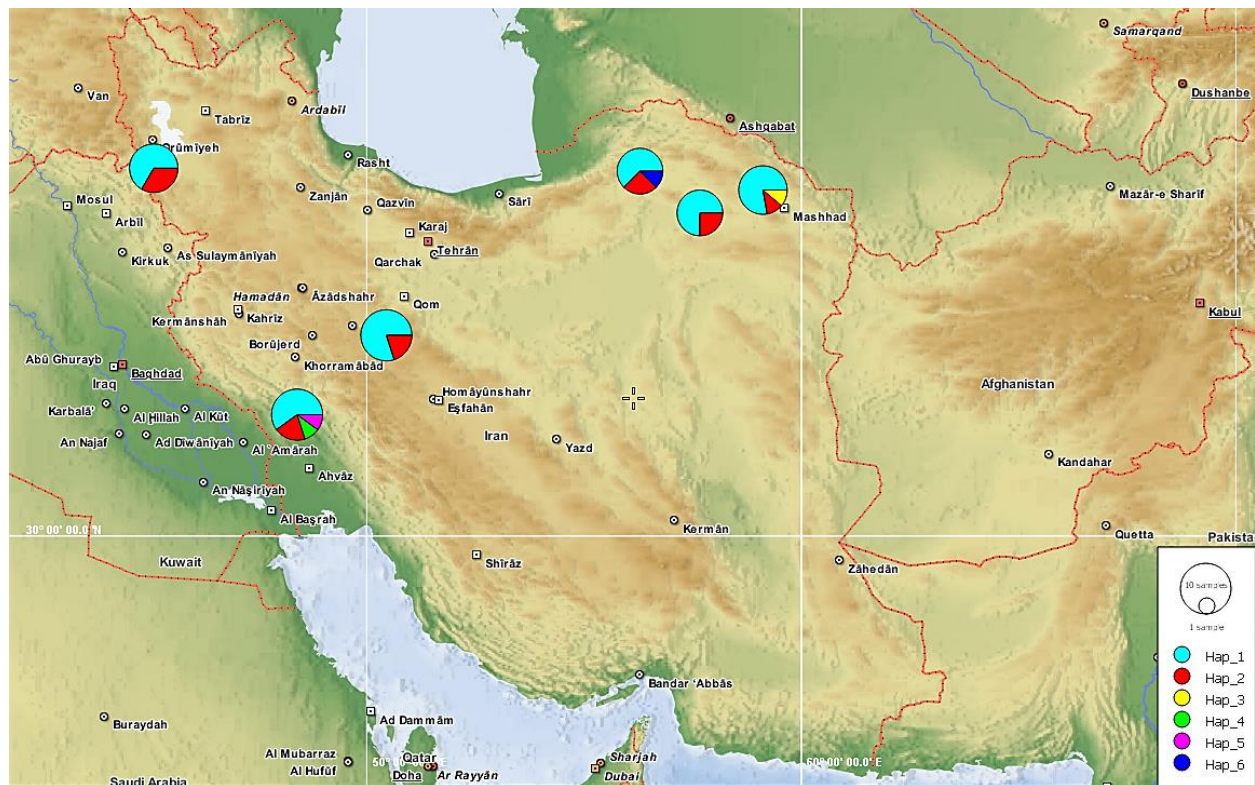
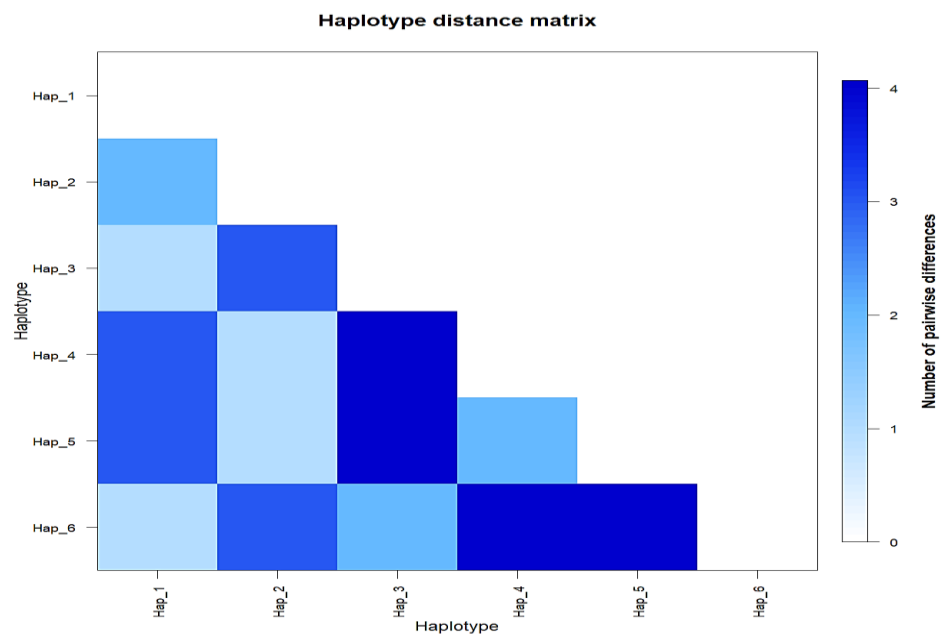


Table S1. Analysed sequences of *Spodoptera exigua* obtained from NCBI GenBank with sampling site country, accession numbers, and quantity of analyzed specimens (N), including Iranian sequences from this study.

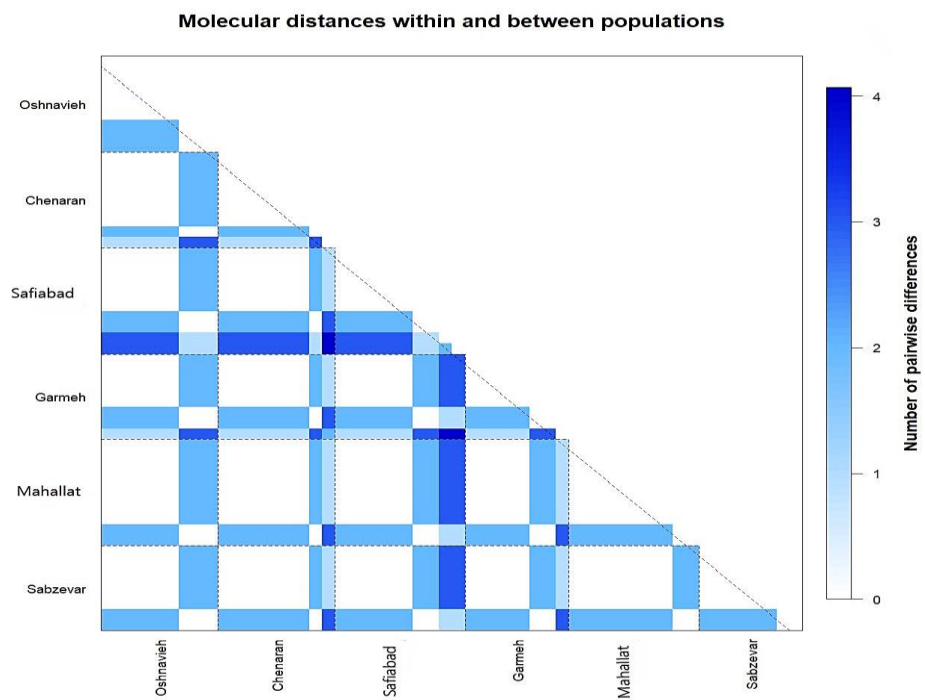
Country	N	Accession numbers
India	2	MZ297458, MZ297462
China	2	MK860943, MK860944
Jamaica	2	MT881741, MT881725
Indonesia	2	MN457694, MZ323866
Pakistan	2	HQ991336, MT449726
Malta	2	MW306009, MW306011
USA	2	MW665995, EU779856
Finland	1	JF853552
Italy	2	HQ565253, KX045943
Netherland	1	KJ634291
Portugal	1	OQ564362
Canada	2	GU687828, KX281220
Mexico	1	MK318332
Australia	1	OL539272
Germany	1	HM914242
Iran	54	PQ765817-PQ765820, PQ765822-PQ765831, PQ765833-PQ765846, PQ765848-PQ765854, PQ765856- PQ765869, PQ765871- PQ765875



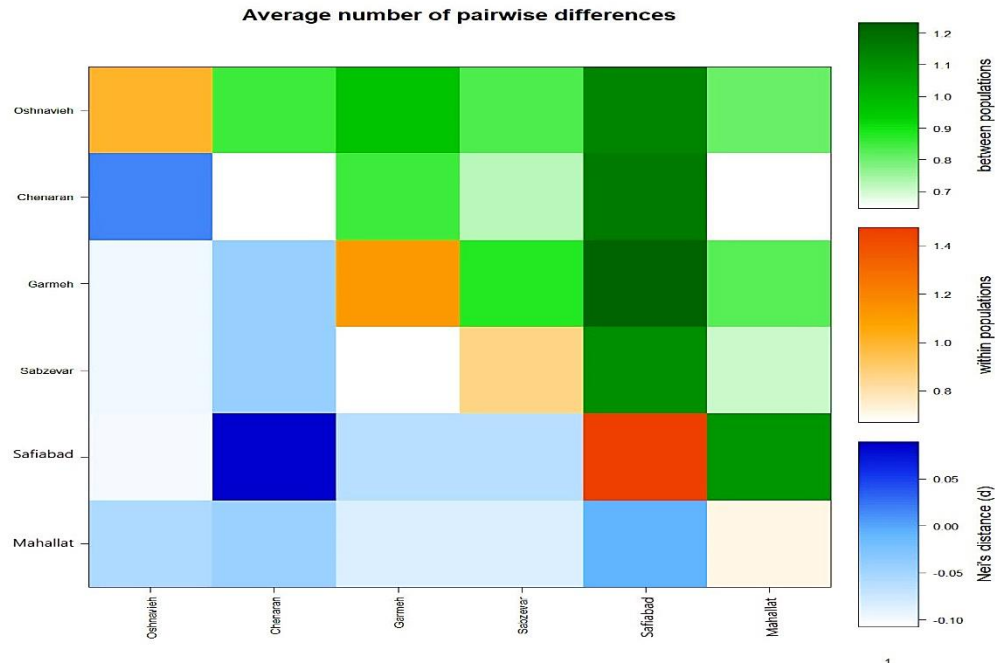
Appendix 1. Mapping haplotypes.



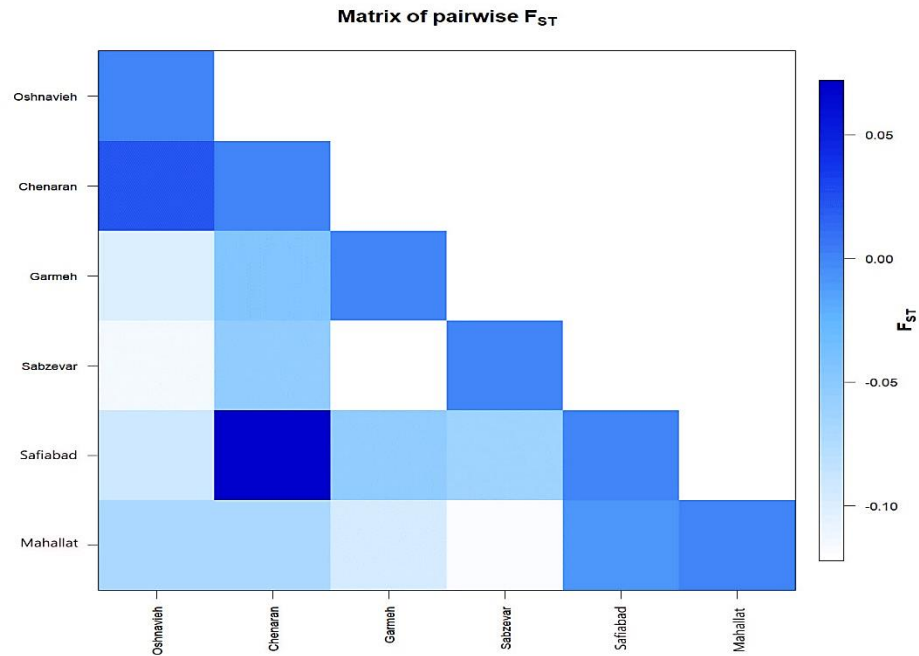
a



b



c



d

Appendix 2. AMOVA results for the *COI* gene study of *Spodoptera exigua*. (a) Haplotype distance matrix; (b) Nei's within and between population distances; (c) Number of pairwise differences between localities, and (d) Comparison of F_{ST} values of all populations.