

**Table S3.** Generalized linear model fit to the data on PCR presence/absence data. The model used fit the year and region from which strains were collect (see Supplementary Table 1), plus an interaction term, to the presence or absence of P-element in that strain, and used a binomial error model. (I.e, the call in R `glm(formula = cbind(present,absent) ~ year * region, family = "binomial")`)

	odds-ratio estimate	std error	z	p-value
(Intercept)	-9.11E+02	1.75E+02	-5.216	1.83E-07 ***
year	4.53E-01	8.68E-02	5.218	1.81E-07 ***
region(Americas)	-1.27E+03	4.76E+02	-2.664	0.00772 **
region(Europe)	-2.33E+02	2.24E+02	-1.041	0.29799
interaction year x region(Americas)	6.31E-01	2.37E-01	2.663	0.00773 **
interaction year x region(Europe)	1.16E-01	1.11E-01	1.045	0.29625

\*\*\*p<0.001, \*\*p<0.01