# Genetic and physiological studies of heat tolerance in hexaploid wheat (*Triticum aestivum* L.)

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# Abbreviations

| Symbol | Definition |
|---|---|
| ANOVA | Analysis of variance |
| ATR-MIR | Attenuated total reflectance mid infrared |
| AUSC | Area under SPAD curve |
| ChlC10DAA | Chlorophyll content 10 DAA |
| ChlC13-16DAA | Chlorophyll content within the range from 13 to 16 DAA |
| ChlC13DAA | Chlorophyll content 13 DAA |
| ChlC25DAS | Chlorophyll content 25 DAS |
| ChlC27DAA | Chlorophyll content 27 DAA |
| ChlC28DAS | Chlorophyll content 28 DAS |
| ChlC7-10DAA | Chlorophyll content within the range from 7 to 10 DAA |
| ChlR13 | Chlorophyll loss rate from 10 to 13 DAA |
| ChlR27 | Chlorophyll loss rate from 10 to 27 DAA |
| CL | Culm length |
| cM | Centimorgan |
| D | Drysdale |
| DAA | Days after anthesis |
| DAS | Days after sowing |
| DH | Doubled haploid |
| DMSO | Dimethyl sulfoxide |
| DNA | Deoxyribonucleic acid |
| dNTP | Deoxyribonucleotide triphosphate |
| DTA | Days from sowing to anthesis |
| DTM | Days from anthesis to maturity |
| DTM | Days from sowing to 95% senescence of spike |
| FL | Flag leaf length |
| FLSe | 95% flag leaf senescence |
| Fv/Fm | Flourescence variable/flourescence maximum |
| FW | Flag leaf width |
| G | Genotype |
| G × T | Genotype-by-treatment effect |
| GFD | Grain-filling duration |
| GNS | Grain number $spike^{-1}$ |
| GNSp | Grain number $spikelet^{-1}$ |
| $g_s$ | Stomatal conductance |
| GWS | Grain weight $spike^{-1}$ |
| $H^2$ | Broad-sense heritability |
| HI | Harvest index |
| HSI | Heat susceptibility index |
| KASP | Competitive allele-specific PCR |
| LHCII | Light harvesting complex proteins associated with PSII |
| LOD | Logarithm of odds |
| LSD | Least significant difference |
| LWP | Leaf water potential |
| MGR | Maximum grain growth rate |
| MWSC | Mobilized WSC |
| PC | Principal component |
| PCA | Principal component analysis |
| PCR | Polymerase chain reaction |
| PH | Plant height |
| PSA | Proportion of senescent area |
| PSA25DAS | Proportion of senescent area 25 DAS |
| PSA28DAS | Proportion of senescent area 28 DAS |
| PSA39DAS | Proportion of senescent area 39 DAS |
| PSI | Photosystem I |
| PSII | Photosystem II |
| QTL | Quantitative trait loci |

| Symbol | Definition |
|---|---|
| RFLP | Restriction fragment length polymorphism |
| RGR | Relative growth rate |
| RGRAT | Relative growth rate after treatment |
| RGRBT | Relative growth rate before treatment |
| RGRDT | Relative growth rate during treatment |
| $R_{H/C}$ | Heat-treated/control ratio |
| RWC | Relative water content |
| S.E. | Standard error |
| SGR | Sustained grain growth rate |
| SGW | Single grain weight |
| ShW | Shoot dry weight |
| SNP | Single nucleotide polymorphism |
| SpNS | Spikelet number $spike^{-1}$ |
| SSR | Simple sequence repeat |
| SSS | Soluble starch synthase |
| T | Treatment |
| TIP | Time from anthesis to the inflection point |
| TN | Tiller number |
| TotChl | Total chlorophyll content (chlorophyll a + b) measured by destructive method |
| W | Waagan |
| WSC | Water soluble carbohydrate |
| WSCME | WSC mobilization efficiency |
| WUE | Water use efficiency |
| ZGS | Zadoks' growth stage |

**Abstract**

High temperature is one of the major environmental constraints for wheat production globally. It puts significant pressure on the wheat industry around the world, compromising both the quantity and quality of wheat grain produced. The current study focussed on the impact of brief episodes of very high temperatures during vegetative and grain-filling stages of wheat development using a combined approach of plant physiology and quantitative trait loci (QTL) mapping.

At grain-filling stage, wheat plants were exposed to a brief heat stress (3 days, 37/27 ºC) 10 days after anthesis and the plants evaluated for a number of morphological and physiological traits (Chapters 3, 4, and 6). At the vegetative stage (~ 4 weeks after sowing) plants were challenged with a brief heat treatment (2 days, 40/30 ºC), and growth and senescence related characters were monitored using automated imaging facilities and a SPAD chlorophyll meter (Chapter 7).

In total, 37 bread wheat genotypes were evaluated for different heat responses during the grain-filling stage. Genetic variation was observed among wheat genotypes for various heat responses, particularly for single grain weight, chlorophyll retention, rate and duration of grain-filling, and water soluble carbohydrate content and mobilization (Chapters 3 and 4). Overall, the findings suggested that more than one adaptation process contributed to tolerance. Generally, genotypes with more stable grain weight under heat tended to have particular traits under stress, including the ability to maintain chlorophyll content and rate and duration of grain-filling, and stronger water soluble carbohydrate mobilization efficiency (Chapters 3 and 4). Therefore, these traits may provide appropriate selection criteria for improving heat tolerance in wheat.

A genetic linkage map of a Drysdale/Waagan population was constructed using a 9K SNP array (Chapter 5) and used for QTL analysis (Chapter 6) of heat responses (evaluated using heat susceptibility index) at the grain-filling stage. A region on chromosome 3BS strongly affected heat responses of grain weight, stay-green related traits, grain-filling duration, shoot dry weight and harvest index, explaining 10 to 40% of the phenotypic variation, with Waagan contributing the tolerance allele. Most notably, the results indicated a strong genetic link between stay-green and grain weight maintenance under brief episodes of terminal high temperatures but a lack of a significant association between the *Rht-B1* and *Rht-D1* dwarfing loci and heat tolerance.

Using high-throughput automated imaging facilities in The Plant Accelerator, considerable variation among 77 bread wheat genotypes was observed for growth rate and senescence

responses to a brief heat stress at the vegetative stage (Chapter 7). A subset of 32 genotypes was also screened at the grain-filling stage (Chapter 3) which allowed a comparison of heat responses at these two developmental stages. Growth rate and senescence responses at the vegetative stage showed significant associations with grain weight maintenance and senescence responses at the grain-filling stage. These results suggested a physiological/genetic link between heat responses at the different growth stages, with implications for developing more efficient heat tolerance screening methods.

The present work contributes to the understanding of physiological mechanisms of heat tolerance and its genetic basis in hexaploid wheat, and identifies assays with potential to assist heat tolerance studies and in breeding programs.

## Declaration

This work contains no material which has been accepted for the award of any other degree or diploma in any university or other tertiary institution to Hamid Shirdelmoghanloo, and to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text.

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## Dedication

*To my*

*father "**Ali**" and mother "**Maryam**"*