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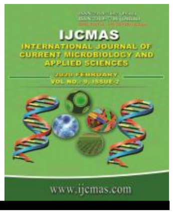

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Wheat Heat Tolerance: Mechanism, Impact and Quantitative Trait Loci Associated with Heat Tolerance

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ABSTRACT

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Heat stress is an abiotic phenomenon that resulting the losses in yield. Wheat consumed by the human in all over world. It has the top first rank in among cereals because of which most significant contribution to the worldwide. Higher temperature alters the primary phenomena such as growth and development and also affected to the physiological responses and biochemical aspects. So we need to development of heat tolerance variety that gives good yield performance towards heat stress. This may be achieved by the knowledge of whole plant mechanism for example mechanism of heat tolerance with plants, morphological responses, anatomical responses, physiological responses and expression of gene. Most strong full tool to know idea about these mechanism is molecular marker breeding. Molecular marker system reveals about that which one gene/ QTLs associated with heat tolerance.

Introduction

Wheat (Triticum aestivum)is one of the most important Rabi cereals crop all over the world. It is having first rank in both area and production. It is a thermostable crop that is cultivated on latitudinal distribution (Sahu *et al.,* 2002). Wheat is consumed by the human in all tropical and subtropical areas in developing as well as developed nations. It is grown mainly optimum temperature 15-18^{0}c (Chaudhary and wardlaw 1978) but mainly in these regions it suffers the chronic heat tolerance during reproductive phase and vegetative growth. Main effect of heat arise in world is the global warming (Iba, 2002).Heat stress affected to the production of wheat arid and semi-arid areas. Approximate 50 countries import wheat from another country due to heat stress that is affected to wheat production (Reynolds *et al.,* 2009). So to consider these problems we need to develop heat tolerance variety for public domain. Genetic diversity for wheat heat tolerance has been well created (Al-Khatib and Paulsen, 1990; Reynolds *et al.,* 2009; Wardlaw, 1989).

If temperature rosefrom optimal temperature due to any reason, thus this temperature reduceswheat yield(Fokar ., 1998; Maestri ., 2002).There are many traits such as earliness, leaf rolling, leaf motif, plant height and grain filling duration has been associated with wheat heat tolerance (Blum and Neguyen, 1997, Fokar ., 1998; Reynolds *et al.*, 2009).There are many another physiological traits associated with wheat heat resistance canopy temperature depression, photosynthetic rate, stomatal conductance and thermal stability (Al-Khatib and Paulsen, 1984; Fokar .,1998; Reynolds *et al*., 2009).

Terminal leaf burning mostly happened due to increase temperature at the time of grain filling duration, high temperature at this time severe loss to wheat production over worldwide (Hays *et al.,* 2007). A major portion affected in south Asia with high temperature in which resulting in losses in yield in India (Joshi *et al*., 2007).

Heat changes the morphological and anatomical structure of wheat plants resulting losses in yield (Stone and Nicolas 1995). However yield under stress is selecting that genotype that is gives good performance under this environment. This approach is very helpful to decide the tolerated variety in which no need extra activity such as to know physiological basis of any trait.

But this point should be always note that a variety gives good performance for heat tolerance, than we cannot consider that this variety gives good yield performance under drought tolerance (Reynolds *et al.*, 2009).But some limitation is there that no chosen early generation for yield heat tolerance in any variety. For selection of heat tolerance, need labor, cost, time and some necessary equipment for breeding programmes.

Although heat tolerance cannot predicted in the field so this is very difficult to furcate from drought stress. Hence there is any other method need to predict the heat resistance such as marker assisted breeding/ marker assisted selection (MAS/MAB). Hence need the QTLs mapping to detect QTLs that is associated with heat resistance with the help of molecular markers (Kato *et al.*, 2000).

It is proved that heat stress is controlled by the quantitative nature and it is inherited from generation to generation and continuously distributed (Blum .,1989; Yang *et al.*, 2002). To detect the QTLs for heat tolerance is being by many plant breeders in different environment breeding programmes on different population (See table).

The main objective of QTLs mapping to detect the quantitative trait that is associated with heat tolerance with the help of molecular marker breeding (Mohammadi *et al.*, 2008). There are many QTLs has been detected with the help molecular marker or genome mapping. They are described below (See table).

Mechanism of heat tolerance

When temperature is raised beyond level of threshold for a limited time than this temperature losses the beyond level of yield expectation. For higher yield, temperature should be normal range from18-22^{0}C. High temperature changed the physiological, morphological, anatomical and biochemical aspects of plants. High temperature may be change the geographical distribution, in which plants can be mature earlier (Porter, 2005). High temperature leads the injury levels of cellular may be death of cells (Schollf .,).

Direct injuries of cells due to heatleads toprotein denaturation and also may be alter the mechanism of cell if there is minimum heat than it can be also inactive of enzymes and reduce the protein synthesis (Howarth, 2005). All these injuries leads to starvation death because of which directly affected to yield contribution characters (Smertenko *et al.,* 1997).

Plants affected in different ways such as high temperatures and low temperature with high night temperatures or high day temperature or high soil temperatures. In addition there are many crops that are very sensitive to heat temperatures. In general heat tolerance is one phenomenon in which plant can be maintaining self-integrity to avoid the high temperatures and can be create good metabolic pathway.

Impact of high temperature on plant

High temperature has adverse effect on plant growth and development because of which resulting losses the yield. It affects the photosynthesis, photorespiration and also reproduction. In addition it also affected to molecular level of gene expression, alters the biochemical reaction and affected the heat shocked protein (HSP) (Marriamma *et al.*, 1997).

Activity of enzymes on plant is affected by the higher temperature due to changing in cellular response. An enzymes always having the thermal kinetic window that means the temperature range in which the Michaelis–Menten constant (Km) of the enzyme is remains within 200% of the optimum. If temperatures arise than even heat shocked protein may be inhibited. A study has been conducted on wheatthat described decrease the protein accumulation in kernel and changed the composition of kernelsdue to high temperature (Monjardino *et al.,* 2005).

Morphological response

Pre and post-harvest losses has been happened due to heat stress. In which some things are included such as sunburn on leaves, stem and branches,scorching of leaves, leaf abscission and senescence, inhibition of root, shoot growth, fruit dropping, discoloration, damage etc. so resulting reduced in yield (Vollenweider *et al.,* 2005).

And higher temperature also alters the phonological process from one to another. For enhance durability of high temperature decline the germination process or may be lost ultimately, this temperature inhibit the growth of emergence. Several plants have been affected by the high temperature in which significant reduction in losses, net assimilation ratio and shoot dry mass.

It also affected to anthesis and reproduction stage of plants with the combination of heat stress and drought stress. For instances, both grain number and grain weight is also affected by the higher temperature in wheat (Ferris *et al.*, 1998). Reproductive process also affected by the higher temperature because of which fertilization can occur or not, leading to loss in yield.

Anatomical response

It is clarify that higher temperature not only affected to plants morphology at cellular level but also affected to subcellular level. This phenomenon is same as happened in drought stress environment. Hence plants reduced the cell size, closer the stomata, it also increase the stomata densities and other cellular activity and enhance the xylem vessels for shoot and root (Anon *et al.,* 2004). The most disadvantage of plants that alteration of subcellular level in chloroplasts because of which significant changes in photosynthesis, For instances photosynthesis reduced by the higher temperature in which by the changing in structural system of thylakoid (Karim *et al.*, 1997).

Physiological responses

High temperature on wheat, reduce the physiological responses such as reduce the spike length, lower no of spikelets, accelerate floral initiation, adversely effect on pollen development etc. the most critical period of grain filling is post anthesis, if at this time temperature is high can be reduce the high yield. Complete sterility may be developed more than 30^0c higher temperature (Oven 1971, Saini and Aspinal 1982).

Previous study has been conducted where outlength of vegetative growth having highly positive correlation association with no of spikelets per spike (Rehman *et al.,* 1997). While shorter length of vegetative growth having adverse effect and reduce the no of spikelets per spike. Higher temperature during floral initiation reduces the kernel number in plants. Temperature increase 4% during development of kernel number than may be kernel number per unit area decrease (Fischer, 1985).

Previous study has been revealed that the time of floret death corresponded with the period when the ear and stem were accumulating dry matter at their most rapid rate and that inadequate assimilate availability may be critical in the loss of florets (Kirby, 1988). It is suggested that wheat yield and wheat quality could be improved to give heat shock treatment in early grain filling stage.

Molecular approach

It has been described that there are many methods to improve the heat tolerance such as traditional, transgenic approach and conventional breeding approach. It is well suggested that heat tolerance is controlled by the multigenic trait that involve in gene expression at different level of stage in different tissue (Bohnert *et al.*, 2006).

Thus to know about the heat tolerance gene, we need some extra powerful tool to detect the heat tolerance genes. The most powerful tool to detect the qualitative and quantitative complex trait is quantitative trait loci with the help of marker system (Roff, 1997. Shah *et al.*, 1999). There are many marker system has been promising to detect the QTL. There is some marker that has been most extensively utilized in plant breeding to detect the heat tolerance QTL(table no)is briefly described here.

SSR

SSR also called the microsatellite marker, it consist of tandem repeat in DNA sequence such as mono, di, tri, tetra and so on. And this tandem repeats found in both prokaryotic and eukaryotic genome (Tautz and Renz 1984; Katti *et al.*, 2001; Toth *et al.*, 2000; Salem *et al.*, 2008). They have another name short tandem repeats marker, microsatellites markers and sequence tagged microsatellite (STMS) marker etc. it is hyper variable marker available in nature. 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 due to repeats of DNA (Schlotterer and Tautz 1992). Slippage of DNA strand during replication originate more time than the point mutation. Microsatellite are differentiate based on inter individual of unique loci called the polymorphism, it can be analysed with the help of PCR analysis. In this technique primer used without radioactive labeled or flurolabeled or radiolabeled to know diverse group of individual with the help of PCR. This unlabeled primer is used analysis with the help of agarose gel electrophoresis or polyacrylamide gel. The unlabeled or fluorolabed primer significantly enhances the research and also panders the research (Wenz *et al.,* 1998). SSR or microsatellite are codominant in nature and also distinguished to heterozygous from homozygous and they are also highly reproducible due to locus specific. Mostly used in both eukaryotic and as prokaryotic (Khan *et al.*, 2017). There are many scientists has been described the which one particular marker for heat tolerance

SNP

Single nucleotide variation arises due to single nucleotide in a genome in individuals of a population knows as SNPs. They found among species, it very individual to individuals and they constitute the more sufficient marker in the genome. 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 and resulting the phenotypic differences (Richard and Beckman 1995). 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. 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)

AFLP

To overcome the difficulties of RAPD analysis that is does not reproducible in any laboratory, so it came. This method has been developed by the (Vos *et al* 1995). It combines the power of RFLP with the flexibility of PCR-based technology by ligating primer recognition sequences (adaptors) to the restricted DNA and selective PCR amplification of restriction fragments using a limited set of primers.

The AFLP may be produce 51-100 per assay, in primers pairs. Number of amplicons per AFLP assay is a function of the number selective nucleotides in the AFLP primer combination, the selective nucleotide motif, GC content, and physical genome size and complexity. DNA fingerprinting is developed by the AFLP technique regardless to DNA resources without prior knowledge of DNA sequence. Most AFLP present in any genome at unique location in which can be exploited as a landmark of physical and genetic mapping. This technique distinguished the closely related individual of the species and also use for genome map (Althoff *et al.,* 2007).

Table.1 Schematic representation of quantitative trait loci with heat tolerance

S. No.	**Trait**	**QTLs Name**	**flanking Marker**	**Type of Marker**	**Population size**	**Cross type**	**References**
1	Grain weight/spike	*Qtgws.iiwbr-2A*	*Gwm497.1*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
		Qtgws.iiwbr-6D.1	*Barc21*		397	HUW510 × HD2808	
		Qtgws.iiwbr-6D.2	*Barc196*		397	HUW510 × HD2808	
2	Grain weight/spike	*Qgws.iiwbr-2A*	*Gwm122*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
3	Grain weight/spike	*Qgws.iiwbr-2A*	*Gwm122*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
		Qgws.iiwbr-2A	*Gwm448*	SSR	397	HUW510 × HD2808	
4	Grain number per spike	*Qgns.iiwbr-2A*	*Gwm448*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
		Qtgns.iiwbr-6D	*Barc196*		397	HUW510 × HD2808	
5	Grain number per spike	*Qgns.iiwbr-2A*	*Gwm448*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
		Qlgns.iiwbr-2A	*Gwm372*	SSR	397	HUW510 × HD2808	
6	Grain number per spike	*Qgns.iiwbr-2A*	*Gwm122*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
		Qgns.iiwbr-2A	*Gwm448*	SSR	397	HUW510 × HD2808	
7	Thousand grain weight	*Qtgw.iiwbr-2A*	*Gwm122*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017

8	Thousand grain weight	*Qtgw.iiwbr-2A*	*Gwm122*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
		Qtgw.iiwbr-2A	*Gwm122*	SSR	397	HUW510 × HD2808	
9	Grain filling duration	*Qlgfd.iiwbr-2B*	*Cfa2278*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
10	Grain filling duration	*Qhthsigfd.iiwbr-2B*	*Gwm257*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
11	Grain filling rate	*Qtgfr.iiwbr-2A*	*Wmc728*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
		Qtgfr.iiwbr-6D	*Barc196*		397	HUW510 × HD2808	
12	Grain filling rate	*Qgfr.iiwbr-2A*	*Gwm448*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
13	Grain filling rate	*Qgfr.iiwbr-2A*	*Gwm122*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
14	Grain yield	*Qtgy.iiwbr-6D*	*Barc196*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
15	Grain yield	*Qgy.iiwbr-2A*	*Gwm448*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
16	Grain yield	*Qgy.iiwbr-2A*	*Gwm122*	SSR	397	HUW510 × HD2808	Bhusal *et al.*, 2017
17	Productive tiller	*QLpt.iiwbr-1B*	*1265440|F|0*	SNP	220	RAJ 4014× k 7903	Shrama *et al.*, 2016
		QLpt.iiwbr-1B^{3}	*1265440|F|0*	SNP	220	RAJ 4014× k 7903	Shrama*et al.*, 2016
		QHpt.iiwbr-2D^{3}	*1259376|F|0*	SNP	220	RAJ 4014× k 7903	Shrama*et al.*, 2016

		QHpt.iiwbr-3B	*1145590|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHpt.iiwbr-3B	*997738|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHpt.iiwbr-6B	*1109194|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
18	Grain filling duration	*QHgfd.iiwbr-1B*	*2249474|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHgfd.iiwbr-1B	*2249474|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHgfd.iiwbr-5A	*1079678|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHgfd.iiwbr-5A	*1079678|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QLgfd.iiwbr-5A	*1079678|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QLgfd.iiwbr-5A	*1079678|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
19	Grain number per spike	*QHgn.iiwbr-2B*	*1161184|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHgn.iiwbr-2B	*1097543|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
20	Grain yield	*QHgy.iiwbr-6B*	*2280984|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHgy.iiwbr-Un	*1039232|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
		QHgy.iiwbr-Un^{3}	*1038216|F|0*	SNP	220	RAJ 4014× k 7903	Shramaet *al.*, 2016
21	water soluble carbohydrates	*Q.Wsc.aww-1B*	*WPT3679-BARC1138B*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
22	thousand kernal	*Q.Tkw.aww-1D*	*CFD0027-*	DArt,	255	RAC875×	Bennet *et al.*, 2012

	weight		*WPT-1799*	SSR		KUKRI	
23	physiological maturity	*Q.Phys.aww-2A*	*CFA2263-WPT6361*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
24	Ear emergence time	*Q.Eet.aww-2B*	*WPT7757-BARC0013A*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
25	thousand kernal weight	*Q.Tkw.aww-2B*	*BARC0091-WPT-0335*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
		Q.Vig.aww-2B	*WPT7200-WPT5128*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
26	flag leaf width	*Q.Flw.aww-2B*	*WPT7200-WPT5128*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
27	normalixed difference vegetative index	*Q.Ndvi.aww-2B*	*CFD0050A-WPT3378*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
28	canopy temperature: vegetative	*Q.Ctveg.aww-2D*	*WPT-6003-PPD-D1*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
29	canopy temperature: grain fill	*Q.Ctgf.aww-2D*	*WPT-6003-PPD-D1*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
30	Ear emergence time	*Q.Eet.aww-2D*	*PPDD1-WPT0330*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
		Q.Vig.aww-2D	*BARC0328B-WPT6574*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
31	normalixed difference vegetative index	*Q.Ndvi.aww-2D*	*WPT0021-WPT4559*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
32	canopy temperature: vegetative	*Q.Ctveg.aww-3A*	*WPT-0714-GWM0002*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
33	water soluble carbohydrates	*Q.Wsc.aww-3A*	*BARC0324-WPT4077*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
34	Grain yield	*Q.Yld.aww-3B-1*	*WMC0043-WPT6973*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
35	thousand kernal weight	*Q.Tkw.aww-3B*	*WPT-6973-WPT-9510*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
36	normalixed difference vegetative index	*Q.Ndvi.aww-3B*	*WPT6973-WPT9510*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
37	flag leaf width	*Q.Flw.aww-2B*	*WPT7200-WPT5128*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
38	kernels per	*Q.Kpsm.aww-3B*	*WPT8021-*	DArt,	255	RAC875×	Bennet *et al.*, 2012

	metre sq		*GWM0114B*	SSR		KUKRI	
		Q.Vig.aww-3B	*WPT8021-GWM0114B*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
39	Grain yield	*Q.Yld.aww-3B-2*	*WPT8021-GWM0114B*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
40	canopy temperature: grain fill	*Q.Ctgf.aww-3B*	*WPT-8021-GWM0114B*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
41	kernels per metre sq	*Q.Kpsm.aww-3D*	*CFD0034-WMC0533*	SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
42	Grain yield	*Q.Yld.aww-3D*	*CFD0034-WMC0533*	SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
43	normalixed difference vegetative index	*Q.Ndvi.aww-3D-1*	*WPT6262-WPT7894*	Dart	255	RAC875×KUKRI	Bennet *et al.*, 2012
44	physiological maturity	*Q.Phys.aww-4B*	*BARC0114-WPT0391*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
45	normalixed difference vegetative index	*Q.Ndvi.aww-4B*	*WPT0391-WPT3608*	Dart	255	RAC875×KUKRI	Bennet *et al.*, 2012
46	SPAD	*Q.Spad.aww-4D*	*GWM0297B-WMC0457*	SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
47	Grain yield	*Q.Yld.aww-4D*	*WMC0457-BARC0288*	SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
48	Ear emergence time	*Q.Eet.aww-5A*	*GWM0186-WPT1370*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
49	kernels per metre sq	*Q.Kpsm.aww-5A*	*CFA2141-WPT5231*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
50	flag leaf width	*Q.Flw.aww-5B*	*BARC0088-WPT4936*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
51	Ear emergence time	*Q.Eet.aww-5B*	*WPT9103-WMC0099*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
52	physiological maturity	*Q.Phys.aww-6B*	*BARC0247-BARC0134*	SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
53	SPAD	*Q.Spad.aww-6B-2*	*BARC0134-WPT5480*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
54	Grain yield	*Q.Yld.aww-7A-1*	*WPT9207-WPT4748*	Dart	255	RAC875×KUKRI	Bennet *et al.*, 2012
55	canopy temperature: vegetative	*Q.Ctveg.aww-7A*	*WPT-5153-CFA2028*	DArt, SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012
56	Ear emergence time	*Q.Eet.aww-7A-1*	*CFA2028-WMC0083A*	SSR	255	RAC875×KUKRI	Bennet *et al.*, 2012

57	normalixed difference vegetative index	*Q.Ndvi.aww-7A*	*CFA2028-WMC0083A*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
58	water soluble carbohydrates	*Q.Wsc.aww-7B*	*WPT9887-WPT0745*	Dart	255	RAC875× KUKRI	Bennet *et al.*, 2012
59	Ear emergence time	*Q.Eet.aww-7B*	*GWM0297-BARC0065*	SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
60	canopy temperature: vegetative	*Q.Ctveg.aww-7B*	*WPT-4230-WMC0517B*	DArt, SSR	255	RAC875× KUKRI	Bennet *et al.*, 2012
61	Grain Yield	*QGY-1A*	*agg/cac-6-agg/cac-6*	AFLP	167	SeriM82× Babax	Hassan *et al.*, 2018
		QGY-1B	*aag/ctc-6-gwm301b*	AFLP, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QGY-2B	*aag/ctc-13-acc/ctc-9*	AFLP	167	SeriM82× Babax	Hassan *et al.*, 2018
		QGY-2D	*wPt-6657-gdm035*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QGY-3A	*wPt-2478-gwm369*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QGY-7A	*wPt-4748-aca/cag-8*	DArt, AFLP	167	SeriM82× Babax	Hassan *et al.*, 2018
62	water soluble carbohydrates	*QWSC-3B*	*wPt-2757-barc147*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QWSC-4A	*act/cag-3-agg/cta-12*	AFLP	167	SeriM82× Babax	Hassan *et al.*, 2018
		QWSC-5A	*wPt-3563-gwm617a*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QWSC-7D	*cfd0014-gwm473*	SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
63	Proline content (lgg^{-1})	*QPro-5A*	*aac/ctc-12-gwm304*	AFLP, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QPro-5B	*acc/ctc-3-gwm133*	AFLP, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QPro-7A	*wPt-2260-aca/cac-8*	DArt, AFLP	167	SeriM82× Babax	Hassan *et al.*, 2018
64	*Fv/Fm* maximum efficiency of photosystem II	*QFv/Fm-1D*	*wPt-5503-wPt-9380*	DArt	167	SeriM82× Babax	Hassan *et al.*, 2018
		QFv/Fm-2B	*act/ctc-1-wPt-0047*	AFLP, DArt	167	SeriM82× Babax	Hassan *et al.*, 2018
		QFv/Fm-3B	*aag/ctc-9-wPt-8238*	AFLP, DArt	167	SeriM82× Babax	Hassan *et al.*, 2018

		QFv/Fm-6A	*wmc0256-acc/ctg-6*	SSR, AFLP	167	SeriM82× Babax	Hassan *et al.*, 2018
		QFv/Fm-6B	*wPt-2899-wPt-4764*	Dart,	167	SeriM82× Babax	Hassan *et al.*, 2018
		QFv/Fm-7B	*wPt-3723-gwm132c*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
65	cytoplasmic membrane stability	*QCMS-2B*	*act/ctc-1-wPt-0047*	AFLP, DArt	167	SeriM82× Babax	Hassan *et al.*, 2018
		QCMS-3B	*wPt-1804-aca/cag-9*	DArt, AFLP	167	SeriM82× Babax	Hassan *et al.*, 2018
		QCMS-4B	*wPt-1708-wmc048a*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QCMS-7A	*cfa2049-wPt-4553*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
		QCMS-7B	*wPt-3723-gwm132c*	DArt, SSR	167	SeriM82× Babax	Hassan *et al.*, 2018
66	75% green	*Q75%G .ksu-2A*	*Xgwm356/CGT.TGCG-349*	SSR,AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
		Q75%G .ksu-2A	*CGT.TGCG-349/CTCG.ACC-242*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
		Q75%G .ksu- 3B	*CGT.CTCG-146/GTG.AGCT-205*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
67	25% green	*Q25%G .ksu-2A*	*Xgwm356/CGT.TGCG-349*	SSR, AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
		Q25%G .ksu-2A	*CGT.TGCG-349/CTCG.ACC-242*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
68	50% green	*Q50%G .ksu-2A*	*CGT.TGCG-349/CTCG.ACC-242*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
		Q50%G .ksu-6A	*CGT.GTG-343/CGA.CGCT-406*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
69	maximum rate of senescence	*QMrs .ksu-2A*	*Xgwm356/CGT.TGCG-349*	SSR, AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
		QMrs .ksu-2A	*CGT.TGCG-349/CTCG.ACC-242*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
70	time to	*QTmrs .ksu-2A*	*Xgwm356/C*	SSR,	101	Karl 92 ×	Vijayalakshmi *et al.*,

	maximum rate of senescence		*GT.TGCG-349*	AFLP		Ventnor	2010
		QTmrs .ksu-6A	*CGT.GTG-343/CGA.CGCT-406*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
		QTmrs .ksu-6B	*CGT.CTCG-406/CGA.CAT-324*	AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
71	percent greenness at maximum senescence	*QPgms .ksu-3A*	*Xgwm5/Xbarc1165*	SSR	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
		QPgms .ksu-6B	*Xbarc198/CGT.CTCG-406*	SSR, AFLP	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
72	*Fv/Fm* chlorophyll fluorescence	*QFv/Fm .ksu-7A*	*CGA.CGCT-272/Xbarc121*	AFLP, SSR	101	Karl 92 × Ventnor	Vijayalakshmi *et al.*, 2010
73	thylakoid membrane damage 4/7	*QHttmd.ksu-6A*	*Xbarc113/AGCTCG347*	SSR,AFLP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHttmd.ksu-6A	*Xbarc113/AGCTCG347*	SSR,AFLP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
74	chlorophyll content4/7	*QHtscc.ksu-6A*	*Xbarc113/AGCTCG347*	SSR,AFLP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHtscc.ksu-6A	*Xbarc113/AGCTCG347*	SSR,AFLP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
75	thylakoid membrane damage7/10	*QHttmd.ksu-7A*	*Xbarc121/barc49*	SSR	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHttmd.ksu-7A	*Xbarc121/barc49*	SSR	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHttmd.ksu-7A	*Xbarc121/barc49*	SSR	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
76	chlorophyll content4/7/10	*QHtscc.ksu-7A*	*Bin754/Bin45*	SNP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHtscc.ksu-7A	*Xbarc121/barc49*	SSR	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHtscc.ksu-7A	*Xbarc121/barc49*	SSR	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
77	plasma membrane damage7/10	*QHtpmd.ksu-7A*	*Xbarc121/barc49*	SSR	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHtpmd.ksu-7A	*Xbarc121/barc49*	SSR	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
78	chlorophyll content4/7	*QHtscc.ksu-1B*	*gwm18/Bin1130*	SSR, SNP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHtscc.ksu-1B	*gwm18/Bin1130*	SSR, SNP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
79	thylakoid	*QHttmd.ksu-1D*	*Bin747/Bin1*	SNP	101	Karl 92 ×	Talukder *et al.*, 2014

	membrane damage 4		*596*			Ventnor	
	chlorophyll content7	*QHtscc.ksu-1D*	*Bin747/Bin1596*	SNP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
80	plasma membrane damage7/10	*QHtpmd.ksu-1D*	*Bin747/Bin1596*	SNP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHtpmd.ksu-2B	*Bin178/Bin81*	SNP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
		QHtpmd.ksu-2B	*Bin178/Bin81*	SNP	101	Karl 92 × Ventnor	Talukder *et al.*, 2014
81	SSI	*QSsi.moh-1B*	*gwm190*	SSR	144	Kauz × MTRWA 116	Mohammadi *et al.*, 2008
		QSsi.moh-5B	*gwm133A*	SSR	144	Kauz × MTRWA 116	Mohammadi *et al.*, 2009
		QSsi.moh-7B	*gwm63B*	SSR	144	Kauz × MTRWA 116	Mohammadi *et al.*, 2009
82	HSI_kernel number of main spike	*QHknm.tam-2B*	*gwm111.2*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
83	HSI_kernel number of main spike	*QHknm.tam-2B*	*gwm111.2*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
84	HSI_kernel number of main spike	*QHknm.tam-3B*	*gwm389*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
85	HSI_kernel number of main spike	*QHknm.tam3B*	*barc147*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
86	HSI_kernel weight of main spike	*QHkwm.tam-3B*	*wmc527*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
87	HSI_kernel weight of main spike	*QHkwm.tam-3B*	*wmc326*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
88	HSI_single kernel weight of main spike	*QHskm.tam-1A*	*cfa2129*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
89	HSI_single kernel weight of main spike	*QHskm.tam-1A*	*cfa2129*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
90	HSI_single kernel weight	*QHskm.tam-2A*	*gwm356*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010

	of main spike						
91	HSI_single kernel weight of main spike	*QHskm.tam-2A*	*gwm294*	SSR	64	Cutter × Halberd	Mason *et al.*, 2010
92	HSI of thousand grain weight	*QHthsitgw.bhu-2B*	*Xgwm935–Xgwm1273*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
93	HSI of thousand grain weight	*QHthsitgw.bhu-7B*	*Xgwm1025–Xgwm745*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
94	HSI of thousand grain weight	*QHthsitgw.bhu-7D*	*Xgwm3062–Xgwm4335*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
95	HSI of grain yield	*QHthsiYLD.bhu-7B*	*Xgwm1025–Xgwm745*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
96	HSI of grain yield	*QlsYLD.bhu-7B*	*Xgwm1025–Xgwm745*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
97	HSI of grain fill duration	*QHthsigfd.bhu-2B*	*Xgwm935–Xgwm1273*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
98	canopy temperature depression	*QHtctd.bhu-7B*	*Xgwm1025–Xgwm745*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
99	DM	*Qls-dm.bhu-7D*	*Xgwm3062–Xgwm4335*	SSR	148	NW1014 × HUW468’	Paliwal *et al.*, 2012
100	Flag leaf cuticular waxes	*QWax.tam08-1B*	*wmc419*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
		QWax.tam08-5A	*wmc713*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
		QWax.tam09-1B	*wmc156*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
		QWax.tam09-5A	*gwm205*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
101	Temperature depression of flag leaf	*QTdl.tam09-2D*	*cfd56*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
		QTdl.tam09-3B	*barc164*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
		QTdl.tam09-5A	*barc141*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
		QTds.tam09-3B	*wmc418*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015

		QTds.tam09-5A	*gwm293*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
		QTds.tam09-5B	*gwm160*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
102	Temperature depression of main spike	*QTds.tam09-3B*	*wmc418*	SSR	121	Karl92×Halberd	Mondal *et al.*, 2015
105	Plant height	*QPh.cau-1B.3*	*bar308b*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
106	Plant height	*QPh.cau-2D.2*	*gwm296*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
107	Plant height	*QPh.cau-2D.3*	*cfd53*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
113	Plant height	*QPh.cau-4D.2*	*barc105*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
117	Plant height	*QPh.cau-6D*	*barc54*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
148	Grain weight per spike	*QGws.cau-2D.3*	*gwm157*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
155	HSI Thousand grain weight	*QHsitgw.cau-4B.2*	*WMC652*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
156	HSI Thousand grain weight	*QHsitgw.cau-5B*	*barc59*	SSR	203	ND3338 × JD6.	Guan *et al.*, 2018
160	Single grain weight	*QTL11 (QHsgw.aww-3B)*	*wsnp_BE497169B_Ta_2_1*	SNP	144	Drysdale × Waagan	Shirdelmoghanloo *et al.*, (2016)
162	Single grain weight	*QTL27 (QHsgw.aww-6B),*	*wsnp_Ex_c11573_18650189*	SNP	144	Drysdale × Waagan	Shirdelmoghanloo *et al.*, (2016)
163	HSI Grain yield	*QHY.bhu-1DL*	*wmc216-cfd19*	SSR	138	Berkut × Krichauff	Tiwari *et al.*, 2013
164	HSI Thousand grin weight	*QHTgw.bhu-1DS*	*wPt9664-cfd083*	DArt, SSR	138	Berkut × Krichauff	Tiwari *et al.*, 2013
165	HSI Thousand grin weight	*QHTgw.bhu-6BL*	*gwm626-wPt4924*	DArt, SSR	138	Berkut × Krichauff	Tiwari *et al.*, 2013
166	HSI Grain filling duration	*QHGfd.bhu1-2DL*	*gwm349-wPt9797*	DArt, SSR	138	Berkut × Krichauff	Tiwari *et al.*, 2013
167	HSI Grain filling duration	*QHGfd.bhu2-2DL*	*cfd233-cfd044*	SSR	138	Berkut × Krichauff	Tiwari *et al.*, 2013
168	HSI Grain filling duration	*HGfd.bhu1-7AL*	*wmc065-wmc139*	SSR	138	Berkut × Krichauff	Tiwari *et al.*, 2013
169	HSI Canopy temperature	*QHCt.bhu-1DS*	*wPt9664-cfd083*	DArt, SSR	138	Berkut × Krichauff	Tiwari *et al.*, 2013
170	HSI Days of anthesis	*QHDa.bhu-1BL*	*wPt3227-wPt0705*	Dart	138	Berkut × Krichauff	Tiwari *et al.*, 2013

180	SDS heat	*Qsdsheat.tam-1D*	*barc119-gwm337*	SSR	64	Cutter × Halberd	Beecher *et al.*, 2012
181	SDS stability	*Qsdssta.tam-7A*	*gwm60-barc108*	SSR	64	Cutter × Halberd	Beecher *et al.*, 2012
182	Stay green	*QSg.bhu-1A*	*Xgwm691-Xgwm752*	SSR	142	Chirya 3 × Sonalika	Kumar *et al.*, 2010
183	maximum quantum efficiency of photosystem II	*QHst.cph-3B*	*1218388s-Xgwm389*	SSR, SNP	420	IPK-9705 × IPK-2845	Sharma *et al.*, 2017
184	maximum quantum efficiency of photosystem II	*QHst.cph-1D*	*985618p-1698203p*	PAV	420	IPK-9705 × IPK-8183	Sharma *et al.*, 2017
185	maximum quantum efficiency of photosystem II	*QHst.cph-3B*	*1178540p-1127409s*	PAV-SNP	420	IPK-9705 × IPK-28703	Sharma *et al.*, 2017

There are much more variation for heat tolerance that is also varies on development and growth stage but for wheat, reproduction and grain filling stage is more prone to higher temperature. Various plant parts have been most affected by the cellular responses.

Therefore to reduce yield in wheat, understanding the idea about heat tolerance, so we need powerful tool. A extensively used of molecular marker in plant breeding has resulted to detect many QTLs for trait of interest. But in this review paper, we have described QTLs for heat tolerance.

Mostly SSR, SNPs, AFLP etc. used to detect reliable information for heat tolerance QTLs. It seems that this technology reveals about the reliable information without any false report.

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.

Al- Khatib, K. and Paulsen, G.M., 1984. Mode of high temperature injury to wheat during grain development. *Physiologia plantarum*, *61*(3), pp.363-368.

Al- Khatib, K. and Paulsen, G.M., 1990. Photosynthesis and productivity during high- temperature stress of wheat genotypes from major world regions. *Crop Science*, *30*(5), pp.1127-1132.

Althoff, D.M., Gitzendanner, M.A. and Segraves, K.A., 2007. The utility of amplified fragment length polymorphisms in phylogenetics: a comparison of homology within and between genomes. *Systematic biology*, *56*(3), pp.477-484.

Anon, S., Fernandez, J.A., Franco, J.A. *et al.*, (2004) Effects of water stress and night temperature preconditioning on water relations and morphological and anatomical changes of Lotus creticus

Beecher, F.W., Mason, E., Mondal, S., Awika, J., Hays, D. and Ibrahim, A., 2012. Identification of quantitative trait loci (QTLs) associated with maintenance of wheat (Triticum aestivum Desf.) quality characteristics under heat stress conditions. *Euphytica*, *188*(3), pp.361-368.

Bennett, D., Reynolds et al.,, M., Mullan, D., Izanloo, A., Kuchel, H., Langridge, P. and Schnurbusch, T., 2012. Detection of two major grain yield QTL in bread wheat (Triticum aestivum L.) under heat, drought and high yield potential environments. *Theoretical and Applied Genetics*, 125(7), pp.1473-1485.

Bhusal, N., Sarial, A.K., Sharma, P. and Sareen, S., 2017. Mapping QTLs for grain yield components in wheat under heat stress. *PloS one*, 12(12), p.e0189594.

Blum, A., Shpiler, L., Golan, G. and Mayer, J., 1989. Yield stability and canopy temperature of wheat genotypes under drought-stress. *Field Crops Research*, *22*(4), pp.289-296.

Blum, A., Sullivan, C.Y. and Nguyen, H., 1997. The effect of plant size on wheat response to agents of drought stress. II. Water deficit, heat and ABA. *Functional Plant Biology*, *24*(1), pp.43-48.

Bohnert, H.J., Gong, Q., Li, P., andMa, S. (2006) Unravelling abiotic stress tolerance mechanisms: getting genomics going. Curr. Opin. Plant Biol., 9, 180–188.

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.

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.

Chowdhury, S.I. and Wardlaw, I.F., 1978. The effect of temperature on kernel development in cereals. *Australian Journal of Agricultural Research*, *29*(2), pp.205-223.

Ferris, R., Ellis, R.H., Wheeler, T.R., and Hadley, P. (1998) Effect of high temperature stress at anthesis on grain yield and biomass of field grown crops of wheat. Plant Cell Environ, 34, 67–78.

Fischer, R.A. (1985)Number of kernels in wheat crops and the influence of solar radiation and temperature. J. Agric. Sci., 105, 447–461.

Fokar, M., Blum, A. and Nguyen, H.T., 1998. Heat tolerance in spring wheat. II. Grain filling. *Euphytica*, *104*(1), pp.9-15.

Guan, P., Lu, L., Jia, L., Kabir, M.R., Zhang, J., Lan, T., Zhao, Y., Xin, M., Hu, Z., Yao, Y. and Ni, Z., 2018. Global QTL analysis identifies genomic regions on chromosomes 4A and 4B harboring stable loci for yield-related traits across different environments in wheat (Triticum aestivum L.). *Frontiers in plant science*, *9*, p.529.

Hays, D., Mason, E., Do, J.H., Menz, M. and Reynolds et al.,, M., 2007. Expression quantitative trait loci mapping heat tolerance during reproductive development in wheat (Triticum aestivum). In *Wheat production in stressed environments* (pp. 373-382). Springer, Dordrecht.

Howarth, C.J. (2005) Genetic improvements of tolerance to high temperature, in Abiotic Stresses: Plant Resistance Through Breeding and Molecular Approaches (eds M. Ashraf and P.J.C. Harris), Howarth Press, Inc., New York, pp. 277–300.

Iba, K., 2002. Acclimative response to temperature stress in higher plants: approaches of gene engineering for temperature tolerance. *Annual Review of Plant Biology*, *53*(1), pp.225-245.

Joshi, A.K., Ortiz-Ferrara, G., Crossa, J., Singh, G., Sharma, R.C., Chand, R. and Parsad, R., 2007. Combining superior agronomic performance and terminal heat tolerance with resistance to spot blotch (Bipolaris sorokiniana) of wheat in the warm humid Gangetic Plains of South Asia. *Field crops research*, *103*(1), pp.53-61.

Kamran, A., Iqbal, M., Navabi, A., Randhawa, H., Pozniak, C. and Spaner, D., 2013. Earliness per se QTLs and their interaction with the photoperiod insensitive allele Ppd-D1a in the Cutler× AC Barrie spring wheat population. Theoretical and applied genetics, 126(8), pp.1965-1976.

Karim, M.A., Fracheboud, Y., and Stamp, P. (1997) Heat tolerance of maize with reference of some physiological characteristics. Ann. Bangladesh Agri., 7, 27–33.

Kato, K., Miura, H. and Sawada, S., 2000. Mapping QTLs controlling grain yield and its components on chromosome 5A of wheat. *Theoretical and Applied Genetics*, *101*(7), pp.1114-1121.

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.

Kirby, E.J.M. (1988) Analysis of leaf, stem and ear growth in wheat from terminal spikelet stage to anthesis. Field Crops Res, 18, 127–140.

Kumar, J., Mir, R.R., Kumar, N., Kumar, A., Mohan, A., Prabhu, K.V., Balyan, H.S. and Gupta, P.K., 2010. Marker- assisted selection for pre- harvest sprouting tolerance and leaf rust resistance in bread wheat. *Plant breeding*, 129(6), pp.617-621.

Li, S.P., Chang, X.P., Wang, C.S. and Jing, R.L., 2013. Mapping QTL for heat tolerance at grain filling stage in common wheat. *Scientia Agricultura Sinica*, 46(10), pp.2119-29.

Liu, S. and Anderson, J.A., 2003. Marker assisted evaluation of Fusarium head blight resistant wheat germplasm. *Crop Science*, 43(3), pp.760-766.

Maccaferri, M., Sanguineti, M.C., Corneti, S., Ortega, J.L.A., Salem, M.B., Bort, J., DeAmbrogio, E., del Moral, L.F.G., Demontis, A., El-Ahmed, A. and Maalouf, F., 2008. Quantitative trait loci for grain yield and adaptation of durum wheat (Triticum durum Desf.) across a wide range of water availability. *Genetics*, 178(1), pp.489-511.

Maestri, E., Klueva, N., Perrotta, C., Gulli, M., Nguyen, H.T. and Marmiroli, N., 2002. Molecular genetics of heat tolerance and heat shock proteins in cereals. *Plant molecular biology*, *48*(5-6), pp.667-681.

Mariamma, M., Muthukumar, B., Veluthambi, K., and Gnanam, A. (1997) Effects of high temperature stress on the expression of low molecular weight heat shock proteins in rice leaves. J. Plant Physiol., 151, 763–765.

Mason, R.E., Mondal, S., Beecher, F.W., Pacheco, A., Jampala, B., Ibrahim, A.M. and Hays, D.B., 2010. QTL associated with heat susceptibility index in wheat (Triticum aestivum L.) under short-term reproductive stage heat stress. *Euphytica*, 174(3), pp.423-436.

Mohammadi, M.O.H.T.A.S.H.A.M., Karimizadeh, R.A. and Naghavi, M.R., 2009. Selection of bread wheat genotypes against heat and drought tolerance based on chlorophyll content and stem reserves. *J. Agric. Soc. Sci*, *5*(5), pp.119-122.

Mohammadi, V., Zali, A.A. and Bihamta, M.R., 2008. Mapping QTLs for heat tolerance in wheat.

Mondal, S., Mason, R.E., Huggins, T. and Hays, D.B., 2015. QTL on wheat (Triticum aestivum L.) chromosomes 1B, 3D and 5A are associated with constitutive production of leaf cuticular wax and may contribute to lower leaf temperatures under heat stress. *Euphytica*, 201(1), pp.123-130.

Monjardino, P., Smith, A.G., and Jones, R.J. (2005) Heat stress effects onprotein accumulation of maize endosperm. Crop Sci., 45, 1203–1210.

Owen, P.C. (1971) Responses of a semi-dwarf wheat to temperatures representing a tropical dry season. II. Extreme temperatures. Exp. Agric., 7, 43–47.

Paliwal, R., Röder, M.S., Kumar, U., Srivastava, J.P. and Joshi, A.K., 2012. QTL mapping of terminal heat tolerance in hexaploid wheat (T. aestivum L.). *Theoretical and Applied Genetics*, *125(3)*, pp.561-575.

Porter, J.R., 2005. Rising temperatures are likely to reduce crop yields. *Nature*, *436*(7048), pp.174-174.

Rahman, M.S., Wilson, J.H., and Aitken, V. (1977) Determination of spikelet number in wheat. II. Effect of varying light level on ear development. Aust. J. Agric. Res., 26, 575–581.

Reynolds et al.,, M., Foulkes, M.J., Slafer, G.A., Berry, P., Parry, M.A., Snape, J.W. and Angus, W.J., 2009. Raising yield potential in wheat. *Journal of experimental botany*, *60*(7), pp.1899-1918.

Richard I and JS Beckman (1995) How neutral are synonymous codon mutations? Nat Genet 10: 259

Roff, D.A. (1997) Evolutionary Quantitative Genetics, Chapman & Hall, New York, NY

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.

Sahu, G.K., Kar, M. and Sabat, S.C., 2002. Electron transport activities of isolated thylakoids from wheat plants grown in salicylic acid. *Plant Biology*, *4*(03), pp.321-328.

Saini, H.S. and Aspinal, D. (1982) Abnormal sporogenesis in wheat (Triticum aestivum L.) induced by short periods of high temperature. Ann. Bot., 49, 835–846.

Salem, K.F.M., El-Zanaty, A.M. and Esmail, R.M., 2008. Assessing wheat (Triticum aestivum L.) genetic diversity using morphological characters and microsatellite markers. *World Journal of Agricultural Sciences*, *4*(5), pp.538-544.

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

Shah, M.M., Gill, K.S., Baenziger, P.S. *et al.*, (1999) Molecular mapping of loci for agronomic traits on chromosome 3A of bread wheat. Crop Sci., 39, 1728–1732.

Sharma, P., Sareen, S. and Saini, M., 2017. Assessing genetic variation for heat stress tolerance in Indian bread wheat genotypes using morpho-physiological traits and molecular markers. *Plant Genetic Resources*, *15*(6), pp.539-547.

Shinozaki, K. and Yamaguchi-Shinozaki, K., 1999. *Molecular responses to cold, drought, heat and salt stress in higher plants* (Vol. 1). Austin, TX: RG Landes Company.

Shirdelmoghanloo, H., Lohraseb, I., Rabie, H.S., Brien, C., Parent, B. and Collins, N.C., 2016. Heat susceptibility of grain filling in wheat (Triticum aestivum L.)

linked with rapid chlorophyll loss during a 3-day heat treatment. *Acta physiologiae plantarum*, *38*(8), p.208.

Smertenko, A., Draber, P., Viklicky, V., and Opatrny, Z. (1997) Heat stress affects the organization of microtubules and cell division in Nicotiana tabacum cells. Plant Cell Environ., 20, 1534–1542.

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 VD, Baum BR, Johnson DA. Efficient validation of single nucleotide polymorphisms in plants by allele-specific PCR, with an example from barley. Plant Mol Biol Rep 2003;21:281–8.

Stone, P.J. and Nicolas, M.E., 1995. Effect of timing of heat stress during grain filling on two wheat varieties differing in heat tolerance. I. Grain growth. *Functional Plant Biology*, *22*(6), pp.927-934.

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.

Talukder, S.K., Babar, M.A., Vijayalakshmi, K., Poland, J., Prasad, P.V.V., Bowden, R. and Fritz, A., 2014. Mapping QTL for the traits associated with heat tolerance in wheat (Triticum aestivum L.). *BMC genetics*, 15(1), p.97.

Tashiro, T. and Wardlaw, I.F., 1990. The response to high temperature shock and humidity changes prior to and during the early stages of grain development in wheat. *Functional Plant Biology*, *17*(5), pp.551-561.

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

Tiwari, C., Wallwork, H., Kumar, U., Dhari, R., Arun, B., Mishra, V.K., Reynolds et al.,, M.P. and Joshi, A.K., 2013. Molecular mapping of high temperature tolerance in bread wheat adapted to the Eastern Gangetic Plain region of India. *Field crops research*, 154, pp.201-210.

Tóth, G., Gáspári, Z. and Jurka, J., 2000. Microsatellites in different eukaryotic genomes: survey and analysis. *Genome research*, *10*(7), pp.967-981.

Vijayalakshmi, K., Fritz, A.K., Paulsen, G.M., Bai, G., Pandravada, S. and Gill, B.S., 2010. Modeling and mapping QTL for senescence-related traits in winter wheat under high temperature. *Molecular Breeding*, 26(2), pp.163-175.

Vollenweider, P. and Gunthardt- Goerg, M.S. (2005) Diagnosis of abiotic and biotic stress factors using the visible symptoms in foliage. Environ. Pollut., 137, 455–465.

Vos, P., Hogers, R., Bleeker, M. *et al.*, (1995) AFLP: a new technique for DNA fingerprinting. Nucleic Acid Research, 23, 4407–4414.

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.

Yang, J., Zhang, J., Wang, Z., Zhu, Q. and Wang, W., 2001. Hormonal changes in the grains of rice subjected to water stress during grain filling. *Plant Physiology*, 127(1), pp.315-323.

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