

Table x.1

Target Control Ratio and Minimal population size when the target is a known gene.

a) Target controlled by single marker

Target-Marker	Target Control Ratio (TCR %)					Nmin
Distance (cM)	BC1	BC2	BC3	BC5	BC10	
1	99.0	98.0	97.1	95.1	90.5	7
3	97.1	94.3	91.5	86.3	74.4	7
5	95.2	90.7	86.4	78.4	61.4	7
10	90.9	82.7	75.2	62.2	38.7	7
15	87.0	75.8	65.9	50.0	25.0	7
20	83.5	69.7	58.3	40.6	16.5	7
25	80.3	64.5	51.8	33.4	11.2	7
30	77.4	60.0	46.4	27.9	7.8	7

b) Target controlled by marker bracket

Target-Marker	Target Control Ratio (TCR %)					Nmin
Distance (cM)	BC1	BC2	BC3	BC5	BC10	
1	100.0	100.0	100.0	100.0	99.9	7
3	99.9	99.8	99.7	99.6	99.1	8
5	99.8	99.5	99.3	98.8	97.5	8
10	99.0	98.0	97.1	95.2	90.6	9
15	97.8	95.7	93.6	89.6	80.3	10
20	96.3	92.6	89.2	82.6	68.2	11
25	94.3	89.0	84.0	74.7	55.8	12
30	92.2	85.0	78.3	66.5	44.3	12

TCR(%) is the probability that an individual at the given BC generation has the desired genotype at the target given that it has the desired genotype at the flanking marker(s). Nmin is the minimum number of individuals that should be genotyped at each BC generation to obtain at least one individual with the desired genotype at the flanking marker(s) with risk $\alpha_M=1\%$. See text for details.

Table x.2**Target Control Ratio and Minimal population size when the target is a QTL.**

Confidence Interval Length (cM)	Number of markers	Optimal marker positions (distance from marker to expected QTL position, cM)					TCR (%)		N _{min}
							BC1	BC3	
10	1	0.0					98.5	95.6	7
	2	-3.6	+3.6				99.9	99.6	8
	3	-4.7	0.0	+4.7			100.0	99.9	8
	4	-5.4	-1.4	+1.4	+5.4		100.0	99.9	8
	5	-5.9	-2.2	0.0	+2.2	+5.9	100.0	100.0	8
20	1	0.0					97.0	91.5	7
	2	-6.2	+6.2				99.6	98.7	8
	3	-8.5	0.0	+8.5			99.8	99.5	9
	4	-9.9	-2.6	+2.6	+9.9		99.9	99.8	9
	5	-10.8	-4.1	0.0	+4.1	+10.8	100.0	99.9	9
40	1	0.0					94.4	84.5	7
	2	-10.4	+10.4				98.7	96.4	9
	3	-14.9	0.0	+14.9			99.5	98.5	10
	4	-17.7	-4.8	+4.8	+17.7		99.7	99.2	11
	5	-19.6	-7.8	0.0	+7.8	+19.6	99.8	99.5	11
60	1	0.0					91.9	78.5	7
	2	-14.0	+14.0				97.8	93.6	10
	3	-20.5	0.0	+20.5			99.0	97.1	11
	4	-24.6	-6.8	+6.8	+24.6		99.5	98.4	13
	5	-27.5	-11.2	0.0	+11.2	+27.5	99.7	99.0	13

TCR(%) is the probability that an individual at the given BC generation has the desired genotype at the target given that it has the desired genotype at the flanking marker(s). N_{min} is the minimum number of individuals that should be genotyped at each BC generation to obtain at least one individual with the desired genotype at the flanking marker(s) with risk $\alpha_M=1\%$. See text for details.

Table x.3**Example of optimal populations sizes computed by the *popmin* program.**

Maximal duration (n)	Generation (BC _k)	Population size (N _k)	Cumulated genotypings (G _k = $\sum_{i \leq k} N_i$)	Probability of success (S _k)	Cumulated probability ($\sum_{i \leq k} S_i$)	Averaged genotypings ($\sum_{i \leq k} G_i S_i$) / ($\sum_{i \leq k} S_i$)
1	BC ₁	23961	23961	.99	.99	23961
2	BC ₁	290	290	.05	.05	290
	BC ₂	499	789	.94	.99	764
3	BC ₁	117	117	.02	.02	117
	BC ₂	171	288	.72	.74	283
	BC ₃	370	658	.25	.99	378
4	BC ₁	72	72	.01	.01	72
	BC ₂	95	167	.46	.47	165
	BC ₃	143	310	.37	.84	229
	BC ₄	303	613	.15	.99	287
5	BC ₁	52	52	.01	.01	52
	BC ₂	64	116	.30	.31	114
	BC ₃	86	202	.34	.65	160
	BC ₄	130	332	.24	.89	206
	BC ₅	259	591	.10	.99	245

Selection for the reduction of linkage drag with two markers located at 2 cM on each side of the target. BC schemes with different total durations n, each with a global risk of $\alpha=1\%$. The probability of success is the probability to obtain a double recombinant genotype at the given generation. See text for details.

Table x.4
Optimal positions of markers for background selection on non-carrier
chromosomes.

Markers per chromosome	Generation	Optimal marker positions (cM)			RGC (%)	
		d*	d*-	d*+	Selection	No selection
2	BC ₁	18.6	10.4	27.0	93.4	75
	BC ₂	21.4	10.0	32.8	95.2	87.5
	BC ₃	22.9	7.1	38.6	96.9	93.75
3	BC ₁	8.4	0	17.9	97.1	75
	BC ₂	11.0	0	23.5	97.6	87.5
	BC ₃	12.6	0	29.7	98.3	93.75
4	BC ₁	4.5	0	14.4	98.5	75
	BC ₂	6.5	0	19.5	98.6	87.5
	BC ₃	7.8	0	25.2	98.9	93.75

Results are given for a chromosome of length 100 cM, for different numbers of markers per chromosome, at different backcross generations. Optimal marker positions are described by the distance d* (in Haldane centimorgans) from the telomere to the first marker on each chromosome end. Other markers are evenly located on the rest of the chromosome. RGC(%) with selection is the expected Recipient Genome Content for individuals that are homozygous for the recipient allele at all markers. RGC with no selection is recalled for comparison. d*- and d*+ give the range of d values for which RGC is not decrease by more than 1% compared to the value at d*. Data from Servin and Hospital (2002).

Table x.5
Efficiency of a typical marker-assisted backcross scheme.

Generation	Population Size	Homozygosity at selected markers (%)		RGC%	No selection
		Carrier chromosome	Non-carrier chromosomes		
BC ₁	70	38.4	60.6	79.0	75.0
BC ₂	100	73.6	87.4	92.2	87.5
BC ₃	150	93.0	98.8	98.0	93.7
BC ₄	300	100.0	100.0	99.0	96.9

Results of simulations averaged over 1000 replicates. See text for details of the selection strategy. RGC% gives the efficiency of selection over the complete genome (marker and non-marker loci). No selection give the RGC% values if no selection on markers was performed for comparison.