## Poster Presentations Ecological/Genetical Issues

## P EGI 35

**Combined resistance to Bacterial Wilt and Fusarium Wilt in common bean Genotypes derived from a segregating population** A. Wendland

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Bacterial wilt (*C. flaccumfaciens* pv. *flaccumfaciens* - *Cff*) and Fusarium wilt (*F. oxysporum* f. sp. *phaseoli* - *Fop*) present similar symptoms derived from the obstruction of xylem vessels. A mapping population obtained by crossing Ouro Branco (resistant) x CNFP 10132 (susceptible), contrasting for bacterial wilt was evaluated for both diseases. The 12 more resistant genotypes of the generation F5:7 were inoculated in Embrapa Rice and Beans greenhouse by injecting 20 uL of bacterial suspension ( $10^8$  UFC.mL<sup>-1</sup>) of isolates Cff33 and Cff25, ten days after planting. The inoculation of suspension of  $10^6$  conidia.mL<sup>-1</sup> of the isolates Fop101 and Fop102 was made by dipping cut roots during 5 min with subsequent transplant. The control was also inoculated with water. Evaluations were made at 15, 18 and 20 days after inoculation with *Cff,* and 21 days after inoculation with *Fop*, using severity scales of 1 = no symptoms to 9 = dead plants. Data were submitted to analysis of variance and means compared by Skott-Knott test at 5% probability. Plants were considered resistant when the mean rate was at 1 to 3. The more resistant genotypes for both diseases were identified as OBxCNFP 10132.42, OBxCNFP 10132.27 (clear grains) and OBxCNFP 10132.66, OBxCNFP 10132.162 (black grains) as well presented the morphological characteristics and commercial grain favorable to consumers.

## P EGI 36

Host Plant Determination of *Brachytrupes megacephalus* Lefebvre, 1827 (Orthoptera, Grillinae) Using Faeces Analysis in the Region of Oued Righ (Algerian Sahara)

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In the southeast of the Algerian Sahara (Touggourt), the host plant determination of *Brachytrupes megacephalus* was studied by faeces analysis (microscopic observations). The experimentation was conducted in mid August until the end of September 2014. The main results of faeces analysis showed that the plants consumed by *B. megacephalus* belong to 8 families: Arecaceae (*Phoenix dactylifera*), Apocynaceae (*Nerium oleander*), Asteraceae (*Chrysanthemum*), Myoporaceae (*Myoporum sandwicense*), Plumbaginaceae (*Armeria maritima*), Rosaceae (*Prunus armeniaca*), Solanaceae (*Solanum lycopersicum*) and Triochylaceae (*Cherry fantasia and White Kristina*). *Phoenix dactylifera* is the most preferred host species by the adults of Brachytrupes megacephalus, with a consumption rate 85,87%.