# Anchoring the genetic map of near-isogenic introgression lines carrying wild emmer QTL-fragments for drought tolerance to the physical map of *Triticum diccocum*

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Until now wheat breeders had to rely on genetic maps due to the lack of the genome sequence. However, genetic and physical distances may differ significantly from each other, especially in centromeric and telomeric regions. This biased picture might lead to incorrect assumptions and estimations about the size and complexity of QTL-regions, the selection of suitable molecular markers and their suitability to transfer respective QTLs into near-isogenic lines (NILs). The rising availability of cereal genomic sequences and their annotations delivers a first standard that offers the possibility to dissolve this distorted picture and to get a better idea about the physical size of QTL-regions and the number of genes involved.

Suitable free open software packages that allow the comparison of genetic and physical data of NILs from their respective parents to our best knowledge doesn´t exist. We therefore developed a very simple Java-program that can be executed as a "*.jar*" file so that scientists without any programming-skills will be able to use it. Furthermore, the source code of the program will be published so that the code can easily be copied or implemented into other software packages.

We tested the algorithm on two promising NILs that carry QTL-regions for drought tolerance from wild emmer (*T. diccocoides*) on chromosome 2BS and 7AS. Both NILs suffer from linkage drag and were previously established with SSR markers that flank the regions of interest. Recently, these NILs, their respective recurrent parents and $F_6$ descendents of the original mapping population were genotyped using the 15k-iSelect Illumina chip to improve the resolution of the previously calculated genetic map. This data and the availability of the physical wild emmer genome finally allowed us to get detailed information on these introgressions. The analysis revealed, e.g. that the centromeric regions of the wild emmer chromosomes were transmitted into both NILs. The physical segments of wild emmer cover significantly more than half of the corresponding physical size of the chromosomes. This may partly explain the linkage drag in both NILs.

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