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SUMMARY OF DOCTORAL THESIS

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Title: Molecular genetic and physiological studies for drought tolerant wheat production
(耐乾性コムギ育成のための分子遺伝学および生理学的研究)

Bread wheat (*Triticum aestivum* L.; $2n = 6x = 42$, AABBDD) is genetically hexaploid and true breeding species with its ancestry linked to three wild grass species. Wheat crop has been widely cultivated throughout the world in very diverse environments, this means it is exposed to different biotic and abiotic stresses. One of most important of the abiotic stresses is drought. Under drought condition wheat undergoes severe physiological and biochemical changes which in the end result yield loss. Breeding for drought is big challenge because of the complex and unpredictable nature of drought environments and complex nature and interaction of the crops with the environment. Not many genes are known which may increase tolerance to drought.

The wild relatives of wheat have adapted to various environmentally harsh conditions including drought. Some of these wild relatives are expected to have drought tolerant genes. *Aegilops tauschii* Coss. is wild relative of wheat, it is widely adaptable and a direct ancestor of bread wheat, and, therefore, *Ae. tauschii* appears to be the most desirable species for wheat improvement among the more than 300 wild species in the tribe Triticeae. It is the D-genome donor to hexaploid bread wheat and is the most promising wild species as a genetic resource for wheat breeding.

The first part of this study discusses the population structure and diversity of the *Ae. tauschii* accessions studied using diversity array technology (DArT) markers, and the second part is about the applicability of *Ae. tauschii*'s drought-related traits for breeding by comparison of their morphological and physiological traits with their corresponding synthetic wheat (SW) lines. SWs are hexaploid amphiploid (AABBDD) produced by crossing *Ae. tauschii* (DD) with durum wheat (AABB).

The population structure and diversity of 81 *Ae. tauschii* accessions collected from various regions of its geographical distribution were analyzed by DArT marker array made by the genomic representation of these line and a previously developed DArT wheat array. Out of 7500 markers (5500 wheat and 2000 *Ae. tauschii*), 4449 were polymorphic (3776 wheat and 673 *Ae. tauschii*). Phylogenetic and population structure studies revealed that the accessions could be divided into three groups, A, B and C. All the accessions of ssp. *strangulata* clustered in one clade in Group C. On the other hand, the three varieties of ssp. *tauschii* did not cluster into a particular clade. Accessions classified as var.

anathera were present only in Group A, while those classified as var. *meyeri* appeared in Group C, with only one (KU2109) in Group A. The two *Ae. tauschii* subspecies could also be separately clustered, suggesting that the current taxonomy might be valid. DArT markers are effective to detect very small polymorphisms. The information obtained about *Ae. tauschii* in the current study could be useful for wheat breeding. In addition, the new DArT array from this *Ae. tauschii* population is expected to be an effective tool for hexaploid wheat studies.

Few genes are available to develop drought-tolerant bread wheat cultivars. One way to enhance bread wheat's genetic diversity would be to take advantage of the diversity of wild relatives of wheat, i.e. to introduce useful genes from this wild species into common wheat. In this study, I compared the expression of traits encoded at different ploidy levels and evaluated the applicability of *Ae. tauschii* drought-related traits (photosynthesis, stomatal conductance, intercellular CO_2, transpiration rate, SPAD reading, water potential, water use efficiency and dry weights of roots and shoot) using 33 *Ae. tauschii* of the above mentioned 81 accessions along with their corresponding SW lines under well-watered and drought conditions. I found wide variation in *Ae. tauschii,* and even wider variation in the SW lines.

The SW group showed better tolerance to drought in terms of higher rood dry weight, shoot dry weight and total dry weight and less percent reduction in these values due to drought. The *Ae. tauschii* group had higher average photosynthetic rates than the SW group under both well-watered and dry conditions, but the SW accessions had a smaller reduction in photosynthetic rate (20.4% vs. 21.8%). Based on the Euclidian distance, the *Ae. tauschii* group showed greater variation under WWC than under DC, while in SW it was vice versa. Some SW lines were more drought-tolerant than the standard cultivar Cham 6. *Ae. tauschii* from some regions gave better performing SW lines. The traits of *Ae. tauschii* were not significantly correlated with their corresponding SW lines, indicating that the traits expressed in wild diploid relatives of wheat may not predict the traits that will be expressed in SW lines derived from them. I suggest that, regardless of the adaptability and performance of the *Ae. tauschii* under drought, production of SW could probably result in genotypes with enhanced traits due to gene interactions. Based on the results of the present study, it is recommended that the useful traits of the SW lines observed at the hexaploid level be used not only for improving drought tolerance but also for breeding wheat cultivars capable of improving other quantitative characters.

The molecular information provided by the present DArT analyses will elucidate the genetic basis of the morphological and physiological characters at both ploidy levels. The new *Ae. tauschii* array developed, which represents a large and diverse collection, could be an effective tool for hexaploid wheat studies. The aim of this research project is to compare the physiological and morphological characters with molecular information. The results obtained in this thesis will be used to study the genetic disequilibrium of the *Ae. tauschii* lines and also construct association map for drought related characters for SW.