Due to the complexity of resistance breeding to broomrape, however, few improved varieties are developed and released along with some management and protection practices. As a result, *Orobanche* tolerant variety “Hashenge” has been released in Ethiopia from ICARDA breeding lines and promoted to many farmers. The improved variety gave yield advantage of 141% and 211% over susceptible and local checks, respectively, with considerable *Orobanche* reduction compared to the checks. The application of (1-2 x) sub lethal doses of Glyphosate herbicide at early flowering stage further enhanced the management level of the variety explained by higher yield (4 t ha$^{-1}$) and lowest *Orobanche* population. The tolerant variety along with protection practices (1-2 sprays of Glyphosate) is reversing faba bean decline in the highlands and this heralds food and nutrition security to small holder farmers.

**WS34: Moroccan perspective in improving faba bean (*Vicia faba* L.) productivity**

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Faba bean (*Vicia faba* L.) is the major legume grown in Morocco for food and animal feed. Beside its beneficial roles (nutritional, agronomical, environmental), productivity level remains low and variable. This situation is mainly due to susceptibility to biotic and abiotic stresses, low degree of mechanization, limited use of inputs, labor cost and availability, poor seed multiplication systems, and access to market. Thus, it is important to develop strategies for improving productivity and quality, facing climatic changes and extending the use of this crop in different Moroccan farming systems. The improvement activities are focused on developing tolerant germplasm to *Orobanche*, Chocolate spot, *Ascochyta* blight, rust, drought, heat and cold suitable for different agro-ecological areas. Furthermore, local landraces were collected from different faba bean growing regions, characterized, evaluated, conserved in genebank, and integrated in faba bean breeding program. Two faba bean lines are being tested for the second year for registration in Moroccan National Catalogue. Some other promising lines are being increased for submission for registration, and others are included in yield trials. Additional efforts are in progress for better faba bean management under irrigated conditions, screening for cold tolerance for the mountain areas, better weed control specially dicot, and to decrease losses during storage. Also, we are tackling the management of faba bean in association in different situations (agroforestry, association with vegetable crops). This will lead to transferring technical package for optimal faba bean production.

**WS35: Major achievements in faba bean breeding in Tunisia**

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Faba bean (*Vicia faba* L.) is the major food legume crop in Tunisia occupying around 60,000 ha representing almost 80% of the total food legume areas. It contributes to the improvement and the
sustainability of wheat production system. Breeding activities conducted in the Field Crops Laboratory of the National Agricultural Research Institute of Tunisia and the Regional Research Centre on Field Crops of Beja released varieties with high yield potential and tolerant to major stresses. The breeding program has registered catalogue several varieties of small and large seeded faba bean during the last 15 years in the Tunisian plant variety official. Three varieties (Najeh, Chourouk and Shams), among the five small seeded registered varieties, with partial resistance to Orobanche responsible for considerable yield losses in the region and constituting the main constraints of the crop in Tunisia. Advanced research studies conducted on the new varieties showed that many resistance mechanisms are involved. Beside these varieties, the program has registered two other small seeded varieties, Bachaar (moderately resistant to rust, stem nematode and tolerant to drought) and Badi and two large seeded varieties (Mamdouh and Chahbi). Tunisian public and private seed companies are currently producing seeds of most of the released varieties which will contribute to the increase of national faba bean production and development of the crop in near future in the country. In addition, the program has developed integrated production packages in order to improve the productivity through an effective control of the major biotic and abiotic constraints.

WS36: Recent advances in marker assisted selection in faba bean (Vicia faba L.)

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Faba bean is a major food and feed legume in Eurasia and North Africa. Despite being a formerly favoured plant species cytogenetically, faba bean genomics still lags far behind than other model crops. During the 90’s and early 2000s, the use of RILs and molecular markers allowed the production of high resolution linkage maps and the identification of genes and quantitative trait loci (QTLs) controlling biotic (broomrape, Ascochyta) and abiotic (frost) stresses as well as key quality (absence of tannins, vicine-convicine), architectural and yield related traits. Despite these significant efforts, complete translation of marker discovery to faba bean breeding is still to be achieved. The scarcity genome information for faba bean, attributed to the difficulties of assembling/annotating its giant (~13Gb) genome, is hampering breeding applications although recent efforts pave the way to more accurate selective tools. Thus, recent SNP-based genetic maps have allowed the faba bean alignment with model species favoring the application of translational genomics to search for candidate genes involved in phenotypic traits. Moreover, cheaper sequencing technologies are stimulating the production of transcriptome data from multiple cultivars and tissues providing a valuable starting point in the search for relevant positional and functional candidates. A high throughput faba bean SNP chip (50K Axiom, Affymetrix), incorporating all the public transcriptome datasets is underway and will be used within the EUCLEG project to analyse the genetic architecture of key breeding traits using association studies based on candidate genes and genome-wide association studies (GWAS) and to establish prediction equations for genomic selection (GS).