

Table S1. Expected amplicon size with each primer pair from genome assemblies

Locus	Primers	Expected size (kb)	
		HM-1:IMSS	Rahman
13	13.1 F/13.2 R	1.4	0.83
	13.1 F/SINE R	0.21	-
	13.1 F/13.1R	1.1	0.42
17	17.1 F/17.1 R	2.53	2.0
	17.2 F/17.2 R	0.79	0.23
	17.2 R/SINE R	0.13	-
19	19.1 F/ 19.1 R	2.1	1.55
	19.3 F/19.3 R	0.91	0.32
	19.3 F/0.16 SINE F	0.66	-
42	42.1 F/ 42.1 R	3.7	5.2
18	18 F/18 R	0.96	0.24
50	50 F/50 R	0.86	0.16

Primers not matching *E. dispar* are in boldface.