

## **QTL Mapping and QTL×Environment Interaction Analysis of Pod and Seed Related Traits in Cultivated Peanut (*Arachis hypogaea* L.)**

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Pod and seed traits are important agronomy traits, which are closely related to yield in cultivated peanut (*Arachis hypogaea* L.). A RIL population, with 315 families was developed that derived from Jihua 5 with large pod and M130 with small pod, was used to identify molecular markers closely linked to pod and seed traits. A genetic linkage map containing 363 polymorphic loci was constructed using SSR, AhTE, SRAP, and TRAP markers. All polymorphic loci were mapped on 21 linkage groups, which spanned 1360.38 cM with an average distance of 3.75 cM.

A total of 97 QTLs for pod and seed traits were identified by ICIM method under five environments from 2017 to 2018, explaining the phenotypic variations of 2.36%–12.15% , and located on A02, A05, A08, A09, B02, B03, B04, B08, and B09 chromosomes. Among them, 9 QTLs were detected for pod length, 13 QTLs for pod width, 14 QTLs for pod thickness, 11 QTLs for seed length, 13 QTLs for seed width, 13 QTLs for hundred-pod weight, 10 QTLs for hundred-seed weight. Furthermore, 45 stable QTLs were repeatedly detected in more than three environments. QTL clusters were detected on A02, A08, B02, B04, and B08 chromosomes, respectively.