

Nested-association mapping (NAM) based genetic dissection uncovers candidate genes for seed and pod weights in peanut (*Arachis hypogaea*)

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Summary

Multi-parental genetic mapping populations such as nested-association mapping (NAM) have great potential for investigating quantitative traits and associated genomics regions leading to rapid discovery of candidate genes and markers. To demonstrate the utility and power of this approach, two NAM populations, NAM_Tifrunner and NAM_Florida-07 which were developed by U.S. peanut research community, were used for dissecting complex traits of 100-pod weight (PW) and 100-seed weight (SW) in peanut. Two high-density SNP-based genetic maps were constructed with 3,341 loci and 2,668 loci for NAM_Tifrunner and NAM_Florida-07, respectively. QTL analysis identified 12 and 8 major effect QTLs for PW and SW, respectively, in NAM_Tifrunner, and 13 and 11 major effect QTLs for PW and SW, respectively, in NAM_Florida-07. Most of the QTLs associated with PW and SW were localized on chromosomes A05, A06, B05, and B06. A genome-wide association study (GWAS) analysis identified highly significant SNP-trait associations (STAs) for PW and SW. In total, 19 and 28 STAs were identified for PW and SW, respectively, in NAM_Tifrunner. In NAM_Florida-07, 11 and 17 STAs were identified for PW and SW, respectively. These significant STAs were co-localized on similar positions as the detected QTLs, suggesting that PW and SW are regulated by several candidate genes identified on chromosomes A05, A06, B05, and B06. This study demonstrates the utility of NAM population for genetic dissection of complex traits and performing high resolution trait mapping in peanut.

Gangurde, S.S., Wang, H., Yaduru, S., Pandey, M.K., Fountain, J.S., Chu, Y., Isleib, T., Holbrook, C.C., Xavier, A., Culbreath, A.K., Ozias-Akins, P., Varshney, R.K. and Guo, B. Nested-association mapping (NAM)-based genetic dissection uncovers candidate genes for seed and pod weights in peanut (*Arachis hypogaea*). *Plant Biotechnology Journal*, <https://doi.org/10.1111/pbi.13311>