calorie about 30-60 % and also having dietary protein, that is very easy digestible for human. Its grain is produced for several other dishes and consumed by the human (Showemimo *et al.,* 2007) [59]. Now days hybrid (*Zea mays* L.) is most widely cultivated spp. all over world due to high yield compare to other variety of maize and it has economically differ from other maize however other varieties of maize has diversified characters on other variety. Maize populations grow up in several climates such as tropical and sub-tropical climate (Rebourg *et al.,* 2003; Dubreuil *et al.,* 2006) [54, 14]. In ancient time landraces was very popular, but now day's farmers variety and other local varieties are existing: landraces are very resistance to biotic and abiotic factor and it has more diversified than others due to heterogeneous nature and selected by the farmers for cultivation (Prasanna and Sharma 2005) [52]. But due to low yield, landraces did not cultivated by the farmers for longer time. Cultivated maize is developed from the teosinte maize (*Zea mays* purviglumys) and it is distinguished from teosinte maize their morphology and other characters (Wang *et al.,* 1999; Matsuoka *et al.,* 2002; Doebley, 2004; Vigouroux *et al.,* 2005) [72, 44, 13, 69]. To develop good hybrid variety of maize should be good knowledge all about genetic makeup among in the variety to conserve the germplasm (Melchinger *et al.,* 1991; Bernardo 2002) [46, 2].

There are many study has been conducted on analysis of genome mapping such as marker system. Genome mapping is a method to identify the specific allele of a gene that is present in which one position and what is distance between them.

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Molecular marker has scattered all over population to know genome mapping in among variety. Molecular marker is based on DNA technology such as SSR, SNPs, RAPD and AFLP etc. (Govindaraj *et al.,* 2015) [2]. And expression of molecular marker is not influenced by the environment, it also avoiding the genotypic × environmental effects and reveals the actual level of genome mapping analysis with the help of molecular marker (Westman and Kresovich 1997) [75].

There are several population is used for QTL/gene mapping such as mortal and immortal population, in mortal population(it can be segregate) such as f_2 population and BC (back cross) population, but immortal population (it can not be segregate) such as DH (doubled haploid), RIL (Recombinant inbred lines), F_2 derived lines, NIL (near isogenic lines) and other population extensively will be exhibiting for QTL identification (Byrne *et al.,* 1996; Cowen 1988; Edwards *et al.,* 1992, 1987; Knapp 1991; Knapp and Bridges 1990; Tanksley *et al.,* 1982; Szalma *et al.,* 2007) [5, 9, 15, 16, 30, 31, 66]. Genotyping with the help of molecular marker is very crucial role to discriminate desirable Genotype from undesirable ones in many individuals or organism. There are many reliable technology has been participated for better characterization of desirable genotype for breeding material. There are many marker systems is extensively used to analyze the genome mapping (Frascaroli *et al.,* 2013) [20].

Classification of marker
Marker in plant breeding will be utilized to know, genetic diversity, genome mapping, QTL mapping and for genotyping etc. So marker play indispensible role in plant breeding to select best plants for higher yield. To aggregate knowledge of molecular marker is a difficult task, but it is an easy.

1. SSR or microsatellite
SSR also called the microsatellite marker, it consist of tandem repeat in DNA sequence such as mono, di, tri, tetra and so on. This tandem repeats found in both prokaryotic and eukaryotic genome (Tautz and Renz 1984; Katti *et al.,* 2001) [67, 28]. It have another name such as short tandem repeats marker, microsatellites markers and sequence tagged microsatellite (STMS) marker etc. it is hyper variable marker that is available in nature (Jiang 2013) [26]. The variation in these markers found only based on subside the DNA replication, in this, there are many tandem repeats of nucleotide may be matching due to excision or addition repeats of DNA (Schlotterer and Tautz 1992). Slippage of DNA strand during replication originate more time than the point mutation. Polymorphism can be analyzed with the help of PCR. In this technique primer used without radioactive labeled or flurolabeled or radiolabeled to know diverse group of organism. This unlabeled primer is used to analyze with the help of agarose gel electrophoresis or polyacrylamide gel. The unlabeled or fluorolabed primer significantly enhances the research (Wenz *et al.,* 1998) [74]. SSR or microsatellite is codominant in nature and will be distinguished to heterozygous from homozygous and they are also highly reproducible due to locus specific (see table no. 01). These primers most of used in both eukaryotic and prokaryotic (Khan *et al.,* 2017) [29].

Application of SSR marker
It is used in genetic diversity, characterization of germplasm, development of genetic linkage map and also used to identification of QTL detection (Hiremath *et al.,* 2012) [24]. The locus specific study has been conducted in many plant species such as barley (Saghai Maroof *et al.* 1994) [56], jute (Das *et al.,* 2012) [11], wheat (Mukhtar *et al.,* 20O2) [48], chickpea (Nayak *et al.,* 2010) [49], Alfalfa (Li *et al.,* 2009) [39], barley (Saghai Maroof *et al.,* 1994) [57] and also has been study on rice (Wu and Tanksley 1993) [76] etc.

2. SNP
Single nucleotide variation arises due to single nucleotide in a genome in individuals of a population. These variations found in among species, it varies individual to individuals and constitute the more sufficient marker in the genome. In maize 1 SNPs has been found over 60-120 bp (Ching *et al.,* 2002) [7], while in human has been estimated found 1 SNPs over 1000 bp (Sachidanandam *et al.,* 2001) [55]. SNPs are more popular in the genome that has non coding regions. But within the coding sequence that may be changed to result in the amino acid sequence either this is the non-synonymous (Sunyaev *et al.,* 1999) [64], or the synonymous may be not altering the amino acid sequence. Synonymous can be changed the amino acid that can be changed the RNA splicing and may be changed in the modification, resulting the phenotypic differences. Direct analysis of DNA genetic variation sequence has made been possible due to some changes has been improved in DNA sequencing and available of ESTs sequence in the genome (Buetow *et al.,* 1999; Soleimani *et al.,* 2003) [4, 63]. This majority is based on the two approaches molecular mechanism, hybridization of specific alleles, extension of primer and prolificacy attack and ligation of nucleotide (Sobrino *et al.,* 2005) [62]. This is the high throughput genotyping method, allele specific PCR and extension of primer make possible single nucleotide polymorphism in any individuals (see table no. 01). This is the most widely accepted by the plant breeders, due to high rapid method and gives appropriate result; this is the biallelic and codominant marker etc. (Agarwal *et al.,* 2008) [1].

3. RFLP
RFLP is only depending upon short southern blot technique. In this technique DNA digested with the help of restriction endonuclease enzymes, this enzyme produce different fragment of DNA and detects the polymorphism labeled probe with the help of southern blot technique. This profile is generated by the insertion and deletion of DNA bases in DNA or substitution of DNA sequence. The RFLP is highly reproducible, codominant and highly inherited. It is the locus specific and high heritable in plant, due to presence of throughout the genome. So, RFLP marker is very superior to detect the polymorphism in plant. This method provides the numerous sampling together and to be screening simultaneously (see table no 01.). This technique is not widely accepted because it needs high radioactive labeling that is highly expensive, toxic reagents and high quantity genomic DNA that is impossible to isolate without high equipment. And it also want prior sequence information this is reduce the complexity of RFLP technique. These limitations have been overcome to come by PCR based marker (Agarwal *et al.,* 2008) [1].

Application of RFLP marker
This technology most used to construct of genetic linkage map. They are the codominant marker and give high reproducibility. This technology can be separated to homozygous and heterozygotes individuals (Idrees and Irshad 2014) [25].

Table 1: Schematic representation of marker that has been used in genome mapping in maize

S. No.	Marker	Trait	Gene/ QTL	Mapping Population	References
01	SSR	Grain yield (gy), plant height, ear height and grain moisture	13	400 $F_{2:3}$ lines	Sibov et al. 2003 [60]
02	SSR	plant height	13	294 RILs	Ji-hua et al. 2006
03	SSR	Grain Yield and Plant Traits	16	256, $F_{2:3}$ families	Lima et al. 2006 [35]
04	SSR	gray leaf spot	14	37 Inbred lines	Danson et al. 2008 [10]
05	SSR	agronomic traits	51	450 maize RILs	Guo et al. 2008 [23]
06	SSR	Root traits	17	94 RILs	Liu et al. 2008 [36]
07	SSR	Northern leaf blight Resistance	36	400 $F_{2:3}$ progenies	Sabadin et al. 2008 [27]
08	SSR	Phosphorus treatments	69	210, $F_{2:3}$ families	Li et al. 2010
09	SSR	Kernel row number	13	500, F_2 Individuals	Lu et al. 2010
10	SSR	Test weight	5	225 $F_{2:3}$ population	Ding et al. 2011 [12]
11	SSR	Resistance To Aflatoxin	40	250, $F_{2:3}$ families	Warburton et al. 2011 [73]
12	SSR	Root system architecture	36	187 advanced-backcross BC_4F_3	Cai et al. 2012 [6]
13	SSR	kernel size and weight	55 and 28	270 derived $F_{2:3}$ families	Liu et al. 2014 [37]
14	SSR	Ear Fasciation	65	149 $F_{2:3}$ families	Mendes-Moreira et al. 2015 [47]
15	SSR	Nitrogen use efficiency (nue),	19	RILs (181)	Mandolino et al. 2018 [43]
16	SNP	Northern leaf blight	29	25,NAM, RILs	Poland et al. 2011 [50]
17	SNP	Southern Leaf Blight	32	5000 RILs	Kump, et al. 2011 [33]
18	SNP	Kernel Weight Determination	23,59	408 RILs	Prado et al. 2014 [51]
19	SNP	leaf morphology	111	215, 223, 208 and 212 RILs	Ku et al. 2016 [32]
20	SNP	Vitamin E	31	213 $F_{2:3}$	Fenton et al. 2018 [18]
21	SNP	Leaf morphology traits	19,838	866 Teosinte maize, BC_2S_3 RILs	Fu et al. 2019 [21]
22	SNP	Salt tolerance	65	209 doubled Haploid (dh)	Luo et al. 2019 [42]
23	SNP	Water deficit-responsive	213	267 RILs population	Virlouvet et al. 2019 [70]
24	SNP	Tassel-related traits	14	148 f_2 population	Xie et al. 2019 [77]
25	SNP	Plant architecture	21	301 RILs	Yi et al. 2019 [79]
26	SNP	Disease resistance(southern leaf blight (slb), northern leaf blight (nlb), and gray leaf spot)	17	253 RILs	Zuniga et al. 2019 [38]
27	RFLP	Smut of maize	19	280 F_3 lines of cross	Lubberstedt et al. 1998 [41]
28	RFLP	Gray Leaf Spot	15	F_1 cross, and 301 families	Clements, et al. 2000 [8]
29	RFLP	Cell Wall Digestibility and Lignifications in Silage	28	100 RILs	Mechin, et al. 2001
30	RFLP	Root characteristics for hydroponics	11, 7, 9, and 10 and 8	171 F_3 population	Tuberosa et al. 2002 [68]
31	RFLP	Drought tolerance	22	105,$F_{2:3}$ families	Rahman et al. 2011 [53]

Conclusion
In past, conventional method utilized by the plants breeders but it reveals the biased results due to the affected by the environments and estimated the wrong result. So we need to remove the environmental effects. how to overcome these difficulties, there is need good technology that can be remove the biased result that is MAS (Marker assisted selection). MAS is a indirect selection of plants or genotype, select the desirable genotype that is completely dependent on genotype with the help of MAS. The confirmation of quantitative trait loci is most advantageous for marker assisted selection. Development of molecular marker, many studied has been reported for complex traits (quantitative traits) and for agronomic traits that is described in table no 01. in this review paper most of the SSR, SNPs and RFLP markers have been utilized to detects the QTLs (quantitative traits) in which most of the f2, BC (back cross) and RIL population has been used. We have discussing genome mapping in maize how many

QTLs has been identified in maize for particular purpose that is mainly being utilized by breeders at this times. So this review paper will be help to know that was QTLs that is contributes the particular characters.

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