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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 thecereals grown under world wide 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 resietance 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

Maize, Genetic diversity and molecular marker

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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 f_2 population and BC (back cross) population, but immortal population (cannot be segregate) having such as DH (doubled haploid), RIL (Recombinant

inbred lines), F_2 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 fluorolabed 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.,* 20O2), 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	YI *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

				recombinant inbred lines (rils)	
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.

References

Agarwal, M., Shrivastava, N. and Padh, H., 2008. Advances in molecular marker techniques and their applications in plant sciences. *Plant cell reports*, *27*(4), pp.617-631.

Bernardo, R., 2002. *Breeding for quantitative traits in plants* (Vol. 1, p. 369). Woodbury, MN: Stemma press.

Beyene, A., Gibbon, D. and Haile, M., 2006. Heterogeneity in land resources and diversity in farming practices in Tigray, Ethiopia. *Agricultural systems*, *88*(1), pp.61-74.

Buetow, K.H., Edmonson, M.N. and Cassidy, A.B., 1999. Reliable identification of large numbers of candidate SNPs from public EST data. *Nature genetics*, *21*(3), pp.323-325.

Byrne, P.F., McMullen, M.D., Snook, M.E., Musket, T.A., Theuri, J.M., Widstrom, N.W., Wiseman, B.R. and Coe, E.H., 1996. Quantitative trait loci and metabolic pathways: genetic control of the concentration of maysin, a corn earworm resistance factor, in maize silks. *Proceedings of the National Academy of Sciences*, *93*(17), pp.8820-8825.

Cai, H., Chen, F., Mi, G., Zhang, F., Maurer, H.P., Liu, W., Reif, J.C. and Yuan, L., 2012. Mapping QTLs for root system architecture of maize (Zea mays L.) in the field at different developmental stages. *Theoretical and Applied Genetics*, *125*(6), pp.1313-1324.

Ching, A.D.A., Caldwell, K.S., Jung, M., Dolan, M., Smith, O.S.H., Tingey, S., Morgante, M. and Rafalski, A.J., 2002. SNP frequency, haplotype structure and linkage disequilibrium in elite maize inbred lines. *BMC genetics*, *3*(1), p.19.

Cowen NM (1988) The use of replicated progenies in markerbased mapping of QTL''s. Theor Appl Genet 75:857–862

Danson, J., Lagat, M., Kimani, M. and Kuria, A., 2008. Quantitative trait loci (QTLs) for resistance to gray leaf spot and common rust diseases of maize. *African Journal of Biotechnology*, *7*(18).

Das, A., Hari, S.S., Shalini, U., Ganeshkumar, A. and Karthikeyan, M., 2012. Molecular screening of virulence genes from Salmonella enterica isolated from commercial food stuffs. *Biosci Biotech Res Asia*, *9*, pp.363-369.

Ding, D., Zhang, L., Wang, H., Liu, Z., Zhang, Z. and Zheng, Y., 2009. Differential expression of miRNAs in response to salt stress in maize roots. *Annals of botany*, *103*(1), pp.29-38.

Doebley, J., 2004. The genetics of maize evolution. *Annu. Rev. Genet.*, *38*, pp.37-59.

Dubreuil, P. and Charcosset, A., 1998. Genetic diversity within and among maize populations: a comparison between isozyme and nuclear RFLP loci. *Theoretical and Applied Genetics*, *96*(5), pp.577-587.

Dubreuil, P. and Charcosset, A., 1999. Relationships among maize inbred lines and populations from European and North-American origins as estimated using RFLP markers. *Theoretical and applied genetics*, *99*(3-4), pp.473-480.

Dubreuil, P., Warburton, M.L., Chastanet, M., Hoisington, D. and Charcosset, A., 2006. More on the introduction of temperate maize into Europe: large-scale bulk SSR genotyping and new historical elements. *Maydica*, *51*(2), pp.281-291.

Edwards, M., 1992. Use of molecular markers in the evaluation and introgression of genetic diversity for quantitative traits. *Field Crops Research*, *29*(3), pp.241-260.

Edwards, M.D., Stuber, C.W. and Wendel, J.F., 1987. Molecular-marker-facilitated investigations of quantitative-trait loci in maize. I. Numbers, genomic distribution and types of gene action. *Genetics*, *116*(1), pp.113-125.

Fenton, M.E., Owens, B.F., Lipka, A.E., Ortiz, D., Tiede, T., Mateos-Hernandez, M., Ferruzzi, M.G. and Rocheford, T., 2018. High-density linkage mapping of vitamin E content in maize grain. *Molecular breeding*, *38*(3), p.31.

Franco, M.M., Antunes, R.C., Silva, H.D. and Goulart, L.R., 2005. Association of a PIT1, GH and GHRH polymorphism with performance and carcass traits in Landrace pigs. *Embrapa Recursos Genéticos e Biotecnologia-Artigo em periódico indexado (ALICE)*.

Frascaroli, E., Schrag, T.A. and Melchinger, A.E., 2013. Genetic diversity analysis of elite European maize (Zea mays L.) inbred lines using AFLP, SSR, and SNP markers reveals ascertainment bias for a subset of SNPs. *Theoretical and applied genetics*, *126*(1), pp.133-141.

Govindaraj, M., Vetriventhan, M. and Srinivasan, M., 2015. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics research international*, *2015*.

Govindaraj, M., Vetriventhan, M. and Srinivasan, M., 2015. Importance of genetic diversity assessment in crop plants and its recent advances: an overview of its analytical perspectives. *Genetics research international*, *2015*.

Guo, M., Yang, S., Rupe, M., Hu, B., Bickel, D.R., Arthur, L. and Smith, O., 2008. Genome-wide allele-specific expression analysis using massively parallel signature sequencing (MPSS™) reveals cis-and trans-effects on gene expression in maize hybrid meristem tissue. *Plant molecular biology*, *66*(5), pp.551-563.

He, Y., Wang, M., Dukowic-Schulze, S., Zhou, A., Tiang, C.L., Shilo, S., Sidhu, G.K., Eichten, S., Bradbury, P., Springer, N.M. and Buckler, E.S., 2017. Genomic features shaping the landscape of meiotic double-strand-break hotspots in maize. *Proceedings of the National Academy of Sciences*, *114*(46), pp.12231-12236.

Hiremath, P.J., Kumar, A., Penmetsa, R.V., Farmer, A., Schlueter, J.A., Chamarthi, S.K., Whaley, A.M., Carrasquilla- Garcia, N., Gaur, P.M., Upadhyaya, H.D. and Kavi Kishor, P.B., 2012. Large- scale development of cost- effective SNP marker assays for diversity assessment and genetic mapping in chickpea and comparative mapping in legumes. *Plant biotechnology journal*, *10*(6), pp.716-732.

Jiang, W., Bikard, D., Cox, D., Zhang, F. and Marraffini, L.A., 2013. RNA-guided editing of bacterial genomes using CRISPR-Cas systems. *Nature biotechnology*, *31*(3), p.233.

Ji-hua, T., Wen-tao, T., Jian-bing, Y., Xi-qing, M., Yi-jiang, M., Jin-rui, D. and Jian-Sheng, L., 2007. Genetic dissection of plant height by molecular markers using a population of recombinant inbred lines in maize. *Euphytica*, *155*(1-2), pp.117-124.

Karen Sabadin, P., Lopes de Souza Júnior, C., Pereira de Souza, A. and Augusto Franco

Garcia, A., 2008. QTL mapping for yield components in a tropical maize population using microsatellite markers. *Hereditas*, *145*(4), pp.194-203.

Katti, M.V., Ranjekar, P.K. and Gupta, V.S., 2001. Differential distribution of simple sequence repeats in eukaryotic genome sequences. *Molecular biology and evolution*, *18*(7), pp.1161-1167.

Khan, M.A., Kiran, U., Ali, A., Abdin, M.Z., Zargar, M.Y., Ahmad, S., Sofi, P.A. and Gulzar, S., 2017. Molecular markers and marker-assisted selection in crop plants. In *Plant biotechnology: principles and applications* (pp. 295-328). Springer, Singapore.

Knapp, S.J., 1991. Using molecular markers to map multiple quantitative trait loci: models for backcross, recombinant inbred, and doubled haploid progeny. *Theoretical and Applied Genetics*, *81*(3), pp.333-338.

Knapp, S.J., Bridges, W.C. and Birkes, D., 1990. Mapping quantitative trait loci using molecular marker linkage maps. *Theoretical and applied genetics*, *79*(5), pp.583-592.

Ku, L., Ren, Z., Chen, X., Shi, Y., Qi, J., Su, H., Wang, Z., Li, G., Wang, X., Zhu, Y. and Zhou, J., 2016. Genetic analysis of leaf morphology underlying the plant density response by QTL mapping in maize (Zea mays L.). *Molecular breeding*, *36*(5), p.63.

Kump, K.L., Bradbury, P.J., Wisser, R.J., Buckler, E.S., Belcher, A.R., Oropeza-Rosas, M.A., Zwonitzer, J.C., Kresovich, S., McMullen, M.D., Ware, D. and Balint-Kurti, P.J., 2011. Genome-wide association study of quantitative resistance to southern leaf blight in the maize nested association mapping population. *Nature genetics*, *43*(2), p.163.

Leng, P., Ouzunova, M., Landbeck, M., Wenzel, G., Eder, J., Darnhofer, B. and Lübberstedt, T., 2018. Quantitative trait loci mapping of forage agronomic traits in six mapping populations derived from European elite maize germplasm. *Plant Breeding*, *137*(3), pp.370-378.

Li, R., Shi, F., Fukuda, K. and Yang, Y., 2009. Effects of salt and alkali stresses on germination, growth, photosynthesis and ion accumulation in alfalfa (Medicago sativa L.). *Soil Science and Plant Nutrition*, *56*(5), pp.725-733.

Li, Y.G., Jiang, D., Xu, L.K., Zhang, S.Q., Ji, P.S., Pan, H.Y., Jiang, B.W. and Shen, Z.B., 2019. Evaluation of diversity and resistance of maize varieties to Fusarium spp. causing ear rot in maize under conditions of natural infection. *Czech Journal of Genetics and Plant Breeding*, *55*(4), pp.131-137.

Lima, M.D.L.A., de Souza, C.L., Bento, D.A.V., De Souza, A.P. and Carlini-Garcia, L.A., 2006. Mapping QTL for grain yield and plant traits in a tropical maize population. *Molecular breeding*, *17*(3), pp.227-239.

Liu, J.J., Wei, Z. and Li, J.H., 2014. Effects of copper on leaf membrane structure and root activity of maize seedling. *Botanical studies*, *55*(1), p.47.

Lu, D., Cai, X., Shi, Y., Zhao, J. and Lu, W., 2015. Effects of waterlogging after pollination on the physicochemical properties of starch from waxy maize. *Food chemistry*, *179*, pp.232-238.

Lu, Y., Zhang, S., Shah, T., Xie, C., Hao, Z., Li, X., Farkhari, M., Ribaut, J.M., Cao, M., Rong, T. and Xu, Y., 2010. Joint linkage–linkage disequilibrium mapping is a powerful approach to detecting quantitative trait loci underlying drought tolerance in maize. *Proceedings of the National Academy of Sciences*, *107*(45), pp.19585-19590.

Mandolino, C.I., D'Andrea, K.E., Olmos, S.E., Otegui, M.E. and Eyhérabide, G.H., 2018. Maize Nitrogen Use Efficiency: QTL Mapping in a US Dent x Argentine-Caribbean Flint RILs population. *Maydica*, *63*(1), p.17.

Mano, Y. and Omori, F., 2007. Breeding for flooding tolerant maize using" teosinte" as a germplasm resource. *Plant Root*, *1*, pp.17-21.

Martins, M.A., Tomasella, J. and Dias, C.G., 2019. Maize yield under a changing climate in the Brazilian Northeast: Impacts and adaptation. *Agricultural water management*, *216*, pp.339-350.

Matsuoka, Y., Vigouroux, Y., Goodman, M.M., Sanchez, J., Buckler, E. and Doebley, J., 2002. A single domestication for maize shown by multilocus microsatellite genotyping. *Proceedings of the National Academy of Sciences*, *99*(9), pp.6080-6084.

Melchinger, A.E., Messmer, M.M., Lee, M., Woodman, W.L. and Lamkey, K.R., 1991. Diversity and relationships among US maize inbreds revealed by restriction fragment length polymorphisms. *Crop Science*, *31*(3), pp.669-678.

Moreira, R., Chenlo, F., Arufe, S. and Rubinos, S.N., 2015. Physicochemical characterization of white, yellow and purple maize flours and rheological characterization of their doughs. *Journal of food science and technology*, *52*(12), pp.7954-7963.

Mu, X., Chen, Q., Chen, F., Yuan, L. and Mi, G., 2018. Dynamic remobilization of leaf nitrogen components in relation to photosynthetic rate during grain filling in maize. *Plant Physiology and Biochemistry*, *129*, pp.27-34.

Mukhtar, M.S., Rahmanw, M.U. and Zafar, Y., 2002. Assessment of genetic diversity among wheat (Triticum aestivum L.) cultivars from a range of localities across Pakistan using random amplified polymorphic DNA (RAPD) analysis. *Euphytica*, *128*(3), pp.417-425.

Nayak, S.N., Zhu, H., Varghese, N., Datta, S., Choi, H.K., Horres, R., JŘngling, R., Singh, J., Kishor, P.K., Sivaramakrishnan, S. and Hoisington, D.A., 2010. Integration of novel SSR and gene-based SNP marker loci in the chickpea genetic map and establishment of new anchor points with Medicago truncatula genome. *Theoretical and Applied Genetics*, *120*(7), pp.1415-1441.

Poland, J.A., Bradbury, P.J., Buckler, E.S. and Nelson, R.J., 2011. Genome-wide nested association mapping of quantitative resistance to northern leaf blight in maize. *Proceedings of the National Academy of Sciences*, *108*(17), pp.6893-6898.

Prasanna, B.M. and Sharma, L., 2005. The landraces of maize (Zea mays L.): diversity and utility. *Indian Journal of Plant Genetic Resources*, *18*(2), pp.155-168.

Raihan, M.S., Liu, J., Huang, J., Guo, H., Pan, Q. and Yan, J., 2016. Multi-environment QTL analysis of grain morphology traits and fine mapping of a kernel-width QTL in Zheng58× SK maize population. *Theoretical and applied genetics*, *129*(8), pp.1465-1477.

Rebourg, C., Chastanet, M., Gouesnard, B., Welcker, C., Dubreuil, P. and Charcosset, A., 2003. Maize introduction into Europe: the history reviewed in the light of molecular data. *Theoretical and applied genetics*, *106*(5), pp.895-903.

Sachidanandam, R., Weissman, D., Schmidt, S.C., Kakol, J.M., Stein, L.D., Marth, G., Sherry, S., Mullikin, J.C., Mortimore, B.J., Willey, D.L. and Hunt, S.E., 2001. A map of human genome sequence variation containing 1.42 million single nucleotide polymorphisms. *Nature*, *409*(6822), pp.928-934.

Saghai, M.M., Biyashev, R.M., Yang, G.P., Zhang, Q. and Allard, R.W., 1994. Extraordinarily polymorphic microsatellite DNA in barley: species diversity, chromosomal locations, and population dynamics. *Proceedings of the National Academy of Sciences of the United States of America*, *91*(12), pp.5466-5470.

Saghai, M.M., Biyashev, R.M., Yang, G.P., Zhang, Q. and Allard, R.W., 1994. Extraordinarily polymorphic microsatellite DNA in barley: species diversity, chromosomal locations, and population dynamics. *Proceedings of the National Academy of Sciences of the United States of America*, *91*(12),

pp.5466-5470.

Schlötterer, C. and Tautz, D., 1992. Slippage synthesis of simple sequence DNA. *Nucleic acids research*, *20*(2), pp.211-215.

Showemimo, F.A., *et al.*, (2007). Evaluation of divergence of agronomic and nutritional traits in quality protein maize.In Demand-driven technologies for sustainable maizeproduction in West and Central Africa. Proceedings of the fifth biennial regional maize workshop, IITA-Cotonou, Bénin, 3–6 May, 2005.WECAMAN/IITA, Ibadan, Nigeria. 515 pages.

Sibov, S.T., De Souza Jr, C.L., Garcia, A.A.F., Silva, A.R., Garcia, A.F., Mangolin, C.A., Benchimol, L.L. and De Souza, A.P., 2003. Molecular mapping in tropical maize (Zea mays L.) using microsatellite markers. 2. Quantitative trait loci (QTL) for grain yield, plant heigth, ear height and grain moisture. *Hereditas*, *139*(2), pp.107-115.

Sobrino, B., Brión, M. and Carracedo, A., 2005. SNPs in forensic genetics: a review on SNP typing methodologies. *Forensic science international*, *154*(2-3), pp.181-194.

Soleimani, V.D., Baum, B.R. and Johnson, D.A., 2003. Efficient validation of single nucleotide polymorphisms in plants by allele-specific PCR, with an example from barley. *Plant molecular biology reporter*, *21*(3), pp.281-288.

Sunyaev, S.R., Eisenhaber, F., Rodchenkov, I.V., Eisenhaber, B., Tumanyan, V.G. and Kuznetsov, E.N., 1999. PSIC: profile extraction from sequence alignments with position-specific counts of independent observations. *Protein engineering*, *12*(5), pp.387-394.

Szalma, S.J., Hostert, B.M., LeDeaux, J.R., Stuber, C.W. and Holland, J.B., 2007. QTL mapping with near-isogenic lines in maize. *Theoretical and Applied Genetics*, *114*(7), pp.1211-1228.

Tanksley S, Medino-Filho H, Rick C (1982) Use of naturally occurring enzyme variation to detect and map genes controlling quantitative traits in an interspecific backcross of tomato. *Heredity* 49:11-25

Tautz, D. and Renz, M., 1984. Simple sequences are ubiquitous repetitive components of eukaryotic genomes. *Nucleic acids research*, *12*(10), pp.4127-4138.

Twumasi-Afriyie, S., Zelleke, H., Yihun, K., Asefa, B. and Tariku, S., 2002. Development and improvement of highland maize in Ethiopia. *Enhancing the Contribution of Maize to Food Security in Ethiopia, EARO and CYMMIT, Addis Ababa*, pp.31-38.

Vigouroux, Y., Mitchell, S., Matsuoka, Y., Hamblin, M., Kresovich, S., Smith, J.S.C., Jaqueth, J., Smith, O.S. and Doebley, J., 2005. An analysis of genetic diversity across the maize genome using microsatellites. *Genetics*, *169*(3), pp.1617-1630.

Wada N, Feng C, Gulati A (2008) Introduction and overview. In: Gulati A, Dixon J (eds) Maize in Asia: changing markets and incentives. Academic Foundation, New Delhi

Wang, R.L., Stec, A., Hey, J., Lukens, L. and Doebley, J., 1999. The limits of selection during maize domestication. *Nature*, *398*(6724), pp.236-239.

Wang, S., Wang, J., Yu, J. and Wang, S., 2014. A comparative study of annealing of waxy, normal and high-amylose maize starches: The role of amylose molecules. *Food chemistry*, *164*, pp.332-338.

Wang, X., Brown, I.L., Evans, A.J. and Conway, P.L., 1999. The protective effects of high amylose maize (amylomaize) starch granules on the survival of Bifidobacterium spp. in the mouse intestinal tract. *Journal of Applied Microbiology*, *87*(5), pp.631-639.

Warburton, M.L., Brooks, T.D., Windham, G.L. and Williams, W.P., 2011. Identification of novel QTL contributing resistance to aflatoxin accumulation in

maize. *Molecular Breeding*, *27*(4), pp.491-499.

Wenz, H.M., Robertson, J.M., Menchen, S., Oaks, F., Demorest, D.M., Scheibler, D., Rosenblum, B.B., Wike, C., Gilbert, D.A. and Efcavitch, J.W., 1998. High-precision genotyping by denaturing capillary electrophoresis. *Genome research*, *8*(1), pp.69-80.

Westman, A.L. and Kresovich, S., 1997. Use of molecular marker techniques for description of plant genetic variation. *Biotechnology in agriculture series*, pp.9-48.

Wu, K.S. and Tanksley, S.D., 1993. Abundance, polymorphism and genetic mapping of microsatellites in rice. *Molecular and General Genetics MGG*, *241*(1-2), pp.225-235.

Xie, L., Zhang, J., Wang, Q., Meng, C., Hong, J. and Zhou, X., 2011. Characterization of maize chlorotic mottle virus associated with maize lethal necrosis disease in China. *Journal of Phytopathology*, *159*(3), pp.191-193.

Zheng, Z.P. and Liu, X.H., 2013. Genetic analysis of agronomic traits associated with plant architecture by QTL mapping in maize. *Genet Mol Res*, *12*(2), pp.1243-53.

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