

INVESTIGATION OF NOVEL PHENOTYPES AMONGST M4 PLANTS OF A COMMON BEAN TILLING POPULATION GROWN IN FIELD CONDITIONS

PISCHEDDA A.*, POSADINU C. M.*, GALBIATI M.***, PAOLO D.***, BITOCCHI E.***, BELLUCCI E.***, CORTINOVIS G.***, PAPA R.***, SPARVOLI F.**, PORCEDDU A.*, ATTENE G.*, RODRIGUEZ M.*

*) Dipartimento di Agraria, Università degli Studi di Sassari, viale Italia, 39A, 07100 Sassari, Italy

**) CNR-Consiglio Nazionale delle Ricerche, Istituto di Biologia e Biotecnologia Agraria, Via Edoardo Bassini, 15, 20133 Milano, Italy

***) Dipartimento di Scienze Agrarie, Alimentari ed Ambientali, Università Politecnica delle Marche, via Brecce Bianche, 2-8, 60131 Ancona, Italy

Phaseolus vulgaris, phenotyping, EMS mutagenesis, mutant population, TILLING

Common bean (*Phaseolus vulgaris*) is one of the most important legumes in the world for human consumption and genomic studies. Its small genome size and its importance as a reference crop for other legume species, makes it an ideal model for advanced genomic approaches. To this end, in 2009 Porch and colleagues have created a mutant population using the mutagen ethylmethanesulfonate (EMS) which could be suitable for both forward and reverse genetic studies.

The present study is part of the PARDOM project, that aims to investigate common bean genome evolution and adaptation. In detail, we have here searched for phenotypic differences amongst 1670 M4 lines generated from the EMS mutagenized BAT 93. A total of 6657 seeds (nearly four seeds per line) were sown in an open field trial during the spring-summer season in 2021 at the “Az. Sperimentale Mauro Deidda” of the Agricultural Department of University of Sassari in Ottava (Sassari, Italy). M4 individuals were evaluated for different phenotypic traits (e.g., emergence, flowering and ripening date, habitus) and compared to the wild type plants to highlight interesting mutation/peculiarities. The data are under evaluation, but preliminary results showed some interesting phenotypes. This study lays the foundation for future reverse and forward genomic studies that might help

to gain insights into the domestication process and plant adaptation and to collect genetic information to be exploited in future breeding programs.