

University of Hohenheim  
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# Evaluating seed quality traits in common bean (*Phaseolus vulgaris*) to generate genomic prediction models

Master's Thesis by  
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## ABSTRACT

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In common bean (*Phaseolus vulgaris*) breeding, quality traits are monitored to ensure that released varieties are acceptable to market and to ensure high adoption rates. The traits investigated are cooking time, Fe and Zn content. The cooking time trait is of interest primarily because it is a major determinant of consumer acceptability, and short cooking time lowers the demand for fuel. Fe and Zn deficiencies affect more than a third of the world's population, most severely women and children. Quality traits were evaluated for a panel of 67 common bean genotypes from the Mesoamerican genepool. Cooking time was determined by experimentation with an Automated Mattson Cooker. A row-column design was implemented to test for possible sources of variation in the design effects. Machine effects were shown to be a source of variation which should be controlled in Automated Mattson cooker experiments. X-ray fluorescence analysis was performed for Fe and Zn content determination. A GWAS analysis was conducted with the quality traits of interest to detect markers associated with the traits of interest. Significant QTLs were not identified, contrary to published data. A low number of genotypes is the suspected cause of the lack of detection. Genomic prediction modelling was performed for the quality traits, low prediction accuracy was attained for the nutrition traits, and intermediate prediction accuracy was found for the cooking time trait. Genomic selection seems a plausible future tool for accelerated selection cycles for cooking time in common bean.

**Keywords: *Phaseolus vulgaris*, cooking time, Automated Mattson cooker, biofortification, genomic prediction**