



Bayesian approach increases accuracy when selecting cowpea genotypes with high adaptability and phenotypic stability

L.M.A. Barroso^{1*}, P.E. Teodoro^{2*}, M. Nascimento¹, F.E. Torres², A. dos Santos³, A.M. Corrêa², E. Segrilo⁴, C.C.G. Corrêa², F.A. Silva² and G. Ceccon⁵

¹Departamento de Estatística, Universidade Federal de Viçosa, Viçosa, MG, Brasil

²Departamento de Fitotecnia, Universidade Estadual de Mato Grosso do Sul, Aquidauana, MS, Brasil

³Departamento de Melhoramento Genético, Universidade Estadual do Norte Fluminense Darcy Ribeiro, Campos dos Goytacazes, RJ, Brasil

⁴Embrapa Meio-Norte, Teresina, PI, Brasil

⁵Embrapa Agropecuária-Oeste, Dourados, MS, Brasil

*These authors contributed equally to this study.

Corresponding author: P.E. Teodoro

E-mail: eduteodoro@hotmail.com

Genet. Mol. Res. 15 (1): gmr.15017625

Received September 11, 2015

Accepted October 30, 2015

Published March 11, 2016

DOI <http://dx.doi.org/10.4238/gmr.15017625>

ABSTRACT. This study aimed to verify that a Bayesian approach could be used for the selection of upright cowpea genotypes with high adaptability and phenotypic stability, and the study also evaluated the efficiency of using informative and minimally informative *a priori* distributions. Six trials were conducted in randomized blocks, and the grain yield of 17 upright cowpea genotypes was assessed. To represent the minimally informative *a priori* distributions, a probability distribution with high variance was used, and a meta-analysis concept was adopted to represent the informative *a priori* distributions. Bayes factors were used to conduct comparisons between the *a priori* distributions. The Bayesian approach was effective for selection

of upright cowpea genotypes with high adaptability and phenotypic stability using the Eberhart and Russell method. Bayes factors indicated that the use of informative *a priori* distributions provided more accurate results than minimally informative *a priori* distributions.

Key words: *Vigna unguiculata* L.; Bayes factor; Informative prior; Genotype x environment interaction