



Research Opinion & Topics

“Core-collection” Project of the National BioResource Project-Wheat, Japan: 2015 Progress report

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Key words: wheat, DNA marker, polymorphism, core-collection

National Bioresources Project-Wheat (NBRP-Wheat) stores nearly 12,000 accessions of wild species, landraces and historic cultivars of wheat and its relatives (*Triticum* and *Aegilops* species). The main body of the collections derives from the several scientific expeditions dispatched from Kyoto University. In the third term of NBRP-Wheat, we decided to establish core-collections of hexaploid wheat including *Triticum aestivum* and exotic hexaploid wheat, tetraploid wheat (both wild and cultivated, AABB and AAGG species), and diploid wheat (*T. monococcum*, *T. urartu*, and *T. boeoticum*). This is the annual report of the project summarizing the progress made in the fiscal year 2015. We believe that once the core-collections are established, they will facilitate wheat researches using genome data.

Hexaploid wheat core-collection

The hexaploid core-collection is open to public. The F₁ and F₂ seeds between the accessions (female parent) and Norin 61 or Chinese Spring wheat (male parent) are available with specific arrangement. Those who want to use the materials, please contact to nasushu@kais.kyoto-u.ac.jp. We propagated the seed of F₁ (six crosses) and F₂ (71 crosses) that were in short.

Tetraploid wheat core-collection

We have selected the tetraploid core-collection from the genotype data. In short, we genotyped a total of 2,008 AABB and 401 AAGG accessions

by the small number of DArT array markers. Based on the genotype data we established a tetraploid wheat core-collection with the 192 accessions representing the genetic diversity. The core-collection is extensively genotyped by the genotyping-by-sequencing approach (Poland et al., 2012) and the DArTseq available from Diversity Arrays Technology Pty. Ltd. We successfully propagated 190 of 192 accessions for seed delivery, and AABB accessions are also made crosses with durum cultivars Langdon and Kronos. In the fiscal year 2015, we made 190 crosses and got F₁ seeds in 134 combinations. We have recorded some agronomic characters for the accessions in the core-collection.

Diploid wheat core-collection

We finished DNA preparation for the 501 AA genome species. Those include 50 *T. monococcum* and 38 *T. urartu*, and 413 *T. boeoticum* accessions. We added 140 *T. urartu* and one *T. boeoticum* accessions introduced from USDA for genotyping. Genotyping was performed by DArTseq technology. As a result, we established a diploid wheat core-collection of a total of 160 accessions (3 *T. monococcum*, 93 *T. boeoticum*, and 64 *T. urartu*). We propagate them in the fiscal year 2015.

References

Poland JA, Brown PJ, Sorrells ME, Jannink J-L (2012) Development of high-density genetic maps for barley and wheat using a novel

two-enzyme genotyping-by-sequencing
approach. PLoS ONE 7: e32253.