# Biochemical and molecular evaluation of rust resistant bread wheat lines

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**Abstract**

Incorporation of different resistant genes/quantitative trait loci (QTL) against the three wheat rusts (stem, leaf and stripe rust) into a single wheat line using gene-pyramiding and marker-assisted selection (MAS) allows protection against these diseases. However, gene-pyramiding can cause decreases in baking quality characteristics which are important for the milling and baking industry as well as consumers. The aim of the study was to evaluate rust resistant lines for good protein content using molecular marker data as well as biochemical data generated over a two year period. Lines were evaluated for the presence of five rust resistant genes/QTL (*Lr19, Lr34/Yr18/Sr57, QYr.sgi.2B-1, Sr2* and *Sr26*) for two consecutive breeding cycles. These lines were also subjected to sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) and size-exclusion high performance liquid chromatography (SE-HPLC) to determine various protein quality characteristics based on single seed analyses. Results indicated that the most resistant lines did not necessarily had the best bread-making qualities and vice versa. Results also indicated that lines were firstly selected based on rust resistance followed by selection for protein quality alleles and lastly the large polymeric proteins percentage (LUPP%). The best rust resistant lines to be used in future breeding programmes were identified based on both rust resistance and quality characteristics.