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

Poster Communication Abstract – 9.29

THE EFFECTS OF DOMESTICATION ON THE STRUCTURE OF THE NUCLEOTIDE DIVERSITY IN THE COMMON BEAN FROM MESOAMERICA

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Phaseolus vulgaris, crop evolution, nucleotide diversity, selection, linkage disequilibrium

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. The species is characterised by two major geographically distinct gene pools that predate its domestication, and where two independent domestication events occurred: Mesoamerica and the Andes. Many studies have investigated the molecular and phenotypic diversities and the population structure of the common bean, although little information is available on the level and extent of its nucleotide diversity. Here, we focused our attention on investigation of the domestication process in Mesoamerica by sequencing 55 gene fragments from a set of 47 accessions of common bean, most of which were from Mesoamerica (39; as both wild and domesticated forms). Eight additional accessions were included as controls: four from the Andes, two from northern Peru–Ecuador wild populations that are characterised by phaseolin type I (a seed storage protein), and one as a *P.coccineus* and *P. dumosus* accession. Nucleotide diversity, population structure and linkage disequilibrium analyses were carried out, along with identification of loci that show signs of a past genetic sweep, which are indicative of selection during domestication.