Genome mapping: Utilization of molecular markers in genome mapping

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Abstract

Maize is one of the cereals crops grown under worldwide area. Nowadays, maize is the third in among cereals. It’s main utilization as a form of food and fodder in all over the world. Maize consumed by the human and it is also income source of majority over the 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 deteriorated 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 mays L.) belongs to poaceae family and it is cultivated all over the 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 the world (Wada et al., 2008) [171]. 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 (Rebour et al., 2003; Dubreuil et al., 2006) [54, 14]. In ancient time landraces was very popular, but now day’s farmer 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; Doebly, 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.
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 F2 population and BC (back cross) population, but immortal population (it can not be segregate) such as DH (doubled haploid), RIL (Recombinant inbred lines), F2 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) [15, 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 indispensable 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) [20]. 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 fluorolabeled 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 fluorolabeled 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) [15], wheat (Mukhtar et al., 2002) [69], chickpea (Nayak et al., 2010) [69], Alfalfa (Li et al., 2009) [69], barley (Saghai Maroof et al., 1994) [57] and also has been study on rice (Wu and Tanksley 1993) [70] 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) [71], while in human has been estimated found 1 SNPs over 1000 bp (Sachidanandam et al., 2001) [53]. 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 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, 65]. 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) [11].

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 inheritable 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 F2:3 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, F2:3 families | Lima et al. 2006 [15] |
| 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 F2:3 progenies | Sabadin et al. 2008 [27] |
| 08    | SSR    | Phosphorus treatments                      | 69        | 210, F2:3 families | Li et al. 2010 |
| 09    | SSR    | Kernel row number                          | 13        | 500, F2 Individuals | Lu et al. 2010 |
| 10    | SSR    | Test weight                                | 5         | 225 F2:3 population | Ding et al. 2011 [12] |
| 11    | SSR    | Resistance To Aflatoxin                    | 40        | 250, F2:3 families | Warburton et al. 2011 [73] |
| 12    | SSR    | Root system architecture                   | 36        | 187 advanced-backcross BC1F3 | Cai et al. 2012 [6] |
| 13    | SSR    | kernel size and weight                     | 55 and 28 | 270 derived F2:3 families | Liu et al. 2014 [37] |
| 14    | SSR    | Ear Fasciation                             | 65        | 149 F2:3 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 F2:3           | Fenton et al. 2018 [19] |
| 21    | SNP    | Leaf morphology traits                     | 19,838    | 866 Teosinte maize, BC2S: RILs | Fu et al. 2019 [21] |
| 22    | SNP    | Salt tolerance                             | 65        | 209 doubled        | 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 F2 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 (sib), northern leaf blight (nib), and gray leaf spot) | 17        | 253 RILs           | Zuniga et al. 2019 [18] |
| 27    | RFLP   | Smut of maize                              | 19        | 280 F1 lines of cross | Lubberstedt et al., 1998 [41] |
| 28    | RFLP   | Gray Leaf Spot                             | 15        | F1 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 F3 population | Tuberosa et al. 2002 [68] |
| 31    | RFLP   | Drought tolerance                          | 22        | 105, F2:3 families | Rahman et al. 2011 [55] |

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 studies 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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