



Relationship among physiological quality, heterosis, and amylase gene expression in maize seeds

G.E. Oliveira¹, E.V.R. Von Pinho², T. Andrade², J.C. Souza¹, F. Caixeta² and R.A.D.C. Ferreira¹

¹Departamento de Biologia, Universidade Federal de Lavras, Lavras, MG, Brasil

²Departamento de Agricultura, Universidade Federal de Lavras, Lavras, MG, Brasil

Corresponding author: T. Andrade

E-mail: thaisandradeagro@gmail.com

Genet. Mol. Res. 14 (3): 8623-8633 (2015)

Received September 12, 2014

Accepted March 12, 2015

Published July 31, 2015

DOI <http://dx.doi.org/10.4238/2015.July.31.10>

ABSTRACT. In this study, we analyzed heterosis, amylase enzyme gene expression, and the physiological quality of maize seeds with different genotypes and sizes, which were subjected to aging and not subjected to aging. We used seeds from 2 maize lines that differed with regard to physiological quality, the hybrid, and the reciprocal hybrid; they were classified into 2 sizes and were subjected to aging and not subjected to aging. Physiological quality was assessed by performing tests for germination, emergence, emergence speed index, and artificial aging. Expressions of the genes alpha amylase B73, alpha amylase (LOC542522), isoamylase mRNA clone 353244, and the endogenous controls ubiquitin and alcohol dehydrogenase in the seeds were studied using quantitative real-time-polymerase chain reaction. We observed heterosis for seed quality and for expression of amylase genes in the

genotypes studied. We found no difference in seed quality between large and small seeds.

Key words: Quantitative real-time-polymerase chain reaction; Seed quality; *Zea mays*