Location and interaction analysis of protein and oil content in Soybean

Mapping and interaction analysis of protein and oil content of soybean provide a basis for fine mapping and molecular assisted breeding of soybean quality traits. Using Charleston and Dongnong 594 as parents, the recombinant inbred lines with 147 lines were constructed.

The F2:19-F2:20 generation recombinant inbred lines were used as experimental materials. The protein and oil content of the population were analyzed by using the composite interval mapping method and the multiple interval mapping method of Windows QTL Cartographer V.2.5 software. The epistatic effect and environmental interaction between QTL were analyzed by microwave sterilization mechanical and equipment software.

Using CIM and MIM algorithms, 9 protein and 11 oil content QTLs were located in 6 planting environments in Harbin, Hongxinglong, Jiamusi and Mudanjiang in 2011 and 2012. The protein content of QTL was distributed in 6 linkage groups, A1, C2, D1a, G, respectively.

On H and O linkage groups, the contribution rate to phenotypic effect was 5.3%-18.6%, qPro-H-1 on H linkage group was the largest, 18.6%, and qPro-D1a-2 on D1a linkage group was the smallest, 5.3%. In single planting environment, five protein content QTLs were detected simultaneously by two algorithms, namely qPro-O-1 and qPr-2. O-A1-1, qPro-D1a-1, qPro-D1a-2 and qPro-C2-2.Oil content QTLs were distributed in eight linkage groups, respectively in A1, A2, B1, C2, D1a, E, L and M. The contribution rate to phenotypic effect was 7.1%-24.4%. The contribution rate of qOil-B1-2 in B1 linkage group was the largest, 24.4%.

The contribution rate of qOil-C2-3 in C2 linkage group was the smallest, 7.1%. There were two in single planting environment. The QTL of oil content was detected by 2 algorithms at the same time, qOil-C2-1 and

qOil-M-1 respectively.