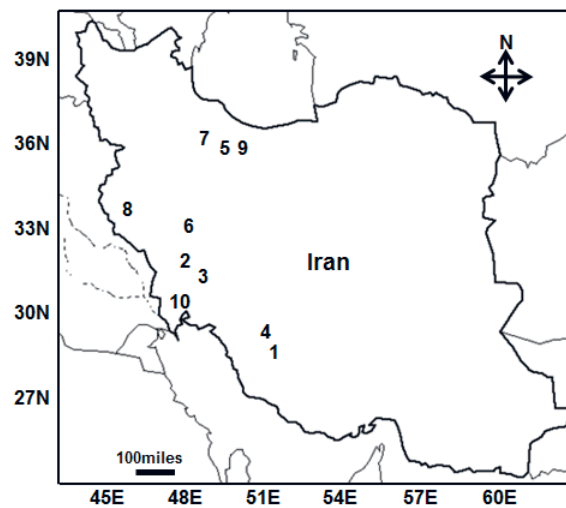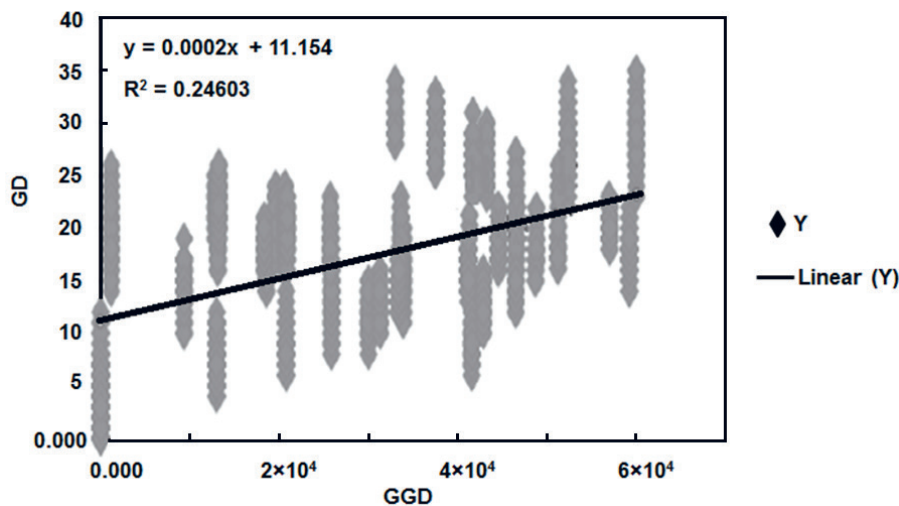# ON-LINE SUPPLEMENTAL MATERIAL

On-line suppl. Tab. 1. Genetic diversity parameters estimated within the populations of *Senecio vulgaris*. N – number of specimens, P – polymorphism percentage, Na – number of different alleles, Ne – number of effective alleles, I – Shannon information index, He – gene diversity, UHe – unbiased gene diversity.

Population	N	P (%)	Na	Ne	I	He	UHe
Pop1	9	55.61	1.187	1.289	0.298	0.189	0.195
Pop2	9	41.50	0.903	1.219	0.221	0.137	0.142
Pop3	7	49.76	1.063	1.241	0.246	0.143	0.151
Pop4	8	32.31	0.701	1.158	0.166	0.098	0.102
Pop5	6	10.54	0.351	1.023	0. 062	0.039	0.044
Pop6	10	39.14	0.876	1.189	0.197	0.128	0.133
Pop7	9	12.51	0.398	1.041	0.074	0.046	0.051
Pop8	8	13.24	0.419	1.054	0.078	0.053	0.059
Pop9	7	15.31	0.442	1.067	0.095	0.072	0.076
Pop10	8	22.32	0.628	1.098	0.125	0.097	0.102

On-line suppl. Fig. 1. Map of Iran, showing localities of the collected populations of *Senecio vulgaris*.

On-line suppl. Fig. 2. Mantel test plot of genetic distance (GD) allied with geographical distance (GGD) in the studied *Senecio vulgaris* populations. A significant positive correlation exist between Nei's genetic distance and geographic distance (km) (r = 0.5, P < 0.01).