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STRUCTURAL ANALYSIS OF THE WHEAT GENES ENCODING NADH-DEPENDENT GLUTAMINE-2-OXOGLUTARATE AMIDOTRANSFERASES (NADH-GOGAT) AND COMPARISON WITH OTHER SPECIES

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Nitrogen uptake is an essential element in crop improvement and breeding for cereal cultivars that absorb and metabolize nitrogen most efficiently for grain or silage production. Maximizing efficient nitrogen utilization is becoming increasingly important for breeders. This aim requires a better understanding of nitrogen metabolism and its regulation, and identification of target genes to monitor N uptake by either direct gene transfer or marked-assisted breeding. One of the enzymes related to nitrogen metabolism is glutamine-2-oxoglutarate amidotransferase (also known as GOGAT). Together with glutamine synthetase (GS), GOGAT maintains the flow of N from NH_4^+ into glutamine and glutamate, which are then used for several other aminotransferase reactions during amino acid synthesis. We focused on *NADH-GOGAT* gene as one of the potential candidate genes for determining grain protein content (GPC). Using a rice *NADH-GOGATI* sequence as an initial query, we identified a GOGAT gene from the wheat B-genome within previously reported wheat genomic DNAs (Goto at al., 1998). We also extracted and assembled 454-reads of cv. Chinese Spring (http://www.cerealsdb.uk.net/search_reads.htm) and the 454-reads of a *Triticum tauschii* accession (http://avena.pw.usda.gov/RHmapping/blast/). From the single wheat gene sequence and 454 reads we were able to assemble the three orthologous genes from the three hexaploid genomes and from the D-genome ancestor *Triticum tauschii*. PCR primer pairs were design for the three distinct GOGAT hexaploid sequences and used to identify genome assignments using DNA from Chinese Spring nulli-tetrasomic lines for the group 3 chromosomes. A comparison of a set of plant *NADH-GOGAT* genes (wheat, *Brachypodium*, rice and sorghum) suggests regions of greater sequence and structure conservation likely related to critical enzymatic functions and metabolic control. We also obtained the *NADH-GOGAT* genomic sequence in the two Italian durum wheat cultivars Svevo and Ciccio, characterized by different grain protein content. Polymorphism between the two cultivars could be analyzed in an RIL population derived by crossing those two cvs and evaluating grain protein content in field trials. Such polymorphisms could then be used to verify the correlation with a QTL for GPC and assess the potential implication of *NADH-GOGAT* gene in controlling this very complex trait.