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QTLs associated with quality traits in oat DH mapping population

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Doubled haploids (DH) improve the efficiency of the genetic analysis due to instant and total homozygosity. Until recently, low production rates limited the use of DH lines in oats (*Avena sativa* L.). In this study, a mapping population of 144 DH plants was generated through anther culture of F_1 plants from the cross Aslak × Matilda, by a method lately developed in our laboratory. A linkage map was built to locate QTLs (quantitative trait loci) for oil content, β-glucan content, and leaf spot disease resistance. A variety of PCR-based DNA markers have been analysed in the DH progeny, including microsatellites, RAPDs (random amplified polymorphic DNAs), REMAPs (retrotransposon-microsatellite amplified polymorphisms), ISSRs (inter simple sequence repeats), SRAPs (sequence characterized amplified regions) and AFLPs (amplified fragment length polymorphism). Resistance to *Pyrenophora avenae* has been evaluated in a greenhouse test and β-glucan and oil content analyses are done from the yield of the field trial. Results from the QTL analyses will be shown and discussed. According to our knowledge, this is the first genetic linkage map of oats based on an anther culture derived DH population. Our final goal is to provide marker-assisted tools for more efficient oat breeding.