



QTL verification of grain protein content and its correlation with oil content by using connected RIL populations of high-oil maize

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ABSTRACT. Maize with high grain protein and oil contents offers great advantages for human food and animal feed. In this study, grain protein contents of 282 and 263 $F_{7,8}$ recombinant inbred lines (RILs) of 2 crosses were evaluated in 4 environments within and between populations. The RILs were developed from crosses between an inbred high-oil maize line and 2 normal dent inbred maize lines. A total of 16 single-population QTLs and 19 joint-population QTLs were identified for protein content, and 21 QTLs were detected for protein-oil in each of the 4 environments tested and in combination. Most of the QTLs for protein content were greatly influenced by variation among populations and environments. Seven QTLs showed generational consistency compared with QTLs detected in the 2 $F_{2,3}$ populations. However, 7 and 6 QTLs were detected in only the RIL and $F_{2,3}$ populations, respectively. Protein and protein-oil QTLs with the same parental effects were detected at bins 3.03-3.05, 5.04-5.06, 6.03-6.05, 8.03-8.04, and 8.04-8.06, demonstrating that tightly linked and/or pleiotropic QTLs are controlling both traits at these bins. Four single-population QTLs and

11 joint-population QTLs identified at bins 3.02-3.03, 3.05, 7.01, 8.02, 8.03, 8.04-8.05, 8.05, 9.03, and 9.05 with intervals <5 cM could be used in marker-assisted selection. Along with the previously detected QTLs qPRO1-8-1 and qPRO1-5-1 at bins 8.03-8.04 and 5.02-5.04, the QTLs detected herein could be used to develop near isogenic lines and chromosome segment substitution lines in future studies.

Key words: High-oil maize; Grain protein and oil content; RIL population; QTL verification; Joint QTL mapping; QTL consistency