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in 100 grams of fresh soil in Maofen plots was 657 individuals, which was significantly ($P < 0.05$) higher than 477 in resistant rootstock plots. During the harvest period, three semi-selective mediums Komada, Elad and Masago were respectively applied to measure the abundances of *Fusarium* spp., *Trichoderma* spp., *Phytophthora* spp., and *Pythium* spp. around the rhizosphere of resistant rootstock and Maofen. It was found that beside *Fusarium* spp. in June and July 2003, the abundance (CFU per gram of fresh soil) of each of the four fungi around the resistant rootstock rhizosphere was lower than that in Maofen plot. It was concluded, as compared with Maofen cultivars, the resistant rootstock showed good resistance to the above soil-borne diseases and obvious repression effects on the four fungal populations.

Key words: Tomato; resistant rootstock; disease incidence; fungi; greenhouse

P43 Identification of AFLP markers linked to the stripe rust resistance gene YrSp in wheat

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Wheat stripe rust (*Puccinia striiformis* West. f. sp. tritici) is a worldwide disease and one of the most widespread and important diseases in China. The stripe rust resistance gene YrSp in the cultivar "Spaldings Prolific", an European wheat stripe rust differential, is effective against stripe rust in China, but it has seldom been used in commercial wheat cultivars. We aim to develop molecular markers linked to stripe rust resistance genes, as this will help in the utilization of MAS (marker-assisted selection) and raise the efficiency of selection in wheat breeding for rust resistance. DNA polymorphisms between the resistant near-isogenic line YrSp/6×Avocet S and the susceptible background parent "Avocet S" were analyzed using the amplified fragment length polymorphism (AFLP) method with the gene donor parent "Spaldings Prolific" as control. A total of 225 combinations of Pst I-primers and Mse I-primers were screened. Genetic linkage of the polymorphic DNA fragments found with YrSp gene were tested preliminarily on 20 segregating F₂ plants, including 10 resistant plants and 10 susceptible plants, derived from a cross between the susceptible parent "Avocet S" and the resistant near-isogenic line "YrSp/6×Avocet S". Five polymorphic DNA fragments were found linked to the YrSp gene. A 420bp DNA fragment amplified by the primers P34 and M54 was not found to exchange with the target gene. All the other 4 DNA fragments, a 170bp amplified by the primers P70 and M62, a 160bp amplified by P70 and M62, a 160bp and a 230bp amplified by P32 and M59, were found to exchange with the target gene in one plant.

All the 5 polymorphic DNA fragments linked to YrSp gene were recovered from gels. Cloning and sequencing of these fragments are now being carried out. It is expected that SCAR markers closely linked to the YrSp gene against wheat stripe rust will be developed shortly. This will promote the utilization of YrSp gene in wheat breeding program for the resistance to stripe rust.

P44 The new resistant chickpea lines to six pathotypes of Ascochyta blight in Iran

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Ascochyta blight is the most important limitative disease reducing production of chickpea in many areas. The resistance lines were considered as the best way to control the disease. So identification of suitable resistance sources against population of pathogen in each area is important. In this study chickpea germplasm of Ferdowsi University was evaluated against six pathotypes of the pathogen. Five hundred-seventy accessions were cultivated in an augmented design with ten blocks and sixty-seven rows. Plants were inoculated with mixture suspension spores of six pathotypes in five to seven leaves stage. Suitable humidity and temperature were provided using a mist irrigation system. When the susceptible lines (ILC1929 and ILC263) died completely, disease severity was scored on a scale of 1 to 9, where 2 and 3 = resistance, 4 and 5 = moderately resistance, 6 and 7 = moderately susceptible and 8 and 9 = highly susceptible. 2, 25, 32 and 41% of the accessions were divided in those groups respectively. The percentage of Kabuli type in the resistance groups was more than Desi type, but in the susceptible groups, Desi type was more frequently observed than Kabuli type. Only one Desi (MCC523) and five Kabuli accessions (MCC54, MCC133, MCC3.11, MCC142 and MCC331) were resistant at different growing stages against six pathotypes of ascochyta blight.

P45 Germplasm screening and EMS mutagenesis for powdery mildew (*Leveillula taurica*) resistance in sainfoin (*Onobrychis viciifolia* Scop)

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