sequence-based finger printing method (Whole Genome Profiling; Amplicon Express, KeyGene Inc.), physical maps for the short and long arms of chromosome 6B have been successfully established using the 6BS- and 6BL-specific BAC libraries, respectively, which consist of 2,667 and 1,842 BAC contigs. The estimated chromosomal coverage is more than 80% of both arms. Overlap analysis between the neighboring clones within the BAC contigs resulted in a total number of 5,079 and 4,889 MTP (Minimal Tiling Path) BACs on 6BS and 6BL, respectively. For the confirmation and the chromosomal assignment of the BAC contigs onto their corresponding genomic regions, we currently are developing a large number of 6B-specific DNA markers using the public marker resources, available EST databases, and the 6B survey sequence. To date, among 3,743 markers tested for their availability, 2,480 were found to be useful for the PCR screening of BACs, and 451 BAC contigs has been anchored by 627 markers to the specific genomic regions on chromosome 6B presumed on the basis of genetic maps, deletion maps and/or Genome Zipper. In parallel, a high-resolution, radiation hybrid map and a genetic map using recombinant inbred lines are under development for further improvement of physical maps. This work was supported by grants from the Ministry of Agriculture, Forestry and Fisheries of Japan (Genomics Agricultural Innovation; KGS-1001 and KGS-1003) and funding from Nisshin Flour Milling Inc.

Poster 5. The distribution, duplication, pseudogenization, and expression of noncollinear genes of wheat chromosome 3B.

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3BSeq is a large, ANR (Agence Nationale de la Recherche)-funded project developed under the umbrella of the IWGSC. It aims to sequence and characterize the largest wheat chromosome (3B) at the molecular level. The complete chromosome sequence is being produced by combining Roche/454 sequencing of BAC pools with whole chromosome shotgun using Illumina technology. Preliminary studies showed that about 50% of the genes identified in wheat are not collinear with the other grass genomes, raising several questions about their origin, fate, and expression in the wheat genome.

A set of 3,005 collinear genes and 2,432 noncollinear genes was defined using the annotation of chromosome 3B and orthologous genes from *Brachypodium*, rice, and sorghum. While waiting for the establishment of the 3B pseudomolecule, deletion bin information was used to determine the gene density per deletion bin and the relative gene order along the chromosome. Collinear genes show a 2-fold increase in gene density from the centromeric regions to the telomeric regions, whereas noncollinear genes have five-fold increase. In addition, noncollinear genes are more likely to be resulting from gene duplication events, with approximately 10% more of the noncollinear genes having duplicates on 3B in comparison to the collinear genes. The same pattern was found for pseudogenes. RNASeq data, collected from 15 different RNA samples, was used to determine that a higher percentage of collinear genes are expressed in comparison to noncollinear genes.

These results provide evidence that noncollinear genes have a higher probability than collinear genes to be duplicated, revert to pseudogenes, and subsequently become nonfunctional. The primary mechanism for this gene duplication and movement on 3B remains to be determined. We found 50% more CACTA superfamilies in the regions surrounding noncollinear genes than collinear genes, suggesting a major role for transposable elements in noncollinear gene movement. These results will shed some light on the evolutionary forces involved in the shuffling of the gene content on 3B and more generally in the accelerated evolution of the wheat genome. Functional analyses are underway to determine the fate of noncollinear duplicated genes in wheat.