Identification of markers closely linked to effective leaf rust resistance genes of wheat

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Leaf rust, caused by *Puccinia triticina*, is the most common and widespread disease of wheat (*Triticum aestivum*) worldwide. Leaf rust causes a reduction of grain quality and yield losses of up to 40%. Epidemics are common due to a breakdown of leaf rust (*Lr*-) resistances by virulent rust races. An example for a breakdown is *Lr37*, which became ineffective within two years in 2006. One option to avoid epidemics is pyramiding of *Lr*-genes. A prerequisite for pyramiding are closely linked molecular markers and knowledge about the genetic background of *Lr*-genes. Today, more than 80 *Lr*-genes have been identified, but only a part of these have been deployed in wheat varieties due to linkage drag. One of the resistance genes showing a high level of resistance in the field is *Lr24* located on chromosome 3DL. The introgression consisting *Lr24* comprises more than 600 Megabases (MB). Hence no physically closely linked markers are available up to now. In order to get detailed information on its localization and to reduce linkage drag, a near isogenic line (NIL) containing *Lr24* was crossed to the susceptible cultivar Monopol. Parental lines and F_2 plants were inoculated with a single spore isolate of a leaf rust isolate avirulent to *Lr24*.The population was rated using the McIntosh scale on leaf material of parental lines and 144 (*Lr24*) F_2 plants at 10 days after inoculation. First results of the analysis proved the dominant inheritance of *Lr24* with 3r:1s segregation ($\chi2=0.39$). This result was validated by microscopical analyses of the fungal development 72h after inoculation. Based on these results kompetitive allele specific PCR markers (KASP) have been developed based on SNPs detected between the near isogenic line (NIL-L*r24*) and the susceptible parental line (Monopol). One of 28 KASP markers analyzed in bulked segregant analysis differentiated exactly between susceptible and resistant lines so that a physical region of 10 MB up and downstream from the marker position was aligned to the reference genome. One candidate gene for *Lr24* was identified. The next step will be allele specific sequencing of the candidate gene in order to identify mutations within the exons. SNPs analyses of additional F_2 populations segregating for effective resistances (e.g.*Lr27, 31, Lr9, Lr19*) are in progress.