

Inheritance and Genetic Diversity of Flowering Types in Barley

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Abstract: There are open and closed types of flowering in barley. Detailed studies of the flowering types may aid our understanding of the complex nature of plant development, gene flow, evolution, and disease control. However, little is known about the regulatory mechanism of this trait. In genetical analyses of this study, from 8 crosses between closed and open flowering barley accessions, 5 generated open flowering F1 plants and their F2 plants segregated as 3 open:1 closed flowering, and 3 generated closed F1 plants and their F2 plants segregated as 1 open:3 closed flowering. Using molecular markers and segregating populations of 'Azumamugi' × 'Kanto Nakate Gold', 'Mikamo Golden' × 'Harrington' and 'Misato Golden' × 'Satsuki Nijo', we mapped 2 cleistogamy (closed type of flowering) loci, *cly1* and *Cly2*, to the long arm of chromosome 2H. Our results suggested that 2 tightly linked genes or multiple alleles at a single locus control the cleistogamy. Genotypes of eight tested cultivars and wild barley lines were suggested as *cly1cly2* (chasmogamous), *cly1Cly2* (cleistogamous) and *Cly1Cly2* or *Cly1cly2* (chasmogamous), indicating gene diversity for flowering types in barley. Epistasis between the two loci, i.e. *Cly1* > *Cly2*, was suggested. This study demonstrated that barley is a good model plant for studying cleistogamy in cereal crops.