A HIGH-DENSITY GENETIC MAP OF WINTER RYE (*SECALE CEREALE* L.) BASED ON DARTSEQ AND *SILICO* DART MARKERS

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WINTER RYE is an important cereal in Middle and Eastern Europe. Its breeding is dominated by hybrids based on cytoplasmic male sterility Pampa. Whereas many genetic maps of rye constructed on numerous marker platforms are available (Milczarski 2007), the one based on DArTseq and silicoDArT markers is still missing. This technology delivers the opportunity to generate a significant number of reproducible markers with minimum missing data and thus is a reasonable choice for the construction of highly saturated genetic map with limited gaps. Such a map could be used for the identification of markers linked to the trait of interest.

MATERIALS AND METHODS

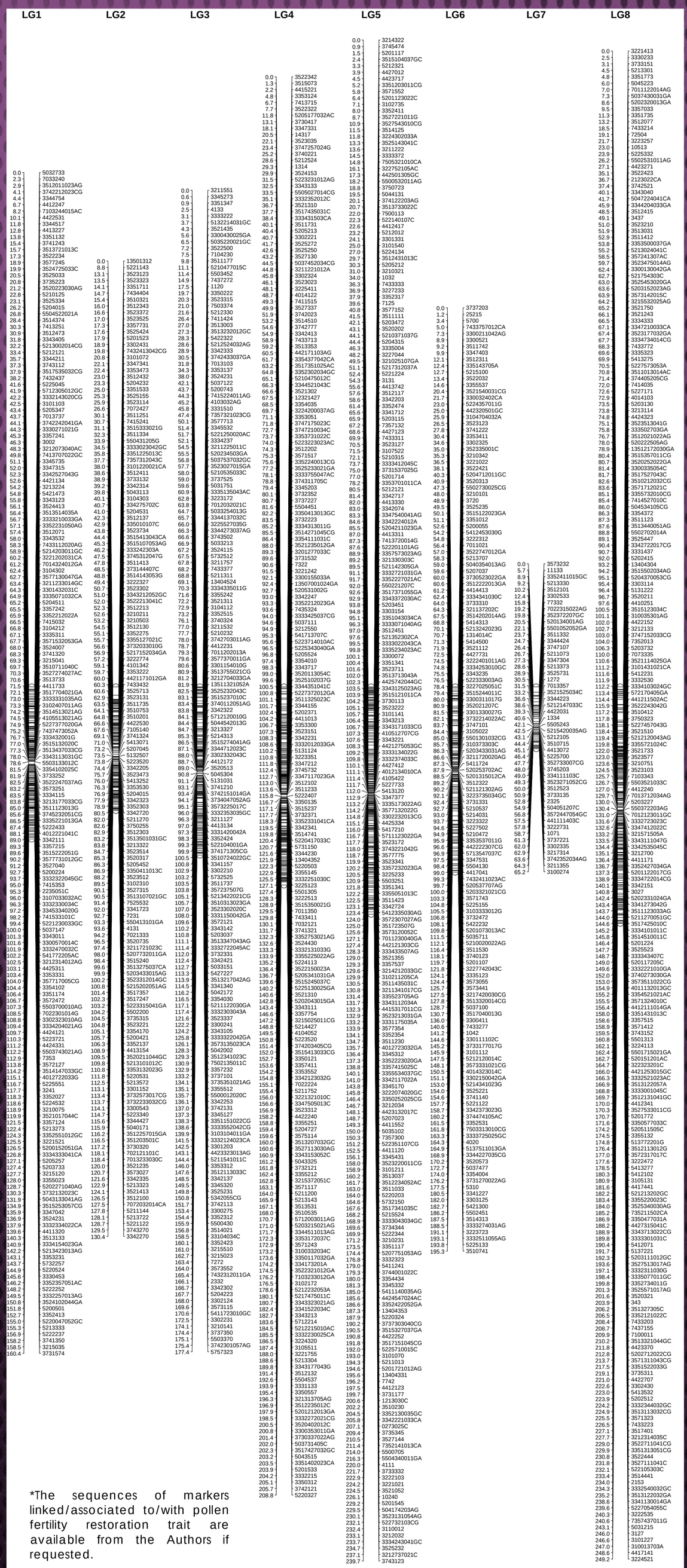
The mapping population based on 190 recombinant inbred lines (F7) derived from a cross S305N/00 x S037R/05 was used for genotyping with DArTseq markers.

The genetic map was constructed under Multi Point Ultra Dense software.

Table 1. Arrangement of mapping data evaluated for the RIL7 mapping population.

Linkage Group	1	2	3	4	5	6	7	8	total
Length (cM)	160	130	177	209	240	196	65	249	1406
No. of skeleton markers	185	153	182	222	238	148	49	236	1413
No. of redundant markers	1501	863	698	1024	1341	776	98	1262	7563
Density (markers/1 cM)	1,32	1,17	1,03	1,06	0,99	0,76	0,75	0,95	1,00
Longest gap (cM)	3,34	8,82	4,81	5,02	4,2	6,46	5,74	7,92	8,82

Figure 1. Genetic map of the population RIL 7 (S64/04/01): S305N/00 x S037R/05 constructed based on DArTseq and silicoDArT markers.



*The sequences of markers linked/associated to/with pollen fertility restoration trait are available from the Authors if requested.

RESULTS

In total 35 991 DArTseq markers (SNP marker) and 128 016 silico DArT were evaluated.

Markers with impaired segregation of Chi2 > 19.4 and missing data above 17 were omitted from the analysis.

Genetic map consisted of eight linkage groups saturated with 2733 skeletal, 14 509 redundant, mainly silico DArT markers and spanned over 1406,31 cM. The largest group covered 249.22 cM whereas the shortest 65.23 cM. The biggest gap was 8.82 cM long. On average there was one marker per 1 cM.

All linkage groups were univocally assigned to rye chromosomes based on the known chromosomal location of the markers on wheat genetic maps using synteny.

Genetic mapping was done twice to verify whether marker order and the number of linkage groups were constructed properly.

SUMMARY

1. Derivation the RIL7 of inbred lines (S64/04/01): S305N/00 x SO37R/05 followed by genetic mapping using DArTseq and silicoDArT markers, enabled the development of a highly-dense genetic map of rye (Figure 1) with limited gaps.
2. Identification of various redundant markers makes it possible choosing suitable marker (variants of the markers) linked to any examined feature.
3. The constructed genetic map is dedicated to the identification of DNA-based markers linked to pollen fertility restoration genes suitable in Pampa sterilizing cytoplasm system.

REFERENCES

- Milczarski P., Banek-Tabor A., Lebiecka K., Stojałowski S., Myśków B., Masojć New genetic map of rye composed of PCR-based molecular markers and its alignment with the reference map of the DS2 x RXL10 intercross. J Appl Genet. 2007;48(1):11-24.
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