

Table 1. Estimates of genetic diversity (θ), recombination (r and C), and growth (g) for *pro*, *rt* and *env* in each twin.

LAMARC's confidence intervals (5% and 95%) around the estimates of each parameter are given between brackets. N_s = Number of sequences.

	Genes	N_s	θ	r (c/ μ)	C	g
Twin A	<i>pro</i>	31	0.44 [0.23 - 0.92]	0.07 [0.02 - 0.17]	0.03 [0.005 - 0.16]	324 [222 - 426]
	<i>rt</i>	28	0.26 [0.14 - 0.6]	0.23 [0.1 - 0.38]	0.06 [0.01 - 0.23]	177 [86 - 277]
	<i>env</i>	33	0.2 [0.13 - 0.33]	0.03 [0.01 - 0.07]	0.01 [0.001 - 0.02]	42 [19 - 66]
Twin B	<i>pro</i>	28	0.2 [0.09 - 0.71]	0.1 [0.003 - 0.47]	0.02 [0.0003 - 0.33]	175 [65 - 480]
	<i>rt</i>	25	0.12 [0.07 - 0.24]	0.14 [0.04 - 0.25]	0.02 [0.003 - 0.06]	81 [27 - 165]
	<i>env</i>	32	0.1 [0.06 - 0.16]	0.02 [0.01 - 0.07]	0.002 [0.001 - 0.01]	13 [(-18) - 41]