

# 大学院入学試験問題用紙

2023 年度 1 期

科 目 名	受 験 専 攻	受 験 番 号	氏 名
英語	農学 専攻 博士後期 課程		

問1 下記の英文を読み(1)～(5)について答えなさい。

(a) Molecular markers have proved valuable in crop breeding, especially in studies on genetic diversity and for assessing relationships in a number of crop species. Among the different molecular genetic markers, RAPD and ISSR markers have been used to generate vast quantities of data, resulting in their rapid application for addressing a diverse range of biological questions (Semagn *et al.* 2006, Agarwal *et al.* 2008, Verma *et al.* 2016, Kalia *et al.* 2017). Because of their efficiency and convenience, these techniques have been applied to taxonomic comparisons of many plant species (Fernández *et al.* 2002, Sudupak 2004, Wu *et al.* 2004, Liu and Wang 2006, Han and Wang 2010, Sultana and Alam 2016, Dasgupta *et al.* 2018). To estimate the genetic distance between cultivars or populations, analyzing a large number of accessions individually within a cultivar or population is desired. Especially, in the estimation of the genetic structure of allogamous species, the diversity existing among individuals within cultivars or populations should be taken into account (Ghérardi *et al.* 1998, Raimondo *et al.* 2012). However, these approaches are laborious and impractical if a large number of populations is to be characterized.

The bulked samples approach is based on mixing equal quantities of genomic DNA, and can reduce the experimental effort, as the large size of a collection makes its management and use difficult (Michelmore *et al.* 1991, Kongkiatngam *et al.* 1996, Taški-Ajduković *et al.* 2014). Hence, this approach has been widely used for estimating genetic variation and relationships among species, cultivars, and populations, such as alfalfa (Yu and Pauls 1993, Segovia-Lerma *et al.* 2003, Taški-Ajduković *et al.* 2014), red clover (Kölliker *et al.* 2001, Dias *et al.* 2008), *Brumus catharticus* (Puecher *et al.* 2001), radish (Muminović *et al.* 2005, Wang *et al.* 2008), *Brassica napus* (Dulson *et al.* 1998), and *Brassica oleracea* (Lázaro and Aguinagalde 1998; Divaret *et al.* 1999), and the efficacy of this strategy has been examined. The bulked samples approach simplifies the marker profile of an individual cultivar or population because it favors the detection of consensus fragments (i.e., common alleles) in each population (Michelmore *et al.* 1991; Yu and Pauls 1993). Segovia-Lerma *et al.* (2003) reported that this approach may reflect a population's general genetic composition more accurately compared to the evaluation of fewer individual genotypes. Although an appropriate bulk size, reflecting genetic diversity existing between individuals within population, depends on the degree of heterozygosity in species, the relationship between an appropriate bulk size and the degree of heterozygosity has not been fully examined for each plant species analyzed in this study.

The genus *Brassica* contains some of the most important arable and forage crop species, such as turnip (*B. rapa*), leaf mustard (*B. juncea*), oil seed rapa (*B. napus*), and cabbage (*B. oleracea*).  
 (b) Their genomes have been denoted as A, B, and C, respectively, and the hybrid taxa, *B. napus*, *B. juncea*, and *B. carinata*, are the known amphidiploids of *B. rapa* × *B. oleracea* (AC), *B. rapa* × *B. nigra* (AB), and *B. oleracea* × *B. nigra* (BC), respectively (U 1935). Among the *Brassica*

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species, *B. rapa* and *B. oleracea* are allogamous species, owing to their self-incompatible nature, and are expected to be genetically heterogeneous, especially in the indigenous varieties. (後略)

\*1 バルク法による解析

- (1) 下線部(a)を和訳せよ。但し、括弧内の引用文献の和訳は必要なしとする。
- (2) DNA マーカーを用いた植物種の類縁関係の推定において、バルク法が広く用いられてきた理由について述べよ。
- (3) バルク法において、適切なバルクサイズを決める際に考慮すべき点は何であるか述べよ。
- (4) Segovia-Lerma ら (2003) は、バルク法についてどのような報告をしているか述べよ。
- (5) 下線部(b)を和訳せよ。但し、括弧内の引用文献の和訳は必要なしとする。

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問1 以下の(1)～(3)について回答せよ。

- (1) 染色体 FISH 法の目的と原理について説明せよ。
- (2) パンコムギにおける異数体の作出例(2つ以上)について説明せよ。
- (3) 食料及び農業のための植物遺伝資源に関する国際条約(ITPGR)の目的を述べ、この条約の必要性について説明せよ。