**Development of a biotech toolbox for bean research**

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Research on common bean genetics and molecular biology faces challenges due to its complex genome, high genetic diversity (within and between Mesoamerican and Andean gene pools), and phenotypic plasticity. Hindered by limited forward genetic methods, the use of low-efficiency protocols (biolistic transformation) and recalcitrance to in vitro regeneration, identifying key genes and traits remains difficult. To face these challenges and to provide the scientific community a structured platform to look for mutants in common bean we recently developed an EMS-mutagenized populations for an approach of TILLING (Targeting Induced Local Lesions In Genomes) in the Meccearly dwarf borlotto type variety (Blumen). This population consists of 2345 M1 lines and we are currently reproducing 1360 M2 plants derived from 340 M1 lines. A Whole Genome Sequencing approach will be applied to exploit this population and a preliminar set of samples is under analysis to evaluate mutation efficiency. In parallel, we are working on the improvement of in vitro protocols and the development of next-generation vectors based on those already tested in other species with low regenerative potential (such as wheat), which would increase the efficiency of transformation and regeneration of bean embryonic axes after biolistics. Altogether, these efforts could be crucial in the frame of global food security, for enhancing crop productivity, genetic diversity and nutritional quality.