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Impact of *mips1*, *lpa1* and *lpa2* alleles for low phytic acid content on agronomic, seed quality and seed composition traits of soybean

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Soybean (*Glycine max* L. Merr) is an important agronomic crop around the world used largely for animal feed. However, approximately 75% of the P in soybean grain is in the form of phytic acid (PA) or phytate, the cation salt form of PA, which cannot be digested by mono- and a-gastric animals including swine, poultry, and aquacultural animals leading to decreased field efficiency and environmental detriment due to P runoff.

Soybean varieties have been developed with a reduced PA content using mutant alleles of three genes involved in the PA pathway: either the combination of *lpa1* and *lpa2* or *mips1*. However, the relationship among these alleles was unknown.

This study was to explore the impact of these three mutant alleles on soybean agronomic, seed quality, and seed composition traits. A population consisting of 30 recombinant inbred lines (RILs) developed from a cross between V03-5901 (*mips1*) x 04-05N32 (*lpa1/lpa2*) was planted along with the parents at two locations in Virginia in 2014 and 2015. The results showed that 1) an additive relationship existed among the three different mutant alleles resulting in lower PA content as more low PA (LPA) mutant alleles were added. 2) The lines with *lpa1* allele had the highest field emergence and so may be a good trait with which to create a commercially viable LPA soybean variety. 3) The interaction between the *mips1* and *lpa2* alleles resulted in raffinose content significantly lower than with either allele on its own. The findings of this study provided breeders with breeding references of developing LPA soybean varieties combined with other desirable traits.