

## Abstract

Barley is an important crop, both in terms of forage production and livestock nutrition. Despite the importance of forage quality to animal performance, barley forage quality has not been used as a selection criterion in barley breeding programs. In order to study the quantitative variability of quality and quantity-related traits and to determine the genomic location which control these traits, an experiment was conducted using one hundred thirty-six doubled haploid(DH) barley lines, their two parents "Nure" and "Tremois", at the research farms of Agricultural and Natural Resource center of Zabol, Iran, in 2015. The experiment was arranged in two replications, alpha lattice design under normal and drought stress conditions. Each plot consisted of four rows that were 2/5 m in length and spaced 50 cm apart. Forage samples were collected at dough stage of maturity and weighted. Then samples were dried at 72<sup>0C</sup> for 48h. Dried samples were scaled and ground. Ground samples scored for forage quality characteristics(DMD, ADF, NDF, ADL, CF, CP, WSC and ash) by NIRs. Other traits (Leaf to Stem ratio, Seed to Forage ratio, number of tiller per plant, plant height) measured on 5 plants that randomly selected in each plot.

The main effect of genotype was highly significant for all studied traits. The maximum correlation observed between wet and dry matter(respectively  $r=0.88^{**}$ ,  $r=0.90^{**}$ ). Factor analysis extracted 4 invisible factors, when accounted for 80% of the variation. Genetics map of this population was recovered from GrainGene. QTL analysis was performed with using of a developed map, consisting DArT, AFLP and locus specific SSR markers. This map is fairly saturated and comprising 396 DArT markers with a total length of 1114 cM an average markers spacing of 2/8 cm. Sixty-eight QTLs controlling different studied traits were identified for all studied traits. Total phenotypic variance explained by these QTLs varies from 7/34 to 24/50%. Highest LOD scores were obtained for QTLs controlling plant height(Qh3Hna), on chromosome 3H, in normal condition. Although numerous QTLs were detected for forage quantity and quality-related traits and some of them were well stable but, major of them appear to be quite unstable in different conditions, therefore grain through marker-assisted selection (MAS) in population would be limited, because, environment plays a tremendous role in the phenotypic expression of forage quantity and quality-related traits and the "Nure/Tremois" population was never developed with the intention of isolating and advancing barley lines for release to the forage.

Key word: Forage quality and quantity, QTL, Double haploid, Drought stress, Nure/Tremois, Variety



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