Recombination rates across A. lyrata linkage groups 1 and 2

Figure 1 shows estimates of recombination rate across the region surveyed, in *A. thaliana*, *A. lyrata*, and an outgroup species, *C. rubella*. Rate estimates are based on physical distances in *A. thaliana*, and genetic mapping data from *A. thaliana* (Arabidopsis Genome Initiative), *A. lyrata* (HANSSON *et al.* 2006; KUITTINEN and AGUADE 2000; KUITTINEN *et al.* 2004), and *C. rubella* (BOIVIN *et al.* 2004). The *A. thaliana* first chromosome is homeologous to two linkage groups in *A. lyrata* and *C. rubella* (hereafter called LG1 and LG2). LG1 shows a very high correlation in estimated recombination rates across the species, and the complete linkage of pericentromeric markers on the *A. lyrata* genetic map suggests conservation of the centromere location (Figure 2; see HANSSON *et al.* 2006). In LG2, recombination rate estimates are substantially higher in both *A. lyrata* and *C. rubella* than in *A. thaliana*. This is most likely due to the fact that, in the first two species without the chromosome fusion, LG2 is a significantly shorter chromosome arm than in *A. thaliana*, which is often associated higher crossing-over per unit of physical distance (KABACK *et al.* 1999). However, other possibilities are that physical distances are disproportionately increased in this region, additional small rearrangements have occurred in this region, or that low marker density and/or incomplete mapping resolution are generating discrepancies. Because of this uncertainty, we did all analyses using both estimates of recombination rates, those based on *A. thaliana* and those based on *A. lyrata*.

BOIVIN, K., A. ACARKAN, R. S. MBULU, O. CLARENZ and R. SCHMIDT, 2004 The Arabidopsis genome sequence as a tool for genome analysis in Brassicaceae. A comparison of the Arabidopsis and Capsella rubella genomes. Plant Physiol **135:** 735-744.

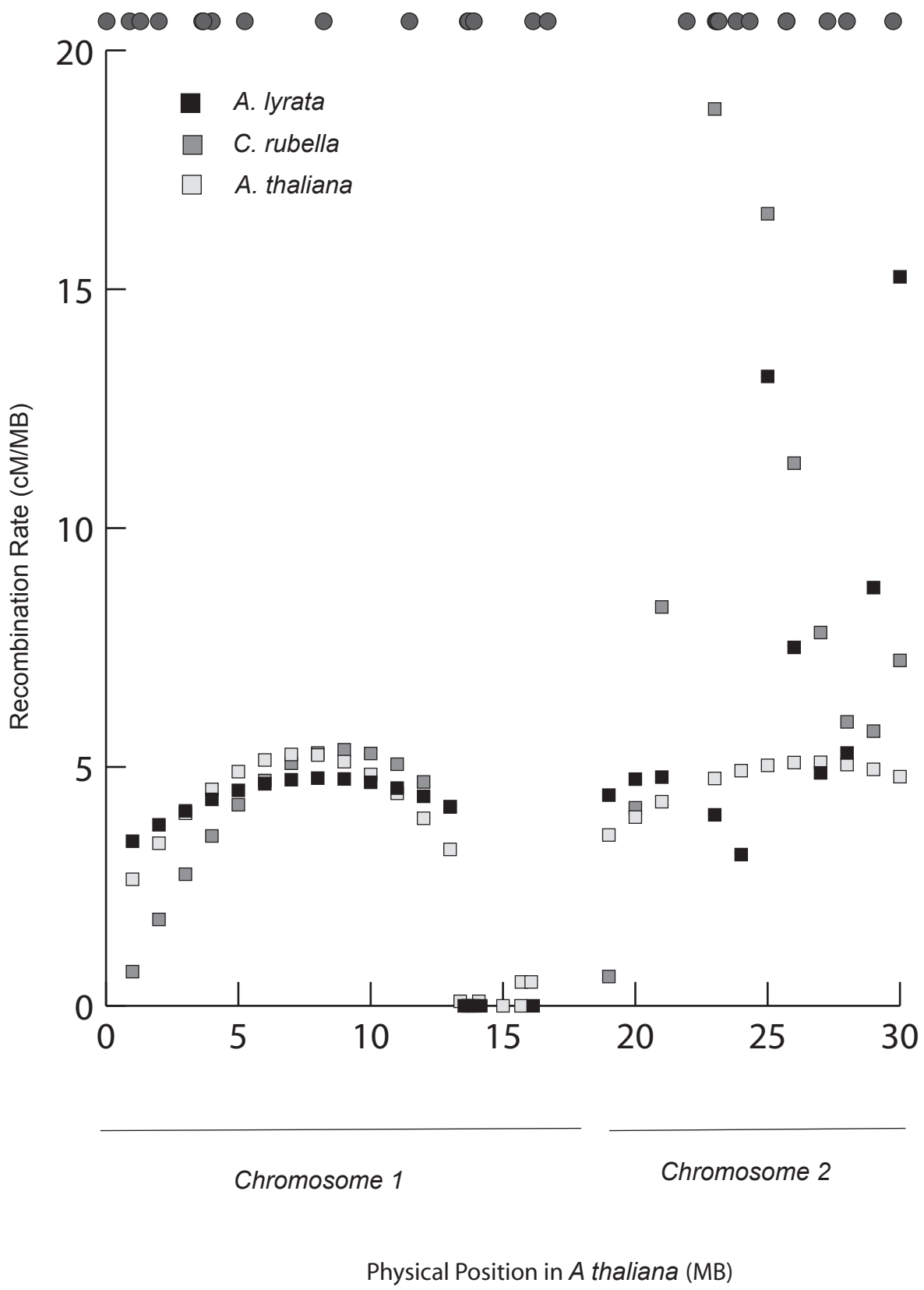
HANSSON, B., A. KAWABE, S. PREUSS, H. KUITTINEN and D. CHARLESWORTH, 2006 Comparative gene mapping in Arabidopsis lyrata chromosomes 1 and 2 and the corresponding A. thaliana chromosome 1: recombination rates, rearrangements and centromere location. Genet Res **In Press**.

KABACK, D. B., D. BARBER, J. MAHON, J. LAMB and J. YOU, 1999 Chromosome size-dependent control of meiotic reciprocal recombination in Saccharomyces cerevisiae: the role of crossover interference. Genetics **152:** 1475-1486.

KUITTINEN, H., and M. AGUADE, 2000 Nucleotide variation at the CHALCONE ISOMERASE locus in Arabidopsis thaliana. Genetics **155:** 863-872.

KUITTINEN, H., A. A. DE HAAN, C. VOGL, S. OIKARINEN, J. LEPPALA *et al.*, 2004 Comparing the linkage maps of the close relatives Arabidopsis lyrata and A. thaliana. Genetics **168:** 1575-1584.

Figure 1- Estimates of scaled recombination rate across the *A. thaliana* chromosome 1, from *A. thaliana*, *A. lyrata*, and *C. rubella*. Light gray squares, *A. thaliana*, black squares, *A. lyrata*; dark gray squares, *C. rubella*. Black circles show the positions of the genes surveyed in this study. LG1 and LG2 refer to the first and second linkage groups in *A. lyrata*.


A. lyrata
C. rubella
A. thaliana
Recombination Rate (cM/MB)
0
5
10
15
20
0
5
10
15
20
25
30
Chromosome 1
Chromosome 2
Physical Position in A thaliana (MB)