

Table 1 Segregation patterns, Chi-square and *P*-values for *Rht3* mapping population

Cross	No. F _{2,3} families			$\chi^2_{(1:2:1)}$	<i>P</i> -value
	Homozygous tall	Heterozygous	Homozygous short		
Burt <i>Rht3</i> × Indian	30	68	33	0.42	0.81

Note: Genotypes of the F₂ plants were determined by progeny testing in F_{2,3} and are represented in 1:2:1 segregation