## PHENOTYPIC AND QUALITATIVE EVALUATION OF FIELD BEANS (VICIA FABA SPP.) POPULATIONS

TORRICELLI R., PAUSELLI M., CESTOLA E., FALCINELLI M.

Department Applied Biology, University of Perugia (Italy)

Vicia faba spp., field beans, phenotypic and qualitative evaluation

Vicia faba spp., originated in the Mediterranean-West Asia region during the Neolithic period and now cultivated in many temperate regions, is one of the oldest legume crops mainly grown for human and animal dietary needs. This crop like other grain legumes, contributes to sustainable agriculture by fixing atmospheric nitrogen. Faba bean has been divided by seed size into three subspecies. The broad bean (V. faba var. major Harz) is mostly grown as a grain vegetable because of its large seed size, while the horse bean (V. faba var. equine Pers.) and tick bean (V. faba var. minor Beck) are grown primarily for animal feed or as a green manure crop; in Europe, these two latter species are referred to as field beans. In the Mediterranean area these species are very important. Disappointingly cultivation of these crops has decreased in the last decades, although in recent years their importance is increasing due to difficulties in sourcing GM-free soya beans and also for their use in organic farming.

Faba beans breeding has proceeded very slowly and with only few interesting results. More than 90 cultivars of *V. faba spp.*, half of which are Dutch, 18 British and 15 Italian, are registered in the European Community Catalogue. However most of the Italian varieties were registered before 1990. Improvement in seed yield and yield stability are the primary objectives of most faba bean breeding programmes. However other objectives such as resistances to the main biotic and abiotic stresses, obtaining genotypes that are free of certain anti-nutritional substances are also important. In the present work, data on the main morpho-agronomic traits and chemical and nutritive characteristics are recorded and determined on landrace accessions of field beans belonging to a collection established in the Umbria Region. The results obtained in the material analyzed enabled us to identify interesting genotypes for further breeding programs.