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 RFLPs are identified, and their regions of overlap determined using all available

cating QTLs affecting the phenotype(s) to lie in intervals of as little as 3 cM by which the segments differed. Some associations between different traits were attrib-

FIGURE 1.—Pedigree of a single BC2F1 plant, based on genotype at DNA markers. Genotype of an interval is inferred from genotype at markers flanking the interval. Overlines represent homozygosity

populations
d. From each
ed the target
gments. [For
he backcross
egments, and
own (Figure

the gap between linkage mapping and physical mapping of QTLs.

MATERIALS AND METHODS

Construction of genetic stocks: The genetic composition

second time to E. Each plant in the six BC2F
(12–64 plants each; total ~200) was genotype
population, one plant was selected which retain
CL segments but was free of the nontarget se
example, one of 64 individuals grown from
of 121.08 to E carried each of the four target s
none of the remaining nontarget segments k

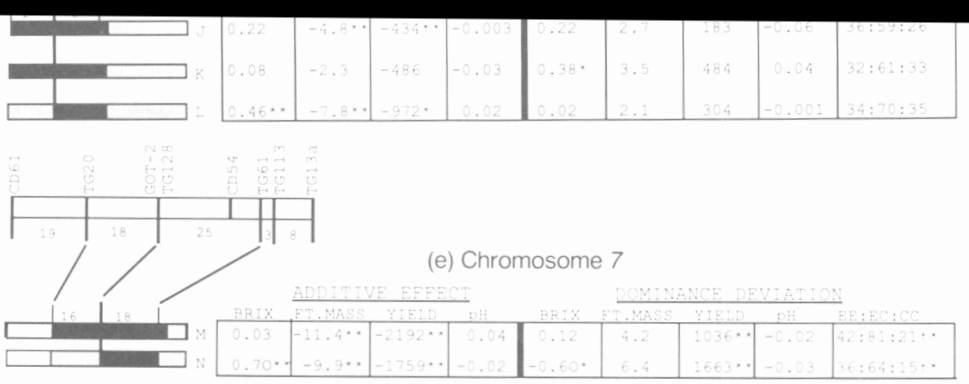
es per fruit, soluble solids
pH were determined as
(1988). Plant yield was
on each plant, when most

[BC1F2] progeny were grown in the field. Several of the BC1F2 families showed partial or complete sterility, and were discarded. From the remaining families, each plant was genotyped. Individuals retaining the target CL segments, but carrying a minimal number of nontarget segments, were selected. [For example, plant #121.08 carried

175 cm between rows. Average
concentration (°Brix), and
described in TANKSLEY and HEW
measured as total weight of frui
fruit were mature.

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)



J	0.22	-4.8**	-434**	-0.003	0.22	2.7	183	-0.06	36:59:26
K	0.08	-2.3	-486	-0.03	0.38*	3.5	484	0.04	32:61:33
L	0.46**	-7.8**	-972*	0.02	0.02	2.1	304	-0.001	34:70:35

nant segments, the marker used to determine segment effects is indicated by a vertical line through the corresponding segments. Additive effects and dominance deviations for soluble solids concentration are expressed in °Brix, mass per fruit and plant yield in grams (g), and pH in original units. * and ** indicate significance at experimentwise error rates of ≥5% and ≥1%, respectively. † and ‡ indicate significant deviation from expected allele (1:1) and genotype (1:2:1) frequencies, respectively.

solids of about 0.6°Brix (PATERSON *et al.* 1988). In is found for segments A, C, D, and E, overlapping in

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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