

# 國立嘉義大學九十三年學年度 農學研究所博士班農藝組招生考試試題

科目：農藝專業英文

## 一、 Please translate the following paragraph into Chinese ( 25 % )

In the sweet pea, purple flower color is dominant to white and gives a typical 3:1 ratio in the  $F_2$ . White-flowered varieties of sweet peas breed true, and crosses between different white varieties usually produce white-flowered progeny. In some cases, however, crosses of two true-breeding white varieties give only purple-flowered  $F_1$  plants. When these  $F_1$  hybrids are self-fertilized, they produce an  $F_2$  consisting of about 9/16 purple-flowered sweet peas and 7/16 white-flowered. The 9:7 ratio is a modification of the 9:3:3:1 ratio. Even though they are not all homozygous for the alleles in question, all the  $F_2$  white-flowered plants breed true when self-fertilized. One-ninth of the purple-flowered  $F_2$  plants ---the C/C P/P genotypes--- breed true.

These results may be explained by the interaction of two genes. The 9/16 purple-flowered  $F_2$  plants suggests that colored flowers appear only when two independent dominant alleles are present together, and that the color purple results from some interaction between them. White flower color would then result from homozygosity for the recessive allele of one or both genes. Thus, gene pair C/c specifies whether or not the flower can be colored, and gene pair P/p specifies whether or not purple flower color will result. An interaction of two genes to give rise to a specific product is a form of epistasis called duplicate recessive epistasis or complementary gene action.

In sum, many types of phenotypic modifications are possible as a

result of interactions between the products of different gene pairs. Geneticists detect such interactions when they observe deviations from the expected phenotypic ratios in crosses. We have discussed some examples in "which two genes assort independently and in which complete dominance is exhibited in each allelic pair. The ratios we discussed would necessarily be modified further if the genes did not assort independently and/or if incomplete dominance or codominance prevailed.

## 二、 Please read the following paragraph, then list at least 5 key points out of the paragraph . ( 25 % )

Sexual reproduction in many angiosperm plants involves self-incompatibility (SI), which is one of the most important mechanisms to prevent inbreeding. SI is genetically controlled by the *S*-locus, and involves highly specific interactions during pollination between pollen and the pistil on which it lands. This results in the rejection of incompatible ('self') pollen, whereas compatible ('non-self') pollen is allowed to fertilize the plant. In *Papaver rhoeas*, S-proteins encoded by the stigma component of the *S*-locus interact with incompatible pollen, triggering a  $Ca^{2+}$ -dependent signalling network, resulting in the inhibition of pollen-tube growth. Programmed cell death (PCD) is a mechanism used by many organisms to destroy unwanted cells in a precisely regulated manner. Here we show that PCD is triggered by SI in an *S*-specific manner in incompatible pollen. This provides a demonstration of a SI system using PCD, revealing a novel mechanism to prevent self-fertilization. Furthermore, our data reveal that the response is biphasic; rapid inhibition of pollen-tube growth is followed by PCD, which is involved in a later 'decision-making' phase, making inhibition irreversible.

Programmed cell death (PCD) has several key diagnostic features. These include nuclear DNA fragmentation, leakage of cytochrome *c* from

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the mitochondria into the cytosol, and cleavage of poly(ADP-ribose) polymerase (PARP). A key enzyme involved in apoptosis in animal cells is caspase-3, which is activated in an autoprocessing cascade and is instrumental in the cleavage of nuclear DNA and PARP. Although it is generally accepted that apoptosis does not occur in plant cells, PCD in plants shares some apoptotic features. The tetrapeptide DEVD is an inhibitor of caspase-3 and has been used to provide evidence for a caspase-like activity in apoptotic animal cells and in plant cells undergoing PCD. We have used these markers and tools to investigate whether PCD is triggered in incompatible pollen as a consequence of the SI response.

### 三、 Please translate the following paragraph into Chinese ( 25 % )

Soybean [*Glycine max* (L.) Merr.] growers using organic production systems have predominately been limited to mechanical cultivation for weed control. Interseeded cover crops such as winter cereal rye (*Secale cereale* L.) have been used in conventional soybean production systems in conjunction with herbicides to reduce tillage and cultivation operations. The objective of this study was to determine if high soybean planting populations in drill-planted (19-cm row) systems or a single mechanical cultivation in row-planted (76-cm row) systems could facilitate the use of interseeded rye in organic soybean production systems. Interseeded winter cereal rye decreased soybean grain yield in 2 of 3 yr in the drill-planted system by 22 and 17%, respectively, and in all 3 yr of the row-planted system by 23, 27, and 23%, respectively. Moisture stress from the interseeded rye was a predominate factor in soybean grain yield reduction. In 2000, the soybean planting population was inversely correlated with late-season biomass of interseeded rye. However, during the drier years of 2001 and 2002, increasing soybean planting density did not significantly reduce late-season biomass of interseeded rye. The interseeded rye reduced late-season weed biomass in both the drill-planted and row systems in 2001. Removal of the interseeded rye with mechanical cultivation in the row system when the soybean was at the V4 growth

stage was ineffective in 2000 but increased soybean grain yield by 1142 and 746 kg ha<sup>-1</sup>, respectively, in 2001 and 2002. These results suggest that some means of controlling winter cereal rye growth is necessary for effective management across a range of precipitation levels.

### 四、 Please translate the following paragraph into Chinese ( 25 % )

The analysis of stress-responsiveness in plants is an important route to the discovery of genes conferring stress tolerance and their use in breeding programs. Proteomic analysis provides a broad view of plant responses to stress at the level of proteins. In recent years this approach has increased in sensitivity and power as a result of improvements in two-dimensional polyacrylamide gel electrophoresis (2DE), protein detection and quantification, fingerprinting and partial sequencing of proteins by mass spectrometry (MS), bioinformatics, and methods for gene isolation. 2DE provides information on changes in abundance and electrophoretic mobility of proteins, the latter reflecting post-translational modifications such as phosphorylation and free-radical cleavage. Here we review the technical aspects of proteomics and demonstrate its use in analyzing the response of rice plants to drought and salinity. More than 2000 proteins were detected reproducibly in drought-stressed and well-watered leaves. Out of >1000 proteins that were reliably quantified, 42 proteins changed significantly in abundance and/or position. We identified several leaf proteins whose abundance increased significantly during drought and declined on re-watering. The three most marked changes were seen with actin depolymerizing factor, a homologue of the S-like ribonucleases and the chloroplastic glutathione-dependent dehydroascorbate reductase. Proteomic comparisons of salt stress-tolerant and stress-sensitive genotypes revealed numerous constitutive and stress-induced differences in root proteins. Among them was caffeoyl-CoA O-methyltransferase, an enzyme of lignin biosynthesis. The abundance of ascorbate peroxidase was much higher in salt-tolerant Pokkali than in salt-sensitive IR29 in the absence of stress.