

(Form No. 13)

SUMMARY OF DOCTORAL THESIS

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Title: *Leymus racemosus*, a wheat wild relative is a potential source for wheat

Improvement for aluminum and heat stress tolerance

(コムギの近縁種、オオハマニンニクはコムギのアルミニウムおよび高温耐性を改良するための潜在的資源である)

The world population is growing exponentially and there is an urgent need to increase and stabilize the world food production. Wheat is the most important food crop worldwide, and thus the food sufficiency could be achieved through development of new stress tolerant and well adapted wheat cultivars with high yield potential. For efficient and successful breeding of outstanding and well adapted cultivars genetic diversity is needed. However, since the available genetic diversity for wheat breeding is very narrow, this study was undertaken to explore the potentiality of genes from *Leymus racemosus*, a wheat wild relative for wheat breeding through physiological and molecular evaluation of wheat - *L. racemosus* introgression lines for aluminum and heat stress tolerance.

Chapter 1 describes the impact of *L. racemosus* chromosomes on wheat tolerance to aluminum (Al) toxicity. The introgression lines and their wheat background Chinese Spring (CS) were evaluated in hydroponics system under various concentration of Al to identify new genetic resources to improve wheat tolerance to Al, and to identify the chromosomes harboring the tolerance genes. Al uptake, oxidative stress, and cell membrane integrity were also investigated. The results indicated that *L. racemosus* chromosomes A and E incorporated in TAC1 and TAC3, respectively, significantly enhanced the Al tolerance of wheat in term of relative root growth. At the highest Al concentration tested (200 μ M), TAC3 had the greatest tolerance. The introgressed chromosomes did not affect Al uptake of the tolerant lines. The improved tolerance conferred by chromosome E was attributing to improved cell membrane integrity.

Chapter 2 describes the impact of *L. racemosus* chromosomes on wheat tolerance and adaptation to heat stress. Wheat - *L. racemosus* chromosome introgression lines and their parent CS were evaluated in a growth chamber at the seedling stage and in the field at the reproductive stage in two heat-stressed environments in Sudan. Optimum and late planting were used to ensure exposure of the plants to heat stress at the reproductive stage. The results revealed the impact of several *Leymus* chromosomes in improving wheat adaptation and tolerance to heat: Three lines possessed enhanced adaptation, whereas two showed high heat tolerance. Two additional lines showed a large number of kernels per spike, while one possessed high yield potential. The findings suggest that these genetic stocks could be used as a bridge to introduce the valuable *Leymus* traits into a superior wheat genetic background, thus helping maximize wheat yield in heat-stressed environments.

Chapter 3 describes the genetic basis of the early heading and maturity observed in three introgression lines under field conditions in Sudan. It was first hypothesized that the vernalization requirement of CS was cancelled in the introgression lines, and this cancellation led to the early flowering. Specific molecular marker analysis revealed that these lines had the dominant *Vrn-A1* allele, whereas CS had the winter recessive *vrn-A1* allele. Unlike the CS winter allele, in the promoter region, the spring *Vrn-A1* allele of all the introgression lines had a large insertion of 220-bp and a small insertion of 131-bp. “In addition, some of the information have been omitted”. Results of molecular marker analysis exclude the possibility of unexpectedly occurred outcrossing and suggested that this insertion is due to genetic events occurred during the maintenance of the introgression lines.

This study indicated clearly the potentiality of utilizing the traits and genes of wheat wild relative *Leymus racemosus* to improve wheat tolerance to aluminum and heat stresses. Moreover, this study revealed the importance of the chromosome addition and substitution lines as potential genetic materials for identification and discovery of new genes, especially when the phenotypic and genotypic evaluation of the wild relative has some limitations.