Fine Mapping of Quantitative Trait Loci Using Selected Overlapping Recombinant Chromosomes, in an Interspecies Cross of Tomato

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somal segments carrying the RFLP and identified and

their regions of overlap determined using all available

of 237 backcross progeny of *L. esculentum* × *L.*

recurrent) × *L. chmielewskii* accession LA1063 (CL), was

determined previously using 79 DNA markers spanning 852

none of the remaining nonlarge segments

Six BC2 individuals with different ge

a different BC2 population, and derive

Genotyping and linkage analysis: RFLP genotypes were determined as described in TANKSLEY and HEWITT (1988),

previously found biparental (F_2) transmission to yield a *larger* recombination fraction than paternal (BC)

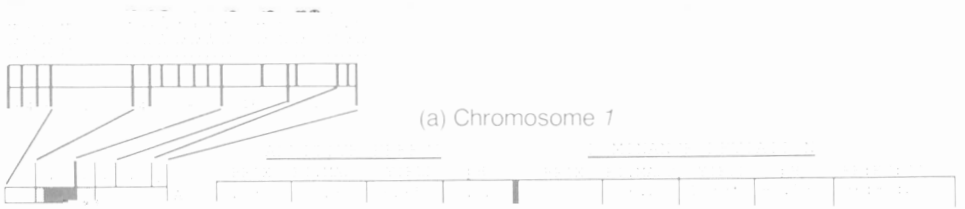

FIGURE 5.—Substitution mapping of QTLs in 5 genomic regions of *L. esculentum* × *L. chmielewskii* BC2F2. (a) Effects at *TG19* linked to different chromosome *1* recombinants. (b) Effects at *CD35* linked to different chromosome *2* recombinants. (c) Effects at *TG32* linked to different

solids of about 0.6° Brix (PATERSON *et al.* 1988). In the present study, phenotypic effects were determined for five CL segments which overlapped at *TG19* (Figure 2a). A significant additive effect on solids of +0.58° Brix was unique to the only segment (E) carrying the CL region from *TG158* to beyond *TG27*, a distance of at least 2 cM. Reductions of fruit mass and yield were found for three segments (C, D, E), which differ from the two segments (A, B) not showing these effects, in that they carry a CL interval of about 3 cM,

is found for segments A, C, D, and E, overlapping in the *TG295-TG19* region. The effect of segment B is large but not significant; if it also carries the factor, the overlapping region would exclude *TG295*. Elevated pH is significant for two segments (B, E) and just shy of significance for two more (C, D). These differ from the only segment not affecting pH (A), in that they carry the CL interval from *TG19-TG17*, about 6 cM. Thus, soluble solids is elevated by one or more CL factor(s) between *TG158* and the *TG27* end

of heterozygotes might be increased by factor(s) near *TG19*, and pH might be increased by factor(s) between

significant additive effect on soluble solids (+0.46°Brix). Segment K shows a significant domi-

per fruit were significant interactions consistently more frequent than the random expectation of 5%. Single-locus additivity and dominance appear to ex-

SLEY and HEWITT 1988), will be important in assessing the role of epistasis in quantitative inheritance. However, both the current results and previous evidence

inbred strains (HALDANE and WADDINGTON, 1931; BURR *et al.* 1988), might permit one to determine orientation of markers as little as 1 cM apart. Physical mapping of genetic markers (COULSON *et al.* 1988; GANAL, YOUNG and TANKSLEY 1989), should improve resolution of both genetic maps and substitution map-

our CL chromosome 5, fewer flanking "preferred sites" would be present, and less shrinkage would be observed.

Recombination shrinkage may be particularly pronounced in wide crosses such as we have studied here, where greater sequence-divergence would result in

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