Maize Genetic Diversity: Utilization of Molecular Markers in Genetic Diversity

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A B S T R A C T

Maize is one of the cereals grown under worldwide area. Global ranking of maize is having third rank 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 has income source of majority overwhelming population. It is also used by the industrial product such as corn starch and other things. Maize having 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 having good resistance for biotic and abiotic factor, but new cultivated species has been deteriorate due to modernization of cultivation. So to maintain the genetic diversity in maize, need some necessary work. Genetic diversity is the total variability present in individual or organism/population. Due to continuous use of maize variety in field and enhance the modern technology has deteriorated potential of genetic diversity. So to conserve this diversity in nature, need to study on population or inbreds (Dubreuil and Charcosset 1999). Genetic diversity such as morphological, biochemical and other molecular characterizations are available (Govindaraj et al., 2015). Morphological and biochemical method has been extensively used (Franco et al., 2001), but these methods are highly sensitive to environmental (Smith and Smith 1992; Beyenne et al., 2006). Molecular marker has scattered all over population to know about relationship among variety or genetic diversity. Molecular marker has been only based on DNA technology such as SSR, SNPs, RAPD and AFLP etc.

Keywords
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Introduction

Maize (Zea maize L.) belongs to poaceae family and it is cultivated all over world. Global ranking of maize has third ranked all over worldwide their own productivity and significance utilization in a form of food and fodder (first and second is rice and wheat
respectively). Maize used by human, and it has also income source of majority overwhelming population (EARO 2000). It used as a form of industrial product such as starch based product, corn starch and other things. Heavy use of maize and maize product, maize demanding has been increased day by day continue in all over world (Wada et al., 2008). Maize having 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). Now days hybrid (Zea mays L.) is most widely cultivated spp. all over world due to more 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 on several climates such as tropical and sub-tropical climate (Rebourg et al., 2003; Dubreuil et al., 2006). 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 having heterogeneous nature and selected by the farmers for cultivation (Prasanna and Sharma 2005).

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).

To develop good hybrid variety of maize should be good knowledge all about relationship among in the variety to conserve germplasm(Melchinger et al., 1991; Bernardo 2002).

Genetic diversity is the total variability present in individual or organism/population. Due to continuous use of maize variety in field and enhance the modern technology has deteriorated potential of genetic diversity. A Loss of genetic diversity in nature due to continue use of homogeneity related variety that is not present in nature, developed by the human effort. So to conserve this diversity in nature, need to study on population or inbreds (Dubreuil and Charcosset 1999).

There are many study has been conducted on analysis of genetic diversity such as morphological, biochemical and other molecular characterizations are available (Govindaraj et al., 2015). Morphological and biochemical method has been extensively used (Franco et al., 2005), but these methods are highly sensitive to environmental effects (Smith and Smith 1992; Beyenne et al., 2006a).

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

There are several population has been used for QTL mapping such as mortal and immortal population, in mortal population(can be segregate) such as f2 population and BC (back cross) population, but immortal population (cannot be segregate) having such as DH (doubled haploid), RIL (Recombinant
inbred lines), F₂ derived lines, NIL (near isogenic lines) and other population extensively has been used 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).

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 from breeding material. There are many marker systems has been extensively used to analyze the genetic diversity and molecular marker assisted selection (Elisabetta Frascaroli • Tobias A. Schrag • Albrecht E. Melchinger 2013).

**Classification of marker**

Marker in plant breeding have been utilized to know, genetic diversity, genome mapping, QTL mapping and for genotyping etc. so marker play indispensible role in plant breeding. To aggregate knowledge of molecular marker is a difficult task, but it is an easy.

**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). 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). The variation in these markers has been only due to 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 individual. This unlabeled primer is used to analyze with the help of agarose gel electrophoresis or polyacrylamide gel.

The unlabeled or fluorolabelled primer significantly enhances the research (Wenz et al., 1998). SSR or microsatellite is codominant in nature and distinguished to heterozygous from homozygous and they are also highly reproducible due to locus specific (see table no. 01). These primers mostly used in both eukaryotic and prokaryotic (Khan et al., 2017).

**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). The locus specific study has been conducted in many plant species such as barley (Saghai Maroof et al., 1994), jute (Das et al., 2012), wheat (Mukhtar et al., 2002), chickpea (Nayak et al., 2010), Alfalfa (Li et al., 2009), barley (Saghai Maroof et al., 1994) and also has been study on rice (Wu and Tanksley 1993) etc.

**SNP**

Single nucleotide variation arises due to single nucleotide in a genome in individuals of a population knows as SNPs. These variations found in among species, it varies individual to individuals and they constitute the more sufficient marker in the genome.
Table 1 Schematic representation of marker that has been more used in genetic diversity in maize

| S.NO. | MARKER TYPE | 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 |
| 02    | SSR         | plant height | 13 | 294 recombinant inbred lines | Ji-hua et al., 2007 |
| 03    | SSR         | Grain Yield and Plant Traits | 16 | 256, F2:3 families | Lima et al., 2006 |
| 04    | SSR         | Root aerenchyma formation | 04 | 141 F2 population | Mano et al., 2007 |
| 05    | SSR         | oil, starch, and protein concentrations in grain | 25 | 298 F2:3 family | Zhang et al., 2007 |
| 06    | SSR         | gray leaf spot | 14 | 37 inbred lines | Danson et al., 2008 |
| 07    | SSR         | agronomic traits | 51 | 450 maize RILs | Guo et al., 2008 |
| 08    | SSR         | Root traits | 17 | 94 Ril | Liu et al., 2008 |
| 09    | SSR         | Northern leaf blight Resistance | 36 | 400 F2:3 progenies | Sabadin et al., 2008 |
| 10    | SSR         | Fusarium ear rot | 16 | 187 Ril | Ding et al., 2009 |
| 11    | SSR         | Phosphorus treatments | 69 | 210, F2:3 families | Li et al., 2019 |
| 12    | SSR         | Kernel row number | 13 | 500, F2 Individuals | Lu et al., 2010 |
| 13    | SSR         | grain oil and starch | 21 | 265 F2:3 families | Wang et al., 2010 |
| 14    | SSR         | Test weight | 5 | 225 F2:3 population | Ding et al., 2011 |
| 15    | SSR         | Resistance To Aflatoxin | 40 | 250, F2:3 families | Warburton et al., 2011 |
| 16    | SSR         | Root system architecture | 36 | 187 advanced-backcross BC4F3 | Cai et al., 2012 |
| 17    | SSR         | gray leaf spot | 161 F2:3 families | Zhang et al., 2012 |
| 18    | SSR         | agronomic traits associated with plant architecture | 18 | 239, RIL | Zheng and Liu 2013 |
| 19    | SSR         | kernel size and weight | 55 and 28 | 270 derived F2:3 families | Liu et al., 2014 |
| 20    | SSR         | Gray leaf spot resistance | 18 | 478 F2:3 population | Liu et al, 2015 |
| 21    | SSR         | Ear Fasciation | 65 | 149 F2:3 families | Moreira et al., 2015 |
| 22    | SSR         | the protein, oil and starch contents | 25, 13, 31 and 15 | 498 RILs | Zhang et al., 2015 |
| 23 | SSR | Grain morphology traits | 18, 26, 23, and 19 | 58, Ril | Raihan et al., 2016 |
|---|---|---|---|---|---|
| 24 | SSR | Grey leaf spot | 12 | 233 f2:3 families | He et al., 2017 |
| 25 | SSR | inflorescence architecture | 19 | 202 and 218 F2:3 family | Zhao et al., 2017 |
| 26 | SSR | Agronomic traits | 15 | 121 Dh population | Choi et al., 2018 |
| 27 | SSR | Maize kernel size And weight | 52 | 150 f7 rils | Lan et al., 2018 |
| 28 | SSR | Forage agronomic traits | 42, 41, 54, and 45 | 250-720 Doubled Haploid lines (dhl), and ril population | Leng et al., 2018 |
| 29 | SSR | Nitrogen use efficiency (nue), | 19 | Recombinant inbred lines (181) | Mandolino et al., 2018 |
| 30 | SSR | Kernel weight | 28 | 40, F2:3 population | Li et al., 2019 |
| 31 | SNP | Northern leaf blight | 29 | 25, Nam, ril | Poland et al., 2011 |
| 32 | SNP | SOUTHERN LEAF BLIGHT | 32 | 5000 RIL | Kump, et al., 2011 |
| 33 | SNP | plant height and biomass as secondary traits of drought tolerance | 23 | 150 F2:3 line | Lu et al., 2011 |
| 34 | SNP | Head smut | 18 | 144, Inbred lines | Wang et al, 2012 |
| 35 | SNP | Kernel Weight Determination | 23,59 | 408 recombinant inbred lines | Prado et al., 2014 |
| 36 | SNP | Fusarium ear Rot resistance | 15 | 940 elite inbred lines | Chen et al, 2016 |
| 37 | SNP | leaf morphology | 111 | 215, 223, 208 and 212 RILs | Ku et al., 2016 |
| 38 | SNP | ear leaf traits | 23, 25, and 17 | 909 ril | Wang et al., 2017 |
| 39 | SNP | Vitamin E | 31 | 213 F2:3 | Fenton et al., 2018 |
| 40 | SNP | amylose biosynthesis | 27 | 464 inbred maize lines | Li et al., 2018 |
| 41 | SNP | Genetic Architecture Of Leaf Angle And Tassel Size | 23 | 213 F2:3 Population | Liu et al., 2018 |
| 42 | SNP | Cob resistance, ear Rot resistance | 28 | 258 Maize inbred | Mu et al., 2018 |
| 43 | SNP | tassel-related traits | 27 | 266 F2:3 families ril | Yl et al., 2018 |
| 44 | SNP | Common rust | 25 | F2:3 population | Zheng et al., 2018 |
| 45 | SNP | Leaf morphology traits | 19,838 | 866 maize-teosinte bc2s3 recombinant inbred lines | Fu et al., 2019 |
| 46 | SNP | Starch content | 9076 | 283 intermated | Lin et al., 2019 |
| 47 | SNP | Salt tolerance | 65 | 209 doubled Haploid (dh) | Luo et al., 2019 |
| 48 | SNP | Southern leaf blight, northern leaf blight, and gray leaf spot | 44 | F2:3 family populations 12 | Martins et al., 2019 |
| 49 | SNP | Delayed maize flowering in response to low Phosphate | 41 | 262 Ril population | Ren et al., 2019 |
| 50 | SNP | Water deficit-responsive | 213 | 267 Ril population | Virlouvet et al., 2019 |
| 51 | SNP | Dynamic plant height | 68 | Inbred lines (117 temperate lines, 135 tropical lines) | Wang et al., 2019 |
| 52 | SNP | Tassel architecture | 19 | 359 inbred lines and an ibm syn 10 population of 273 doubled haploid lines | Wang et al., 2019 |
| 53 | SNP | Tassel-related traits | 14 | 148 f2 population | Xie et al., 2019 |
| 54 | SNP | Plant architecture | 21 | 301 recombinant inbred lines | Yi et al., 2019 |
| 55 | SNP | Disease resistance(southern leaf blight (slb), northern leaf blight (nlb), and gray leaf spot) | 17 | 253 RIL | Zuniga et al., 2019 |

In maize 1 SNPs has been found over 60-120 bp (Ching et al., 2002), while in human has been estimated found 1 SNPs over 1000 bp (Sachidanandam et al., 2001). SNPs are more popular in the genome that has non coding regions.

But within the coding sequence that may be changed results in the amino acid sequence either this is the non-synonymous (Sunyaev et al., 1999), 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 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).

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). 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).

Maize plays indispensible role that is consumed by human in all over worldwide. So we should be enhancing growth of maize, need some any technology that can be fulfill these criteria. So we need good technology. Genetic diversity is the total gene present in among individuals. Modern cultivation is continuing decrease the heterogeneity. So we need to maintain the genetic diversity for future use. There are some molecular work such as marker assisted selection with the help of marker can be detect the genetic diversity present in among individuals. There are mainly in this research paper two molecular marker such as SSR and SNPs mostly used by the many plant breeders and researchers.

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