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Original Article

Assessment of some genetic attributes in wheat (*Triticum aestivum* L.) using gene-specific molecular markers

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ABSTRACT

Twenty-four wheat genotypes were characterized for the presence of three stress related genetic attributes using gene-specific molecular markers. Polymerase chain reaction (PCR) products of approximately 110 bp of 1RS rye chromosome fragment from 16 genotypes were obtained using specific primer pairs indicating the presence of translocation in these lines. The same genotypes were screened for the presence of dwarfing genes where 19 genotypes showed the presence of either the *Rht-B1b* or *Rht-D1b* allele having a semi-dwarf phenotype. Two of the genotypes (Kheri and Sufi) had wild type alleles in both the loci and two other genotypes showed the presence of double dwarf alleles (*Rht-B1b* + *Rht-D1b*). A 16.9 kDa HSP gene was characterized by validating a single-nucleotide polymorphism (SNP) linked with thermo tolerance in wheat. Thirteen of the 24 genotypes, which failed to amplify the specific PCR product due to the presence of an SNP, are expected to show tolerance for heat stress. Among the genotypes, Sonora-64, Balaka, Barkat, Aghrani and BARI Gom-24 (Prodip) tested positive for all the three markers evaluated (rye translocation, dwarfing genes and heat tolerance). These genotypes could be used to improve various stress tolerance attributes in wheat for future breeding programs.

Introduction

Wheat (*Triticum aestivum* L.) belongs to the grass family Gramineae (Poaceae) and is a major cereal crop grown in the world (Food and Agriculture Organization, 2015). In Bangladesh, wheat is grown during the dry winter season and like in other South Asian countries, the crop grown here faces both biotic and abiotic stresses (Chatrath et al., 2007) and hence there is a need for developing high-yielding, stress-tolerant varieties. Although it is easier to characterize stress-related agronomic traits in crops on the basis of field performance, the use of functional or gene-specific polymorphic markers derived from within the genes or linked to a particular character is more efficient and can directly identify the desired traits (Andersen and Lübberstedt, 2003; Gupta and Rustgi, 2004; Poczai et al., 2013).

Translocations from the rye (*Secale cereale* L.) genome, especially those involving the short arm of the rye chromosome 1RS, have been extensively used in wheat breeding, because they confer resistance to various pests and diseases and are reported also to be involved in improving yield potential and water-use efficiency (Singh et al., 1998). *Triticale*, an amphidiploid derived from wheat and rye, has long been used as a bridge parent for facilitating rye gene introgressions into wheat (Sebesta et al., 1995; Sethi, 1989). The relative genomic advantages of these translocations or their unintended pleiotropic detrimental effects depend on the type of wheat and its genetic background, and the origin and position of the rye chromosome fragment in the wheat genome, as well as environmental conditions (Kumlay et al., 2003). Kim et al. (2004) studied the effects of translocations in various rye sources on agronomic performance of various substitution, translocation and translocation lines in 'Pavon-76' grown in humid conditions in the south-eastern part of North America, where the 1RS translocation line was found to be most favorable for agronomic performance. Rabinovich (1998) analyzed 330 wheat genotypes on the basis of geographic origin and genetic background having the 1BL/1RS wheat-rye translocation, 1B(R) substitution and 1AL/1RS translocation. The study showed how translocation sources of different genetic and geographic origins have been used in breeding programs all over the world to

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improve productivity, adaptability and disease and insect resistance in wheat.

The massive increase in wheat and rice yields brought about during the 'Green Revolution' was made possible by the introduction of dwarfing traits into the plants (Khush, 2001). Dwarf plant types have shorter and stiffer straws that can resist lodging and due to less vegetative growth, mobilize more assimilates into the grain resulting in higher yields (Hedden, 2003). Dwarfing genes are present in majority of the modern wheat varieties grown worldwide (Fick and Qualset, 1973). Two homologous semi-dwarfing genes—*Rht-B1b* (formerly *Rht1*) and *Rht-D1b* (formerly *Rht2*), isolated from wheat (Peng et al., 1999) and widely present in commercial cultivars—have been shown to reduce plant height, increase harvest index, improve lodging resistance and consequently increase grain yield (Evans, 1998; Worland et al., 2001). Further analyses of these reduced height (*Rht*) genes, derived from the cultivar 'Norin 10', have shown that they interfere with the action or production of gibberellins (GA) (Hedden, 2003) and hence are also classified as GA-insensitive genes. These GA-insensitive dwarfing genes are probably present in around 90% of the semi-dwarf wheat crops in the world and were responsible for the worldwide green revolution in wheat cultivation (Borlaug, 1968; Gale and Youssefian, 1985; Slafer et al., 1994; Calderini et al., 1995; Worland et al., 1998). Historically, the dwarfing genes *Rht-B1* and *Rht-D1* were first transferred to US cultivars and then to Centro Internacional de Mejoramiento de Maíz y Trigo (CIMMYT, Mexico) lines and varieties which were later sent to other countries for adaptation (Hedden, 2003). However, a different dwarfing gene (*Rht8*, from another Japanese cultivar 'Akakomugi') was found to be widespread among wheat varieties from southern Europe but absent in CIMMYT varieties (Worland et al., 1998). Although several other dwarfing genes have been identified (Gale and Youssefian, 1985), they have not been used extensively in wheat breeding.

Two polymerase chain reaction (PCR)-based, gene-specific perfect markers have been developed by Ellis et al. (2002) from 19 wheat varieties of known *Rht* genotype that included *Rht-B1b* and *Rht-D1b* dwarfs, double-mutant varieties and *Rht-B1a* and *Rht-D1a* tall alleles. Mapping analysis by these researchers placed them on the homologous regions of chromosomes 4B and 4D, respectively, with both markers being strongly associated with reduction in height, and together accounting for 67% of the phenotypic variance in this trait.

Butler et al. (2005) studied the effects of *Rht-B1b* and *Rht-D1b* dwarfing alleles in a recombinant inbred line (RIL) of a spring wheat population under a range of soil moisture conditions and found the best performing lines to be either shorter lines in the tall classes or taller lines in the semi-dwarf classes. Under stressed conditions, the best choice seemed to be related more with the right plant height than just the combination of alleles.

Post-anthesis or terminal heat stress is a limiting factor for wheat production in many parts of the world (Paulsen, 1994). Studies on heat-stress response have found that cytoplasmic effects and nuclear-cytoplasmic interactions were involved in heat tolerance (Talukdar et al., 2015). Wang et al. (2003) stated that the molecular control mechanisms for abiotic stress tolerance were based on the activation and regulation of specific stress related genes and that the stress-response mechanisms and their biological function, regulatory control and metabolic pathway can be examined through the study of heat-shock proteins (HSPs). HSPs function as molecular chaperons which are responsible for protein folding, assembly, translocation and degradation in many cellular processes, for stabilizing proteins and membranes and for assisting in protein refolding under stress conditions that include high temperatures (Wang et al., 2003). Different types of HSPs are synthesized in different tissues in response to the duration and kinds of stress conditions (Zivy, 1987). Expression patterns in several heat-shock protein genes have been linked previously with stress,

Table 1
Names and origins of wheat genotypes studied.

Serial number	Genotype	Origin	Serial number	Genotype	Origin
1	Kheri	Bangladesh	13	BARI Gom-19 (Sourav)	Bangladesh
2	Kalyansona	India	14	BARI Gom-20 (Gaurav)	Bangladesh
3	Sonora-64	CIMMYT, Mexico	15	BARI Gom-21 (Shatabdi)	Bangladesh
4	Sonalika	India	16	BARI Gom-22 (Sufi)	Bangladesh
5	Pavon-76	CIMMYT, Mexico	17	BARI Gom-23 (Bijoy)	Bangladesh
6	Balaka	Bangladesh	18	BARI Gom-24 (Prodip)	Bangladesh
7	Ananda	Bangladesh	19	BARI Gom-25	Bangladesh
8	Kanchan	Bangladesh	20	BARI Gom-26	Bangladesh
9	Akbar	Bangladesh	21	BARI Gom-27	Bangladesh
10	Barkat	Bangladesh	22	BARI Gom-28	Bangladesh
11	Aghrani	Bangladesh	23	Westonia 5907	CSIRO, Australia
12	Protiva	Bangladesh	24	Westonia 5924	CSIRO, Australia

BARI = Bangladesh Agricultural Research Institute; CIMMYT = International Maize and Wheat Improvement Center (Mexico); CSIRO = Commonwealth Scientific and Industrial Research Organisation. Note: Bangladeshi origin varieties were developed from germplasm obtained from international sources.

Table 2
List of polymerase chain reaction primers used in the study.

Trait	Locus	Marker	Primer sequence (5′–3′)	Expected fragment size	Reference
Rye translocation	5s-Rrna-R1	RIS	F:TAATTTCTGCTTGCTCCATGC R:ACTGGGGTGCACTGGATTAG	110	Koebner, 1995
Reduction in plant height	*Rht-B1a*	BF-WR1	F:GGTAGGGAGGCGAGAGGCGAG R: CATCCCCATGGCCATCTCGAGCTG	237	Ellis et al., 2002
	Rht-B1b	BF-MR1	F:CCAGATACACAACTGCTGGC R: TGATCTTGAGGTTCTCGTCG	237	Ellis et al., 2002
	Rht-D1a	DF2-WR2	F:GGCAAGCAAAAGCTTCGCG R: GGCCATCTCGAGCTGCAC	264	Ellis et al., 2002
	Rht-D1b	DF-MR2	F:CGCGCAATTATTGGCCAGAGATAG R: CCCCATGGCCATCTCGAGCTGCTA	254	Ellis et al., 2002
Heat shock protein	*HSP 16.9*	AF-R1	AF: CAGCAATCAACACCACGATG R1: TGCCACTTGTCGTTCTTGTC	307	Garg et al., 2012

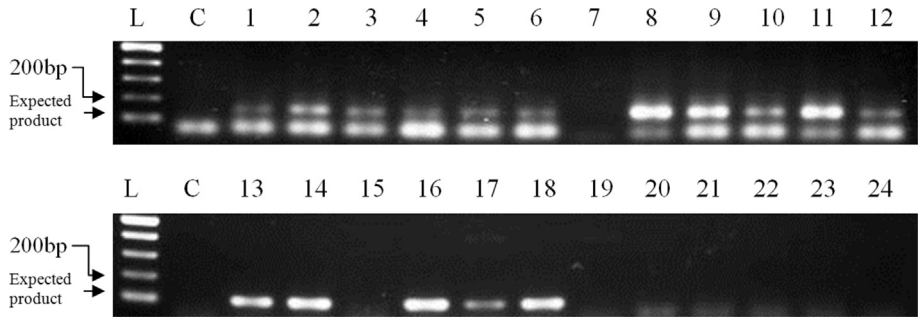

Fig. 1. Amplification profiles of 24 wheat genotypes with rye-specific primers (L = DNA ladder; C = negative (water) control; 1–24 = genotypes under study, as named in Table 1).

defense responses, lifespan and development in a number of organisms (Hoffmann and Willi, 2008).

A single mutation in the gene HSP16.9 was found to be associated with terminal heat stress in wheat. This single-nucleotide polymorphism (SNP) marker analysis explained 29.89% and 24.14% phenotypic variation for grain weight per spike and per thousand grains, respectively (Garg et al., 2012), and thus can be used as a potential marker for screening wheat varieties for heat tolerance.

Some of the molecular markers that could be efficiently used for breeding wheat varieties suitable for growing under abiotic stress conditions are associated with rye translocations, dwarfing genes and HSPs (Koebner, 1995; Ellis et al., 2002; Garg et al., 2012). Development of such varieties can help to reduce stress-related yield loss and increase wheat production; however, no such study for using gene-specific markers in Bangladesh is known. Hence, the aim of the present study was to characterize 24 wheat genotypes, including

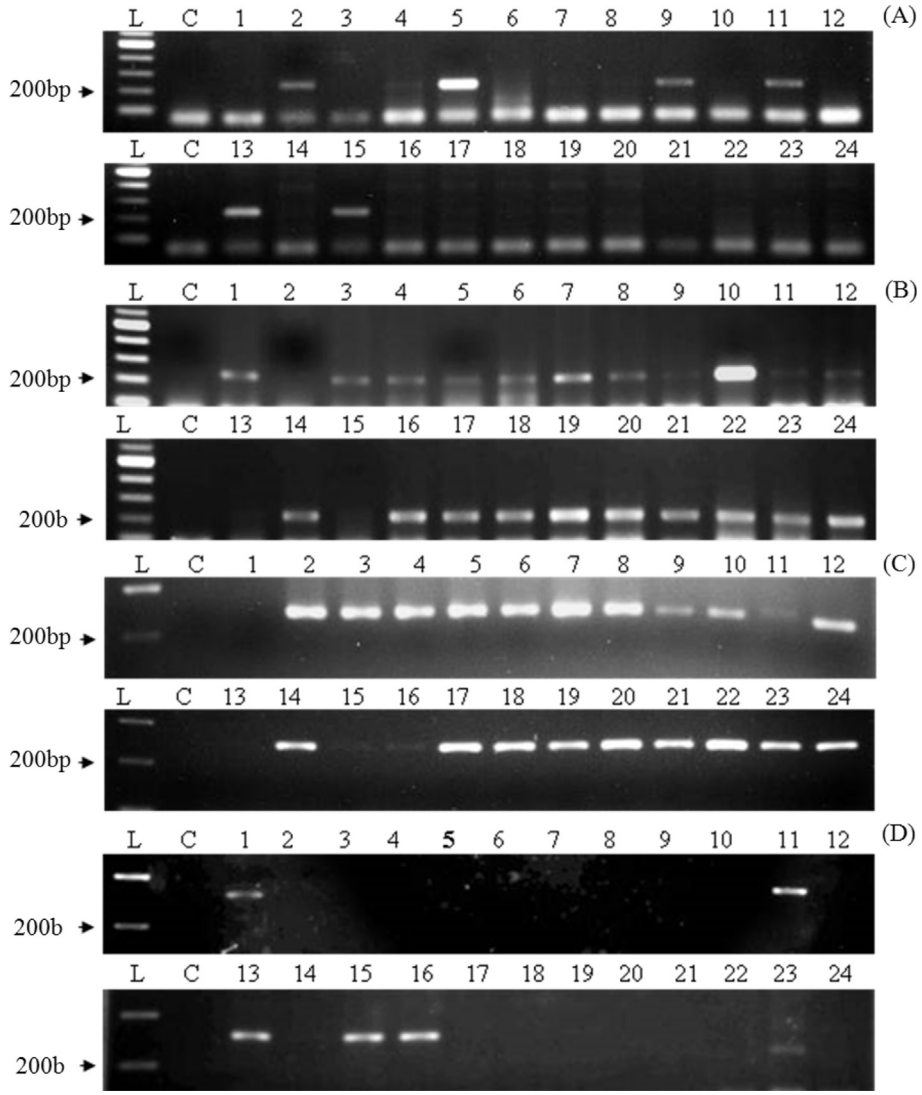

Fig. 2. Amplification profiles for four different dwarfing allele types present in 24 wheat genotypes: (A) *Rht-B1b* (dwarf); (B) *Rht-B1a* (wild); (C) *Rht-D1b* (dwarf); (D) *Rht-D1a* (wild) (L = DNA ladder; C = negative (water) control; 1–24 = genotypes under study, as named in Table 1).

Bangladesh Agricultural Research Institute (BARI) released varieties, using gene specific molecular markers and PCR-based technology.

Materials and methods

Twenty-four (24) wheat genotypes (Table 1) were grown in plastic pots in a greenhouse and approximately 100 mg leaf tissue from a single two-week old seedling from each genotype was used for DNA extraction and further molecular studies. Genomic DNA was extracted using a Plant Genomic DNA Mini Kit (Geneaid; Taiwan), following the manufacturer's instructions and stored at −25 °C until further use. The DNA concentration was measured using a micro spectrophotometer (Nanodrop; Waltham, MA, USA) and all the samples were adjusted to 50 ng/μL prior to PCR analyses.

PCR reactions were prepared in 20 μL total volume with 1X Hotstar Buffer, 1X Hotstar Q solution, 100 ng (2 μL) of template DNA, 4 nmol of dNTPs, 10 pmol each of the forward and reverse primers and 1 unit of Hotstar *Taq* polymerase (Qiagen; Hilden, Germany). Primers and cycling conditions for the PCR (PTC-200, Bio-Rad; Hercules, CA, USA) were selected according to the published protocols (Koebner, 1995; Ellis et al., 2002; Garg et al., 2012, Table 2). The PCR products were separated using electrophoresis (Scie-Plas; Cambridge, UK) with 1.5% agarose gel in TAE buffer at 100 V for 1 h and visualized over ultraviolet light and photographed using a gel documentation system (Alpha Innotech; San Leandro, CA, USA). Each of the 24 genotypes was also grown in the field for observing their height. Average plant height for each genotype was estimated from ten randomly selected plants by measuring from base of plant to the tip of the tallest spike excluding the awns.

Results and discussion

Characterization of rye translocations

PCR analysis of the selected 24 wheat genotypes was carried out using gene specific molecular markers for identifying the presence of rye chromatin translocation in their genomes (Driscoll and Sears, 1971). Specific primer pairs for the 1RS rye chromosome fragment amplified PCR products of approximately 110 bp from 16 out of the 24 wheat genotypes studied (Fig. 1), confirming the presence of rye translocations in them and indicating their greater tolerance to adverse growing conditions (Singh et al., 1998). Eight genotypes which did not produce the band specific for the rye chromatin included some of the best varieties like Shatabdi (serial number 15) and BARI Gom-26 (serial number 20). The absence of rye chromosomes in these indicated that under favorable growing conditions, varieties can perform well without having rye translocations. However, under stress conditions, varieties with the rye translocation might show better adaptation.

Presence of dwarfing genes

DNA samples from wheat genotypes under the present study with unknown *Rht* alleles were analyzed using PCR with *Rht* gene specific molecular markers. Four sets of primers were used for the detection of dwarfing genes having either the *Rht-B1b* or *Rht-D1b* allele while the presence of *Rht-B1a* or *Rht-D1a* indicated the wild type alleles (Fig. 2, Table 3). Out of the 24 genotypes studied, 19 genotypes with either the *Rht-B1b* or *Rht-D1b* allele showed the semi-dwarf phenotype having heights between 78.9 ± 5.5 cm (Westonia 5924) and 94.9 ± 3.9 cm (Kanchan) as shown in Fig. 3. Two of the genotypes—1 (Kheri) and 16 (Sufi)—had wild type alleles in both the loci and were expected to produce tall phenotypes; however, only 'Kheri' showed a tall phenotype and 'Sufi' was a semi-dwarf variety which was probably influenced by some other genetic factors. Three genotypes—2 (Kalyansona), 5 (Pavon-76) and 9 (Akbar)—showed the presence of double dwarf alleles (*Rht-B1b* + *Rht-D1b*) and were expected to show dwarf phenotypes but in fact they were semi-dwarf varieties probably developed by positive selection during breeding.

Butler et al. (2005) evaluated the agronomic performance of the *Rht-B1* and *Rht-D1* genes and reported that the highest grain yield was obtained in an irrigated location with the semi-dwarf combination *Rht-B1b* + *Rht-D1a* while lines carrying both dwarfing alleles produced lower grain yields in every environment. Three of the semi-dwarf genotypes in the present study—11 (Aghrani), 13 (Sourov) and 15

Table 3
Combination of dwarfing (*Rht*) alleles present in the wheat genotypes studied.

Serial number. Genotype	*Rht B1b* (Dwarf)	*Rht B1a* (Wild type)	*Rht D1b* (Dwarf)	*Rht D1a* (Wild type)	Expected phenotype	Actual phenotype
1. Kheri	-[a]	+	−	+	T	T
2. Kalyansona	+	−	+	−	DD	SD
3. Sonora-64	−	+	+	−	SD	SD
4. Sonalika		+	+	−	SD	SD
5. Pavon-76	+	−	+	−	DD	SD
6. Balaka	−	+	+	−	SD	SD
7. Ananda	−	+	+	−	SD	SD
8. Kanchan	−	+	+	−	SD	SD
9. Akbar	+	−	+	−	DD	SD
10. Barkat	−	+	+	−	SD	SD
11. Aghrani	+	−	−	+	SD	SD
12. Protiva	−	+	+	−	SD	SD
13. BARI Gom-19 (Sourav)	+	−	−	+	SD	SD
14. BARI Gom-20 (Gaurav)	−	+	+	−	SD	SD
15. BARI Gom-21 (Shatabdi)	+	−	−	+	SD	SD
16. BARI Gom-22 (Sufi)	−	+	−	+	T	SD
17. BARI Gom-23 (Bijoy)	−	+	+	−	SD	SD
18. BARI Gom-24 (Prodip)	−	+	+	−	SD	SD
19. BARI Gom-25	−	+	+	−	SD	SD
20. BARI Gom-26	−	+	+	−	SD	SD
21. BARI Gom-27	−	+	+	−	SD	SD
22. BARI Gom-28	−	+	+	−	SD	SD
23. Westonia 5907	−	+	+	−	SD	SD
24. Westonia 5924	−	+	+	−	SD	SD

T = Tall; SD = Semi Dwarf; DD = Double Dwarf.
[a] Absence (−) or presence (+) of polymerase chain reaction band.

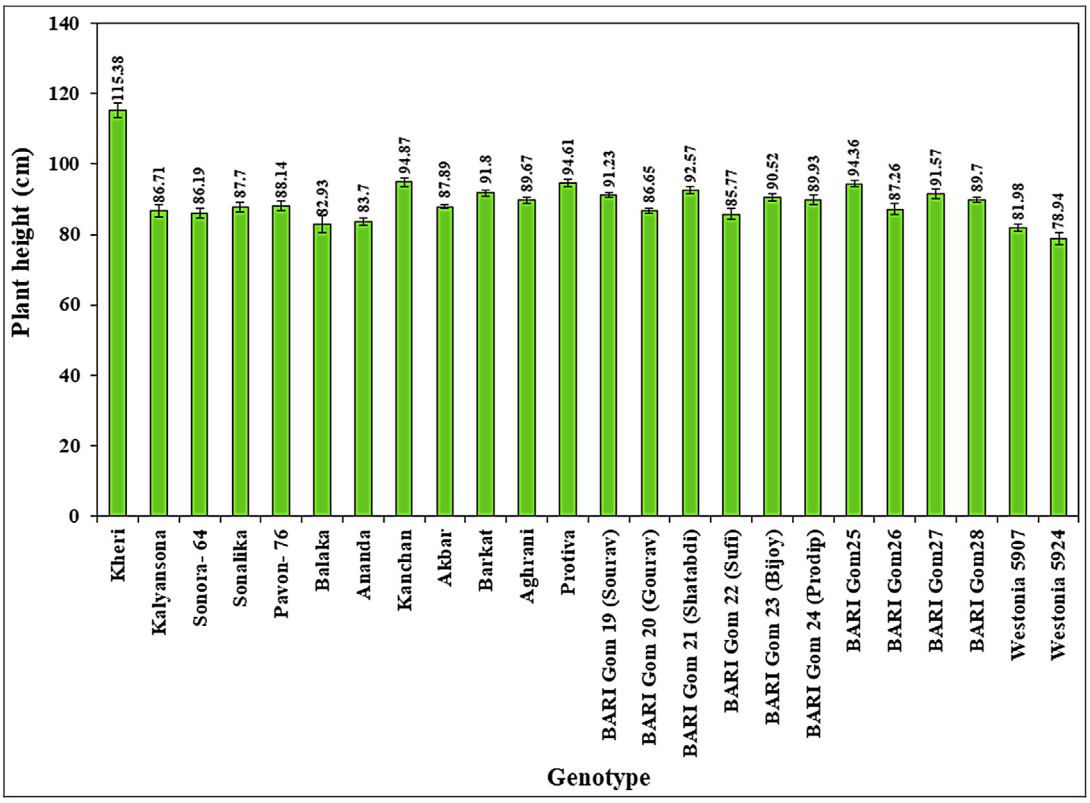

Fig. 3. Mean height distribution of 24 wheat genotypes in the study, where error bars show ±SE.

(Shatabdi)—showed similar dwarfing allele combinations (Table 3) and are expected to give better yield under irrigated conditions. Sixteen other semi-dwarf genotypes showed the presence of the.

Combinations *Rht-B1a* +*Rht-D1b* or *Rht-B1b* + *Rht-D1a* (Table 3) and some of those genotypes (for example, Prodip and Shatabdi) are considered as top varieties in Bangladesh (Rashid and Hossain, 2016). According to Butler et al. (2005), the best performance was observed in shorter lines within the tall class, without any dwarfing allele (like Sufi in the present study), or taller lines within the semi dwarf class carrying the *Rht-B1b* + *Rht-D1a* allele combination as mentioned above.

HSP 16.9 SNP marker

Messenger RNAs encoding HSP16.9 were detected in response to heat-stress in wheat genotypes differing in geographic background (Nguyen et al., 1994). In the present study, allele specific primers based on an SNP present in the HSP16.9 gene (Garg et al., 2012) were used to screen 24 wheat genotypes for their tolerance to heat stress. Thirteen of the 24 genotypes, did not amplify any PCR product, indicating the presence of that specific SNP (Fig. 4). These genotypes are expected to be tolerant to heat stress (Table 4) as the presence of this specific HSP-derived SNP marker was found to be associated with post anthesis heat stress in wheat (Garg et al., 2012). These genotypes along with the specific marker can be used by breeders to improve high temperature tolerance in future wheat breeding programs.

In Bangladesh, large wheat growing areas are vulnerable to various biotic stresses, like diseases or insects and to abiotic stresses, such as heat, drought or salinity (Hossain and Teixeira da Silva, 2013). The breeding of varieties with increased tolerance to these stresses is a pre-requisite to ensure a sustainable yield and

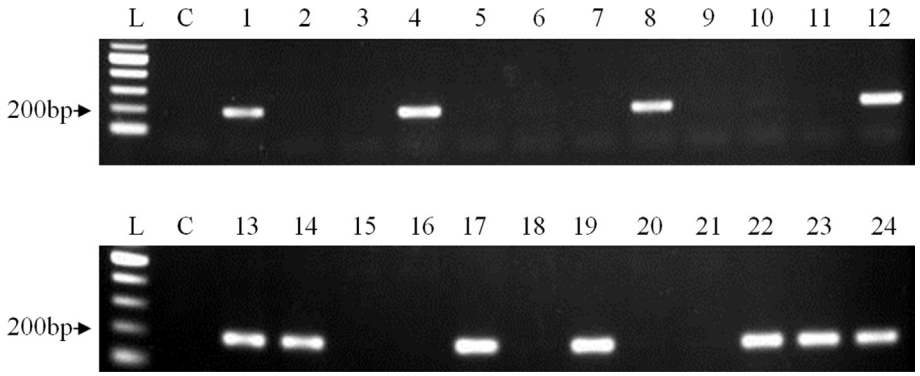

Fig. 4. Amplification profile of 24 wheat genotypes based on a single-nucleotide polymorphism present in the HSP16.9. (L = DNA ladder; C = negative (water) control; 1–24 = genotypes under study, as named in Table 1).

Table 4
Heat tolerance of 24 wheat genotypes assessed through HSP16.9 single-nucleotide polymorphism validation.

Serial number. Genotype	PCR amplification	Expected heat tolerance	Serial number. Genotype	PCR amplification	Expected heat tolerance
Kheri	+	S	13. BARI Gom-19 (Sourav)	+	S
Kalyansona	−	T	14. BARI Gom-20 (Gaurav)	+	S
Sonora-64	−	T	15. BARI Gom-21(Shatabdi)	−	T
Sonalika	+	S	16. BARI Gom-22 (Sufi)	−	T
Pavon-76	−	T	17. BARI Gom-23 (Bijoy)	+	S
Balaka	−	T	18. BARI Gom-24 (Prodip)	−	T
Ananda	−	T	19. BARI Gom-25	+	S
Kanchan	+	S	20. BARI Gom-26	−	T
Akbar	−	T	21. BARI Gom-27	−	T
Barkat	−	T	22. BARI Gom-28	+	S
Aghrani	−	T	23. Westonia 5907	+	S
Protiva	+	S	24. Westonia 5924	+	S

PCR = polymerase chain reaction, S = heat susceptible, T = heat tolerant.
* absence (−) or presence (+) of polymerase chain reaction band.

the knowledge gained on stress tolerance attributes in wheat would lead to major improvements in its production. The aim of the present experiments was to investigate some of the factors related to abiotic stress tolerance in wheat genotypes available in Bangladesh. Twenty-four wheat genotypes were characterized for the presence of rye translocations, dwarfing genes and a heat-shock protein using gene-specific molecular markers. On the basis of these PCR-based markers, it may be concluded that Sonora-64, Balaka, Barkat, Aghrani and BARI Gom-24 (Prodip) are good candidates for stress tolerance and could be used for breeding stress-tolerant wheat genotypes in Bangladesh. However, further studies are necessary to validate these genotypic characters with phenotypes observed in the field.

Conflict of interest

None declared.

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