

## MODULATION OF BIOACTIVE COMPOUNDS IN COMMON BEAN SEED: TWO SIDES OF THE SAME COIN

SPARVOLI F.\*, COMINELLI E.\*, LIBERATORE C.\*, PAOLO D.\*, CAMPION B.\*\*,  
NIELSEN E.\*\*\*, BOLLINI R.\*

\*) Institute of Agricultural Biology and Biotechnology, CNR, Milan, Italy

\*\*) CREA-GB Centro di Ricerca per Genomica e Bioinformatica, Montanaso  
Lombardo, LO, Italy

\*\*\*) Department of Biology and Biotechnology, University of Pavia, Italy

*alpha-amylase inhibitor, lectins, legumes, phytic acid, seed*

Max 3000 characters

Among grain legumes, common bean (*Phaseolus vulgaris* L.) is the most important for human consumption and is a recognized component of healthy diets of the Mediterranean basin. Bean seeds are a rich source of energy (mainly proteins and complex carbohydrates), valuable compounds (folates, vitamins, polyphenols), essential minerals (iron and zinc) and their consumption can contribute to reduce risk of diseases such as obesity, diabetes, cardiovascular problems and colon, prostate and breast cancer. However, despite all these positive characteristics, bean seeds contain important amounts of bioactive compounds (such as the lectins, digestive enzyme inhibitors, phytate, raffinose, phenolic compounds) considered as antinutritional, that may cause adverse negative effect to those who consume them as staple food and/or improperly processed/cooked.

Our group in the last three decades actively contributed in the characterization of natural and induced genetic variability for the identification and exploitation of genotypes with superior nutritional traits. In particular, we identified genotypes devoid of major antinutritional components (lectins,  $\alpha$ -amylase inhibitor, phytic acid). By screening bean EMS mutagenized populations, we identified and described a number of *low phytic acid mutants* (*lpa*) and reported that the *lpa1* mutant also shows a 25% reduction of raffinose as a result of the pleiotropic effect of the *lpa1* mutation. By screening wild and cultivated

bean accessions we also identified several variants in the composition and abundance of major seed proteins. All these different materials were combined to tailor and exploit novel genotypes with specific nutritional traits that turned useful to demonstrate the nutritional/antinutritional role of single components in reducing the predicted glycemic index, improving mineral bioavailability, or discovering unexpected behavior related to the Hard to Cook phenotype.