Cytoplasmic effect of wheat for high temperature tolerance

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Introduction

High temperature is becoming a burning problem for crop production throughout the world. Wheat production is always affected by high temperature through reduction of yield and quality (Wardlaw *et al*., 2002). In a review study done by Budar and Roux (2011), it was found that cytoplasmic genome and the interaction between cytoplasmic and nuclear genome contribute significantly to the adaptation of plants in different environments. Considering this, we have developed NIL population using ten alloplasmic lines and four euplasmic varieties to study traits associated with heat tolerance.

Objective

The objective in this study was to identify the effect of cytoplasm, and cytoplasmic-nuclear genome interaction on traits associated with heat tolerance

Population Development

Four euplasmic wheat varieties (Karl 92, Ventnor, U1275 and Jagger) were backcrossed to a series of ten different alloplasmic lines (Allan,1997). Reciprocal crossing was done using the same parent at BC_5F_1 and/or BC_6F_1 to develop Near Isogenic Line (NIL) for cytoplasm. Twenty four chloroplast markers were run to see polymorphism between the NILs.

Materials and Methods

- Two different experiments were done for phenotyping parental lines and the NIL population.
- All the plants were grown in green house maintaining 16 hours of photoperiod and 20/15°C day/night temperature.
- Plants were tagged during anthesis and tagged plants were taken into growth chambers maintaining 16 hours of light and 35/30°C day/night temperature at ten days after anthesis.
- Parental lines were phenotyped using Randomized Complete Block Design (RCBD).
- Nil populations were phenotyped following split plot design, where varieties were considered as main plot, cytoplasm as subplot and NIL as sub-sub plot.
- Data were collected on Grain filling duration (GFD), Kernels per spike, Chlorophyll content, Chlorophyll fluorescence (FV/Fm) and 1000 seed weight.
- Chlorophyll content and chlorophyll fluorescence data were taken six times in every alternate day starting from thirteenth days of anthesis.
- Data were analyzed using SAS (proc mixed).
- Regression analysis was done for chlorophyll content and chlorophyll fluorescence (FV/FM) data.

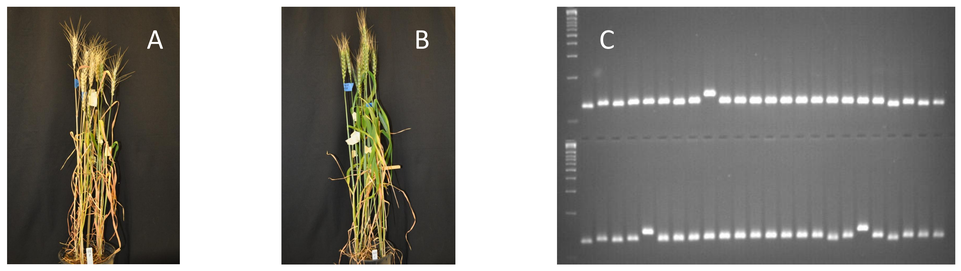

Fig 1: Showing plants at 10 days after heat stress, and polymorphism of WC_2 chloroplast SSR markers in cytoplasmic NIL population. A) plants having U1275 nuclear genome and cytoplasm, B) Plants having alloplasmic line (PI 590259) cytoplasm and U1275 nuclear genome, C) WC_2 chloroplast SSR markers polymorphism in NIL population.

Results and discussion

- In experiment 1, alloplasmic line 3 (PI 590263) and Ventnor showed lowest slope for chlorophyll content and FV/FM among the parental lines.
- Thousand seed weight, seed number per tagged head and days required for physiological maturity showed no significant difference.
- In the NIL population experiment, chlorophyll content, FV/FM and seed number per tagged head showed significant variation.
- For chlorophyll content and FV/FM, significant interaction was found between nuclear and cytoplasmic genome.
- Slope of chlorophyll content was lower in cytoplasm 1 with U1275, cytoplasm 1,4 and 7 with Jagger, cytoplasm 7 with Karl 92, and cytoplasm 8, 9, 10 with Ventnor.

Results and discussion contd.

- On the other hand, cytoplasm 9 with Jagger and cytoplasm 4 and 6 with Ventnor had higher slope.
- For FV/FM, cytoplasm 1 with U1275, cytoplasm 1 and 8 with Jagger, cytoplasm 7, 9 and 10 with Karl 92 and cytoplasm 8, 9, and 10 with Ventnor had lower slope.
- For seed number per tagged head, cytoplasm 1 and 10 had higher number of seed than Jagger.
- Interaction between alloplasmic cytoplasm and nuclear genomes was clearly shown for chlorophyll content and FV/FM

Table 1: Pedigree and polymorphism of chloroplast markers for alloplasmic and euplasmic lines

Lines	Pedigree of alloplasmic lines	Primer Number			
		U1275	Jagger	K-92	Ventnor
PI 590259 (1)	*Aegilops juvenalis*/6*CHR//9*SK (NDM1)/3/7*SPN	15	14	abs	abs
PI 590261 (2)	*A. cylindrica*/CHR//10*SK (NDM2)/3/7*SPN	15	17	10	abs
PI 590263 (3)	*A. variabilis*/9*CHR//13*SK (NDM3)/3/7*SPN	7	13	17	15
PI 590265 (4)	*A. squarrosa*/19*SK (NDM4)//7*SPN	16	13	abs	14
PI 590267 (5)	*A. uniaristata*/2**Triticum durum*/10*SK (NDM5)/3/7*SPN	14	14	13	15
PI 590269 (6)	*A. ventricosa*/*T. durum*//13*SK (NDM6)/3/7*SPN	0	abs	11	11
PI 590271 (7)	*Haynaldia villosa*/*T. durum* //9*SK (NDM7)/3/7*SPN	0	0	0	0
PI 590273 (8)	*T. macha*/17*SK (NDM8)//7*SPN	0	0	abs	0
PI 590275 (9)	*T. macha*/9*SK (NDM9)//7*SPN	0	0	0	0
PI590277 (10)	*T. turgidum*/9*SK (NDM10)//7*SPN	1	1	1	1

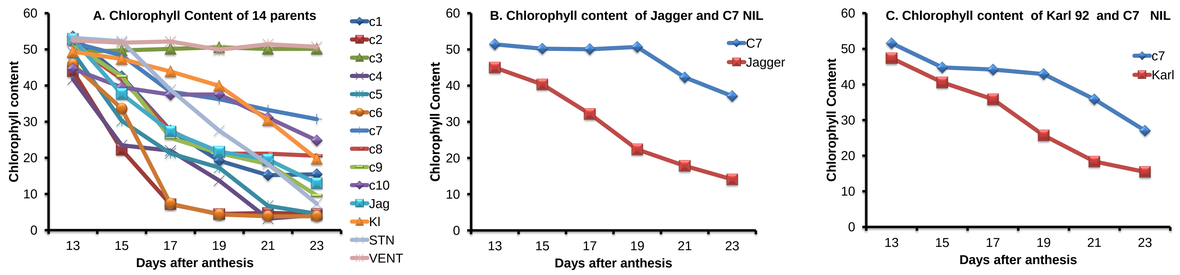

Fig 2: Chlorophyll content comparison under high temperature. A. Comparison among fourteen parental line. B. Comparison between two NILs of Jagger and alloplasmic line 7, C. Comparison between two NILs of Karl 92 and alloplasmic line 7.

Conclusion

Alloplasmic cytoplasm showed response variability with different varietal background. This cytoplasm and nucleus interaction may able to contribute to improve stay green quality. From these experiments, cytoplasm 1, 4,7, 8, 9 and10 may be used in breeding program to improve stay green quality for heat tolerance in wheat.

References

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Acknowledgements

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