Proceedings of the Joint Meeting AGI-SIBV-SIGA
Assisi, Italy – 19/22 September, 2011
ISBN **978-88-904570-2-9**

Poster Communication Abstract – 9.17

COMMON BEAN DOMESTICATION IN MESOAMERICA AND ANDES HIGHLIGHTED BY NUCLEOTIDE DATA

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Phaseolus vulgaris, crop evolution, nucleotide diversity, domestication

Investigations into the evolutionary history of crop species is expected to highlight the structure and organisation of their genetic diversity and the role of the evolutionary forces that have been shaping this diversity. Such knowledge is a crucial prerequisite for efficient conservation and use of existing germplasm for the development of new improved plant varieties. The common bean (*Phaseolus vulgaris* L.) is a diploid ($2n = 2x = 22$) annual species that is predominantly self-pollinating and is the main grain legume for direct human consumption. It represents a rich source of protein, vitamins, minerals and fibre, especially for the poorer populations of Africa and Latin America. A particular evolutionary scenario has characterised this species: the existence of two main geographically distinct gene pools (Mesoamerica and Andes), where two independent domestication events occurred. Here, we analysed a wide collection of wild and domesticated *P. vulgaris* accessions (215) that represent a cross-section of the entire geographical distribution of the common bean, from northern Mexico to northern Argentina. Four gene fragments were sequenced, with the aim of the definition of the nucleotide diversity and the population structure that characterise the wild and domesticated populations from both the Mesoamerica and Andes gene pools. Moreover, the possibility of multiple or single domestication events were investigated, along with the identification of the putative geographical locations of these domestication events within each gene pool.