

DIVERSIFICATION AND MAINTENANCE OF DISEASE RESISTANT GENES IN THE BREAD WHEAT (*TRITICUM AESTIVUM* L.) GENOME

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ABSTRACT

Use of wheat cultivars resistant to yield-reducing pathogens provides a relatively cheap and environmentally friendly method for combating crop disease. Recently available complete genome sequences of wheat (*Triticum aestivum*) and its progenitors (*T. urartu* and *Aegilops tauschii*) allow for investigation into the evolution and diversity of gene families, including those that confer resistance to pathogens, such as Coiled-coil, Nucleotide-binding-site, and Leucine-rich repeat (CNL) genes. The objectives of this study were to identify and analyze the CNL gene orthologs of *T. aestivum*, *T. urartu*, and *A. tauschii*. We identified 609, 318, and 392 CNL genes in *T. aestivum*, *T. urartu*, and *A. tauschii*, respectively. Selection pressure analyses showed that CNL genes experienced purifying selection and exhibit evolutionary patterns similar to that in barley and other grass species. Implementation of a duplication-loss model shows numerous instances where one or two of the three species experienced gene duplication or species-specific loss of their orthologs. Homology to *RPM1*, *RPP13*, *RPS2*, *Lr21*, *Yr10*, *MLA*, and many other characterized resistance genes was observed, providing a basis for functional characterization. Future studies should aim to quantify expression and signaling mechanisms regarding such genes in wheat.