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Poster Abstract – A.38

CHARACTERIZATION OF A BEAN LANDRACE FROM SICILY: THE 'FAGIOLO BADDA DI POLIZZI'

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Inside the project "Piano per la Produzione di Proteine Vegetali in Sicilia" investigations were carried out to characterize a bean population cultivated in the Parco delle Madonie area, the 'Fagiolo Badda di Polizzi'. The producers' interest for this landrace and the appreciation of the consumers could justify the start up of a valorization program through a product certification.

Researches on the morpho-physiological aspects and on the nutritional profile were made in trials conducted between 2005 and 2007. All the Badda bean accessions showed an indeterminate plant growth habit, white flowers and a very delayed flowering time. In particular, a certain variability was seen and described for the size and shape of pods and seeds. Two types of Badda are cultivated, differentiated by the secondary seed colour: the "white Badda" and the "black Badda". Both have ivory has a primary seed coat colour, but the "white Badda" has a brownish spot on the hilum, whereas the "black Badda" shows a black spot. In addition, the secondary colour of the seed coat of the "black Badda" showed two different pigmentations: violet and black, that suggested a genetic differentiation into different sub-populations. Finally, the "black Badda" resulted less susceptible to viral infections than the "white" one.

At the molecular level, three accessions of Badda bean (two 'white' and one 'black') have been compared with control varieties, including one accessions of 'Fagiolo del Purgatorio' from Gradoli (VT), seven landraces of the Borlotto type collected in the Marche region and the cultivars Bat, Jalo, Clio and Big Borlotto. The analyses were carried out using 12 Inter Simple Sequence Repeats (ISSR) primers yielding a total of 140 bands. Although no specific band for the Badda landrace were detected, two amplicons were found only in the accessions of Badda and in Monachello, a bicol-seeded type from the Marche region, morphologically similar to the "black Badda". The dendrogram obtained from the genetic distances based on ISSRs indicated that the Badda type belongs to the Andean gene pool and that it is distinguishable from the tested controls being grouped into a separate cluster. Within the Badda type, the 'white' accessions were not separated from the 'black' one.