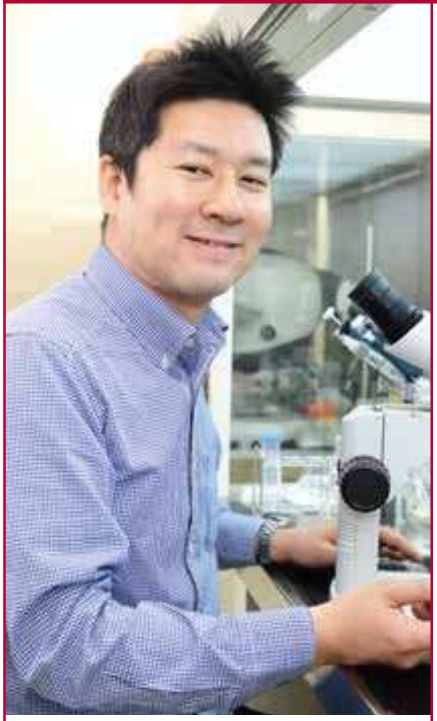

Assoc. Prof.
HISANO Hiroshi

Identification of the genes responsible for transformation amenability in barley

Different plant cultivars of the same genus and species can exhibit vastly different genetic transformation efficiencies. However, the genetic factors underlying these differences in transformation rate remain largely unknown. In barley (*Hordeum vulgare*), 'Golden Promise' is the most useful and well-studied cultivar for genetic transformation. By contrast, cultivar 'Haruna Nijo' is recalcitrant to genetic manipulation, although numerous genomic resources have been developed for this haplotype. Recently, we identified three major genomic regions on chromosomes 2H and 3H in barley important for successful transformation with *Agrobacterium*, utilizing the 'Haruna Nijo' × 'Golden Promise' F_2 generation. We termed these loci as *Transformation Amenability* (*TFA*) responsible for *Agrobacterium*-mediated transformation.

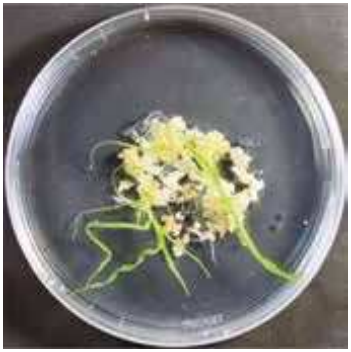

Fig. Green shoots regenerating from callus of barley

The genomic regions identified herein likely include necessary factors (i.e. regeneration from callus) for *Agrobacterium*-mediated transformation in barley. The potential to introduce these loci into any haplotype of barley opens the door to increasing the efficiency of transformation for target alleles into any haplotype of barley by the *TFA*-based selection method. Now we are trying to isolate the genes responsible for *TFAs*.

Genome editing in barley

Genome editing is a new technology of genetic engineering in which DNA is inserted, replaced, or removed from a target genome sequence using artificial restriction enzymes (nucleases). We are now developing a method of mutagenesis by the Clustered Regularly Interspaced Short Palindromic Repeats /CRISPR-associated proteins 9 (CRISPR/Cas9) or other techniques for future breeding and functional genomics in barley.