SUMMARY OF DOCTORAL THESIS

Name: Awad Ahmed Elawad Elbashir

Title: Exploitation and utilization of multiple synthetic derivatives population for breeding wheat with heat stress tolerance
（高温ストレス耐性コムギの育種のための多重合成派生集団の開拓と利用）

Wheat (*Triticum aestivum* L.) is the second most important staple food of the world. It has been widely cultivated in very diverse environments in the worldwide and exposed to different biotic and abiotic stresses. The growth and yield of wheat are adversely affecting by environmental stresses such as high temperature, drought, salinity, etc. High temperature is one of the most important of the abiotic stress. Breeding for heat stress tolerance is a big challenge because of the complex and unpredictable nature of heat stress and complex interaction of crops with the environment. Few genes are known which may increase tolerance to heat stress.

Wild relatives of wheat have adapted to various environments. Some of these wid relatives are expected to have heat stress tolerance genes. *Aegilops tauschii* Coss. is a wild relative of wheat and widely distributed. This species is the direct ancestor of bread wheat, the D-genome donor to hexaploid bread wheat and is a rich genetic resource for wheat breeding. Many *Ae. tauschii* genes have been introduced to bread wheat through amphidiploids between *Ae. tauschii* and tetraploid wheat; these amphiploids are named synthetic hexaploid wheat (SHW). SHW retain wild morphology, such as tough glumes, which precludes threshing and thus the measuring of yield-related characteristics. Synthetic derivative lines, which originate from crosses between SHWs and bread wheat cultivars, are a better choice to uncover the variation in *Ae. tauschii* that may be used for breeding. However, most of the synthetic derivative lines originated from crosses between bread wheat cultivars and a limited number of SHWs. To investigate and use comprehensively the intraspecific variation of *Ae. tauschii* for wheat breeding, I produced multiple synthetic derivatives (MSD) population, in which the intraspecific variation of *Ae. tauschii* was compiled in the genetic background of bread wheat cultivar. I here select heat-tolerant plants from MSD population in terms of their agronomic and physiological traits. Also, I examined the genetic variability of heat stress–adaptive traits and to identify new sources of heat tolerance to be used in wheat breeding programs. In addition, I identify QTLs/genes associated with heat stress-adaptive traits.

I conducted two experiments. First, I grew 1000 BC_1F_3 plants from MSD population under heat stress in Sudan. I selected six BC_1F_4 plants showing good performance and I grew these plants with Norin 61 (N61) in the field at Gezira Research Farm, Sudan and growth chambers in Tottori University, Arid Land Research Center, Japan in season 2015/16. In the field, I used optimum and late sowings to exposure to heat. The experiment was arranged using randomized complete block design with three replications. I used six plants, and I named these plants MNH (MSD population of N61

selected as heat stress tolerant) plus N61 as control, I collected data on days to heading, grain filling duration, plant height, peduncle length, kernel number per spike, thousand kernel weight, biomass, grain yield, canopy temperature, normalized difference vegetation index and leaf area. On the other hand, in the growth chamber, I used two conditions control and hot conditions with the same six plants those I used in field plus N61 as control and the two heat tolerant cultivars 'Gelenson' and 'Bacanora'. I collected photosynthetic rate and stomatal conductance.

In the second experiment I studied 400 BC_1F_4 lines randomly selected from MSD population. The experiment was arranged in an augmented randomized complete block design in four environments (Dongola, Hudieba, Wad Medani optimum sowing and Wad Medani late sowing) in Sudan in season 2015/2016. I used N61 as a control to show the effect of the wild genes on the improvement of N61 heat stress adaptability, and the two heat-tolerant Sudanese cultivars 'Goumria' and 'Imam' as checks to evaluate the heat tress adaptability of the MSD lines. I collected data on plants days to heading and maturity, grain filling duration, plant height, peduncle length, kernel number per spike, thousand kernel weight, grain number per m^2, biomass, grain yield, harvest index, canopy temperature, chlorophyll content and normalized difference vegetation index and heat tolerant efficiency (HTE). In addition, I performed genotyping of these 400 MSD lines to conduct a genome-wide association using 15,616 DArT-seq markers for 400 plants for growth habit, days to heading, canopy temperature at heading and tiller numbers per m^2 in three environments in Sudan.

The results of the first experiment showed that the six plants different response to heat stress in comparison with N61, increasing the photosynthetic rate and stomatal conductance (MNH1, MNH2 and MNH5), and increasing biomass and grain yield (MNH2 and MNH5) in the filed and growth chamber. Also, I identified that MNH2 and MNH5 lines acquired heat tolerant. In addition, I noticed that N61 had relatively good adaptability to heat stress.

The results of second experiment showed wide range of genetic variability in most of the traits in all environments. In all traits examined, I found MSD lines with better performance than their parent N61 and the two adapted Sudanese cultivars. In comparison with N61 and two adapted Sudanese cultivars. Some of the MSD lines showed significantly lower canopy temperature and higher peduncle length, kernel number per spike, thousand kernel weight and biomass values. Using the heat tolerance efficiency, I identified 13 highly heat-tolerant lines and several lines with intermediate heat tolerance and good yield potential. I also identified lines with alleles that can be used to increase wheat yield potential. For genome-wide association study, I detected three QTLs for heading date on chromosomes 2A, 2B and 2D and two QTLs for growth habit on chromosomes 2A and 2D.

The results of these studies indicated that the MSD population, including the diversity of *Ae. tauschii*, is a promising resource to uncover useful quantitative traits derived from this wild species. Also, these researches indicated that the approach is very effective and could be the best way to explore and use the variation in heat tolerance in *Ae. tauschii* in a practical, fast, and economical way. The identified QTLs can be used for marker assisted selection in breeding wheat for improved heat tolerance. In this study, I found rich genetic diversity in the MSD population, which is available for wheat breeding for heat stress tolerance. Corsses will be made between the selected lines and a heat stress sensitive line to facilitate identification of the QTLs associated with the tolerance of these lines.