

Oat QTL on GrainGenes

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This year has seen the addition to the GrainGenes 2.0 database (<https://wheat.pw.usda.gov/GG3/>) of a significant quantity of linkage and association map data for oat. Recent additions include the Oat-2016-Consensus map, bi-parental linkage maps (AC Assiniboia/MN841801, CDC Boyer/94197A1-9-2-2-2-5, Dal/Exeter, Hurdal/Z-597, IL86-1156/Clintland, IL86-6404/Clintland, Kanota/Ogle, Otana/PI269626, Ogle/TAM O-301, Provena/CDC Boyer, Provena/94197A1-9-2-2-2-5, and CDC Sol-Fi/HiFi) and QTL from CORE GWAS analyses of BYDV and Crown Rust resistance. Using the built-in CMap viewer, the relative map positions of markers and QTL can be compared across linkage maps. We used CMap to explore the positional relationships among oat genes characterized using segregation analysis, genes and QTL mapped using RFLP and SSR markers, and QTL mapped after the advent of iSelect and genome-by-sequencing marker technologies. We illustrate two methods of approaching comparative mapping in oat using the GrainGenes resources: 1) Focusing down by exploring matches between linkage groups and a reference genome; and 2) Building up from a specific QTL to identify linked QTL from other mapping efforts.