

**Molecular genetic characteristics of *Darevskia portschinskii* lizard populations based on  
microsatellite markers analysis**

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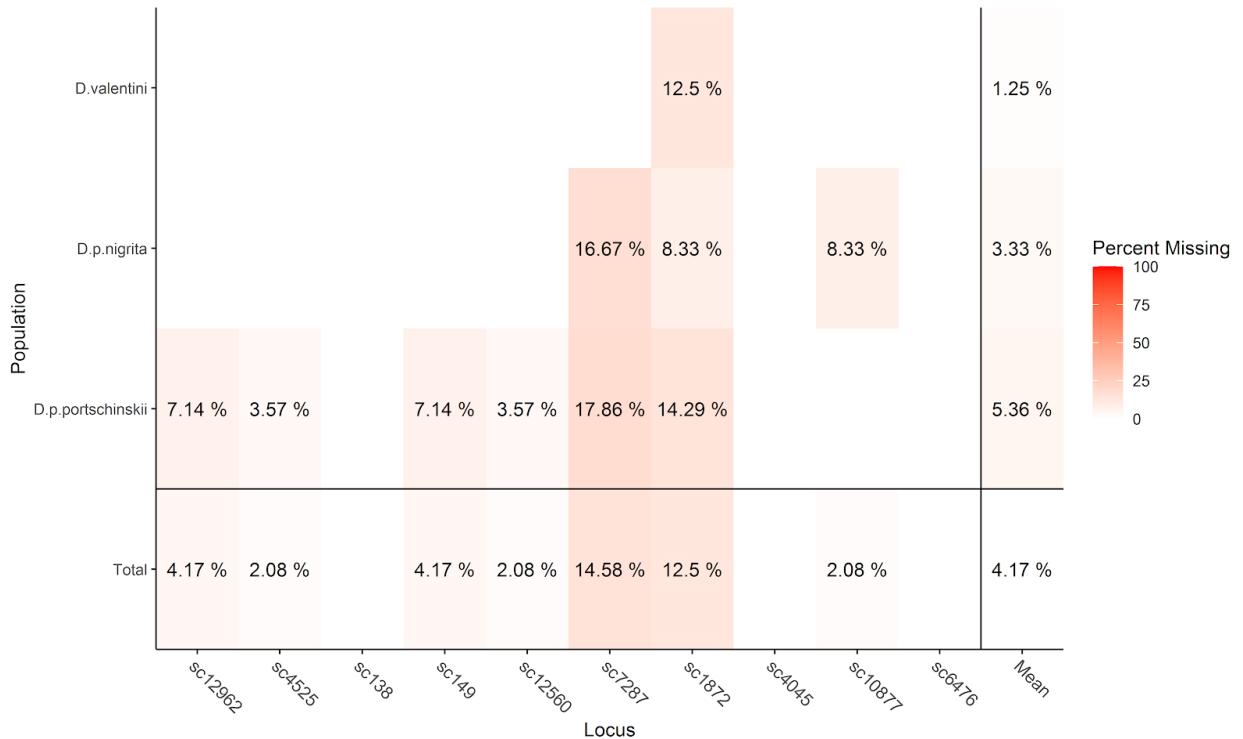
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**SUPPLEMENTARY MATERIAL**

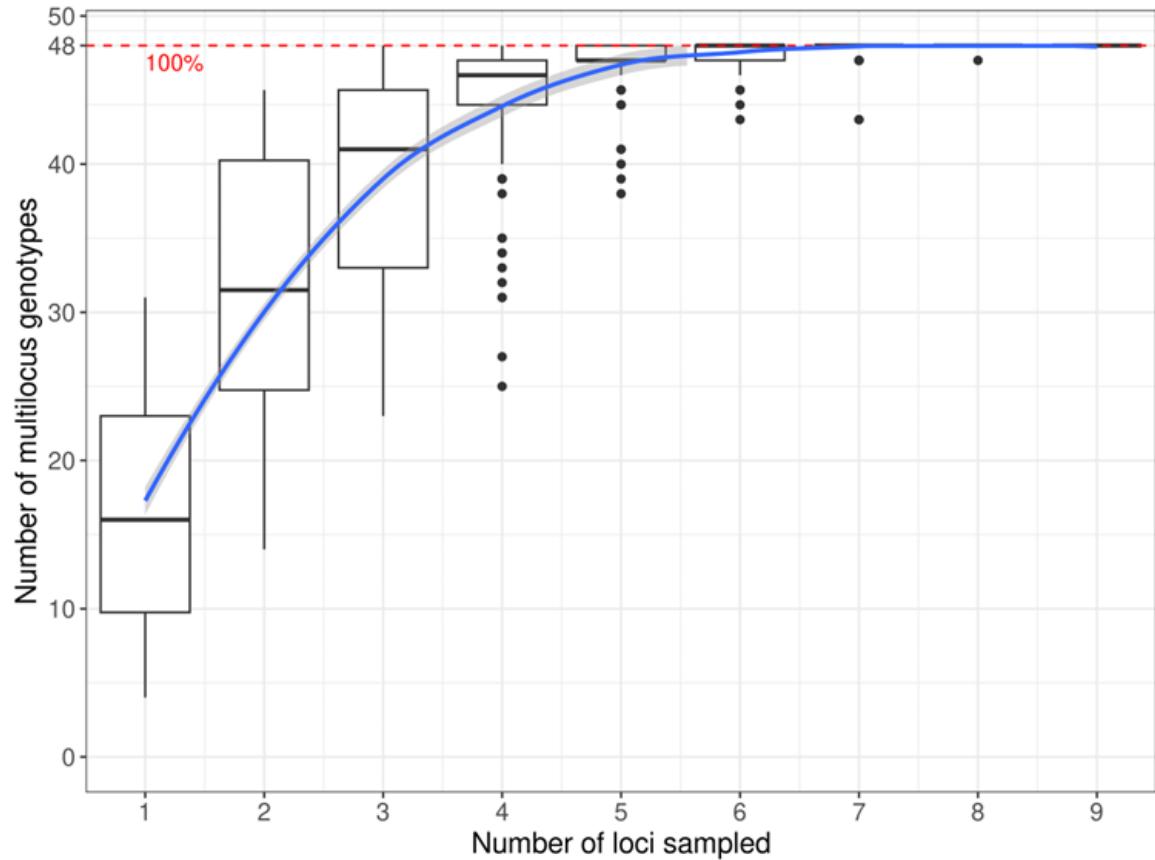
**Table S1.** Microsatellite loci and PCR primers used in the work.

Locus	Microsatellite monomer		Sequence of the primers 5' – 3'
sc12962	GCT	F1	ATGAGTGAGGTGTTATTCCCT
		R1	GTTCTTTCTTCCTCTCAGAA
sc4525	GT	F	CAACAAGGGCAGAAATTAATAC
		R	AGAAACCAGCCCTACAGTTA
sc138	TAA	F	AAGGCTATCAACAACTTCTAGC
		R	GAAACAGCAGTGATGGTATGT
sc149	AAG	F	CCCCTCTTAAGTTCAGTTCTC
		R	GTCCCTACCACCTTTACAAC
sc12560	TA	F	GCAATCTGCTTCACTGTAT
		R	AGAACAAATTATCCAGCAACA
sc6476	TG	F	AGACCCACATTCTAATTCCCTC
		R	AACAAGGGAACTGAAATGAAT
sc10877	AC	F	GAGGTACTATTCTGGGTGG
		R	TACCCTTAAATTGCTTCCTT
sc4045	TGT	F	AGATGGACGGGGTATAAGTAA
		R	AAAATATCAAGATGGACACA
sc7287	CA	F	ATCGACCATTACAGCAAGTAG
		R	CTCAGATGAATCAGCCAATAG
sc1872	GA	F	CGGGATTGAAATACAACCTCT
		R	ACTCCATGATTCTGTAAGTCG

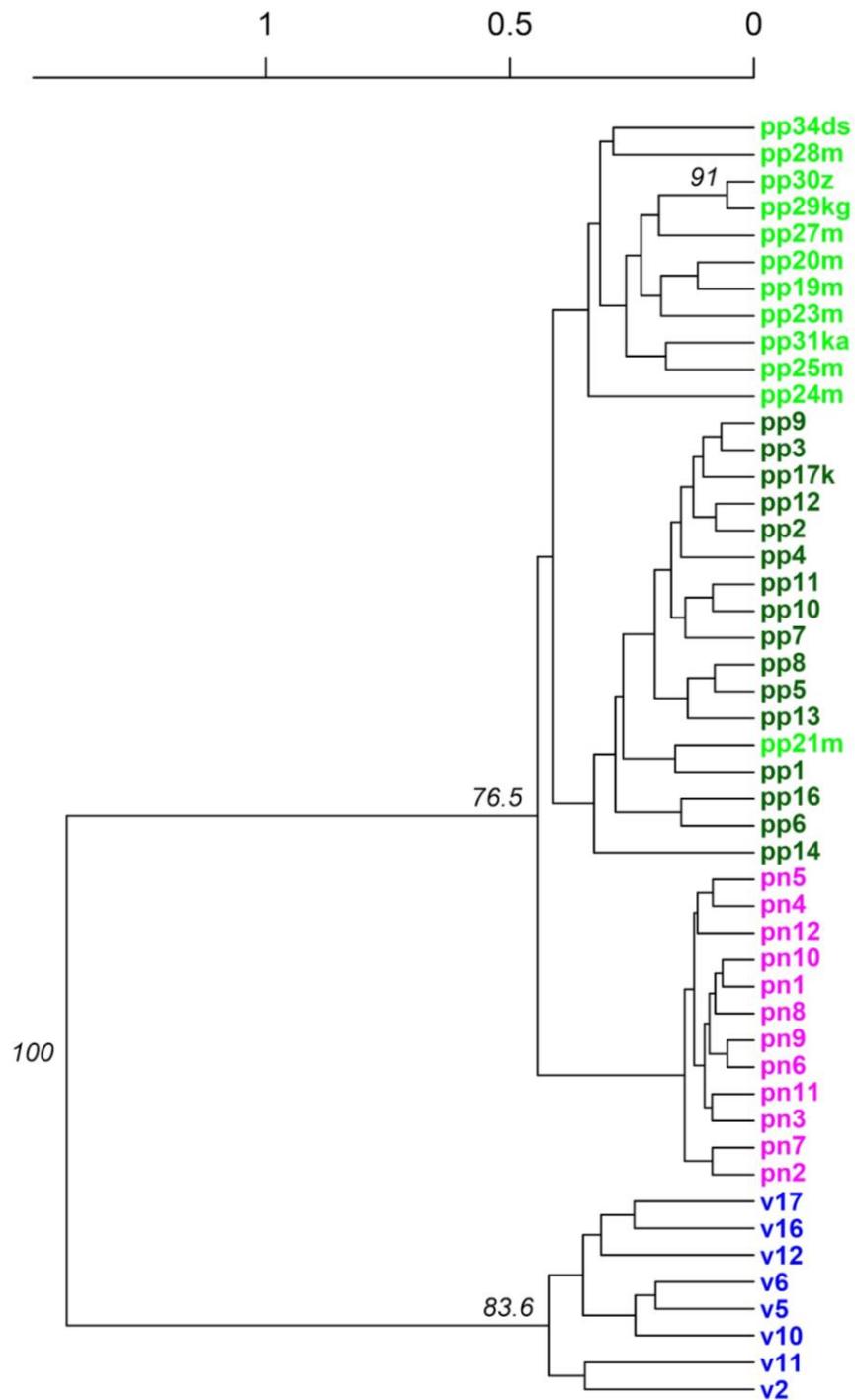
**Fig. S1.** Heatmap of missing data.



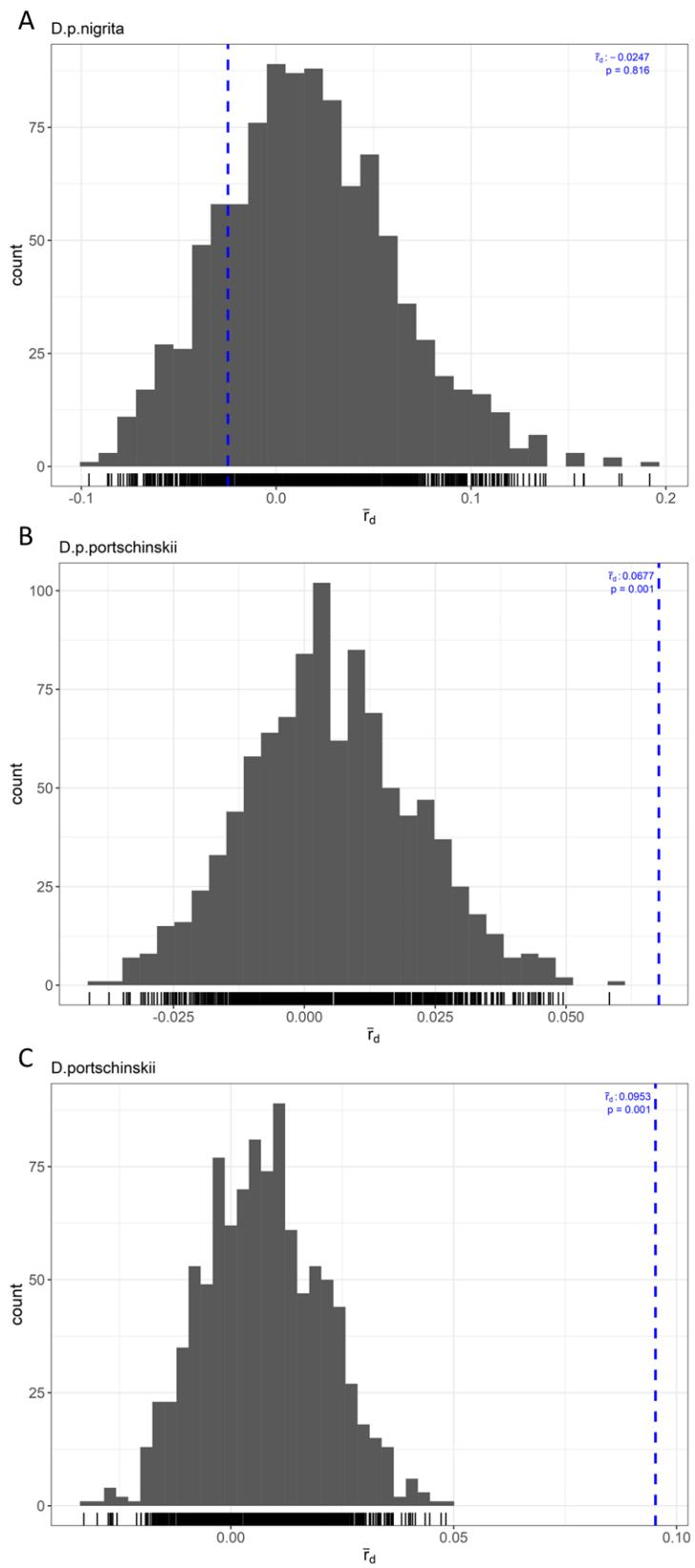
**Fig. S2.** Accumulation curve for multilocus genotypes. The y-axis is the number of multilocus genotypes; x-axis is the number of loci from 1 to 10. 48 multilocus genotypes of *D. valentini* (n=8) and *D. portschinskii* (n=40) (100%) are detected using seven microsatellite loci.



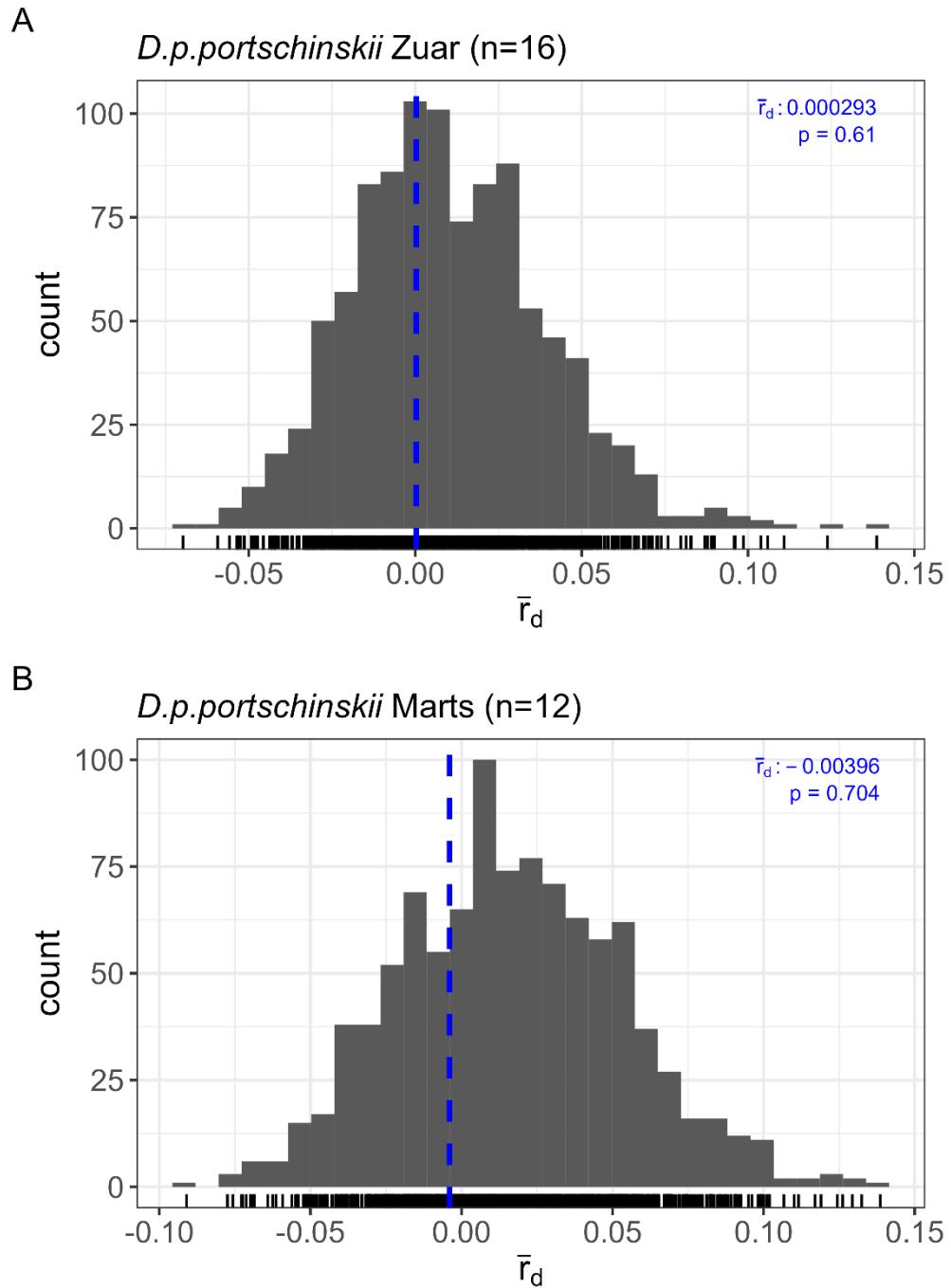
**Fig. S3.** UPGMA Nei distance tree (bootstrap=1000). *D. valentini*; *D. p. nigrita* (“Dzoraget”); *D. p. portschinskii* (“Zuar”); *D. p. portschinskii* (“Marts”). Dark green indicates samples of the subspecies *D. p. portschinskii* from the “Marts” population, green - from the “Zuar” population, magenta indicates samples of the subspecies *D. p. nigrita* from the “Dzoraget” population, blue indicates samples of the species *D. valentini*.



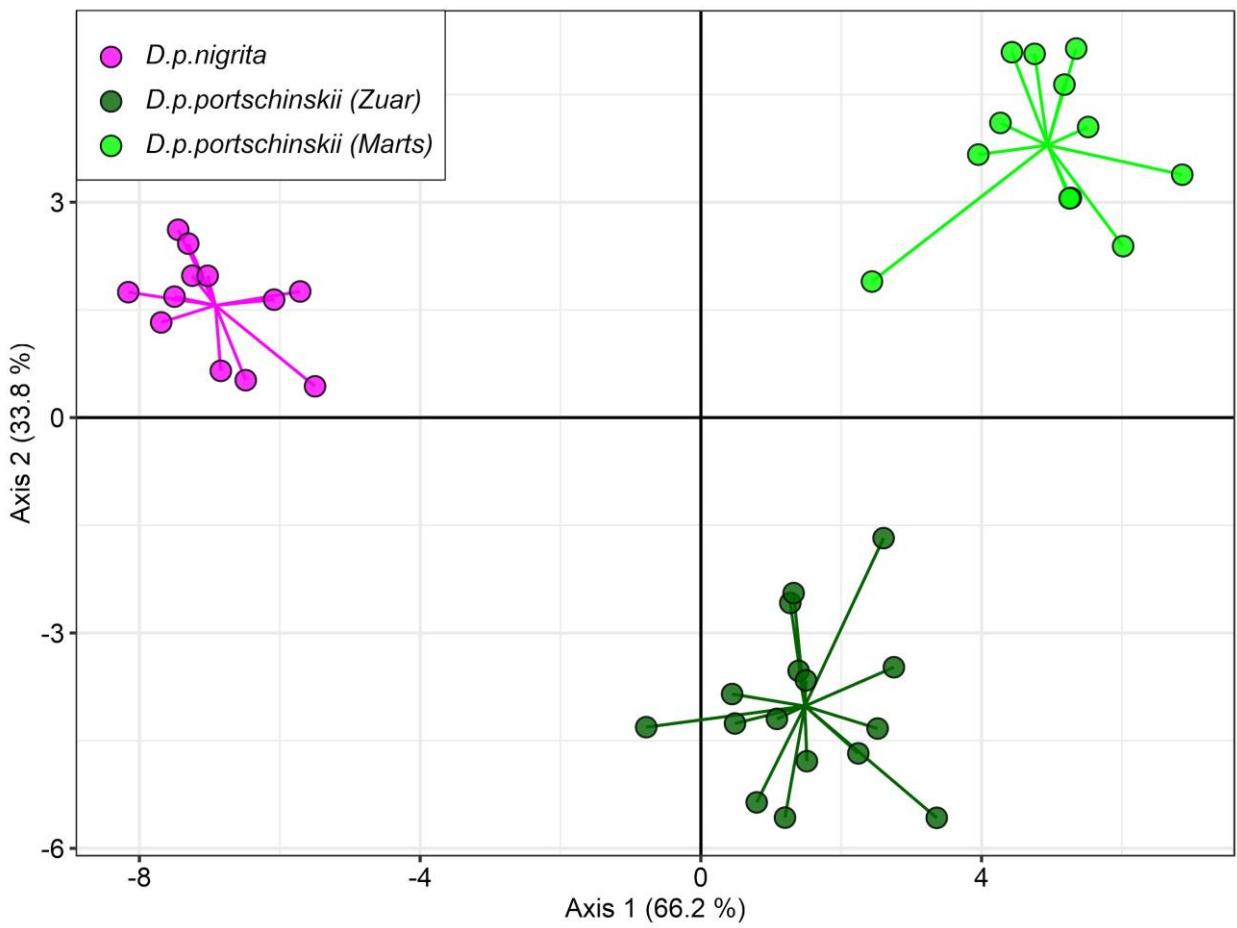
**Fig. S4.** Association index ( $\bar{r}_d$ ) of subspecies *D. p. nigrita* (A) and *D. p. portschinskii* (B), and *D. portschinskii* (C) without division into subspecies.



**Fig. S5.** Association index ( $\bar{r}_d$ ) of *D. p. portschinskii* “Marts” (A) and “Zuar (B)” populations.

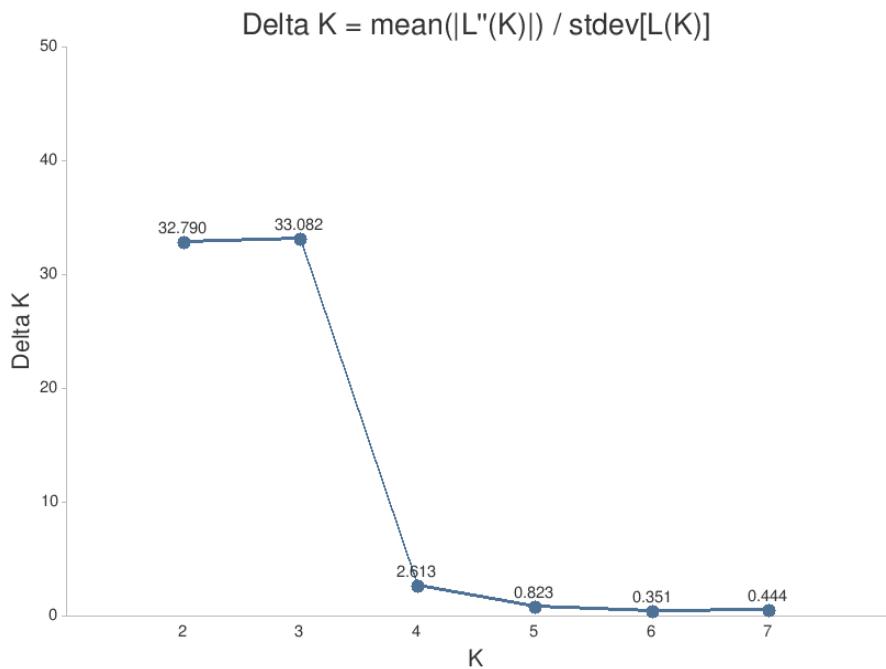


**Fig. S6.** Clustering of *D. portschinskii* individuals based on discriminant principal component analysis (DAPC, K=3).

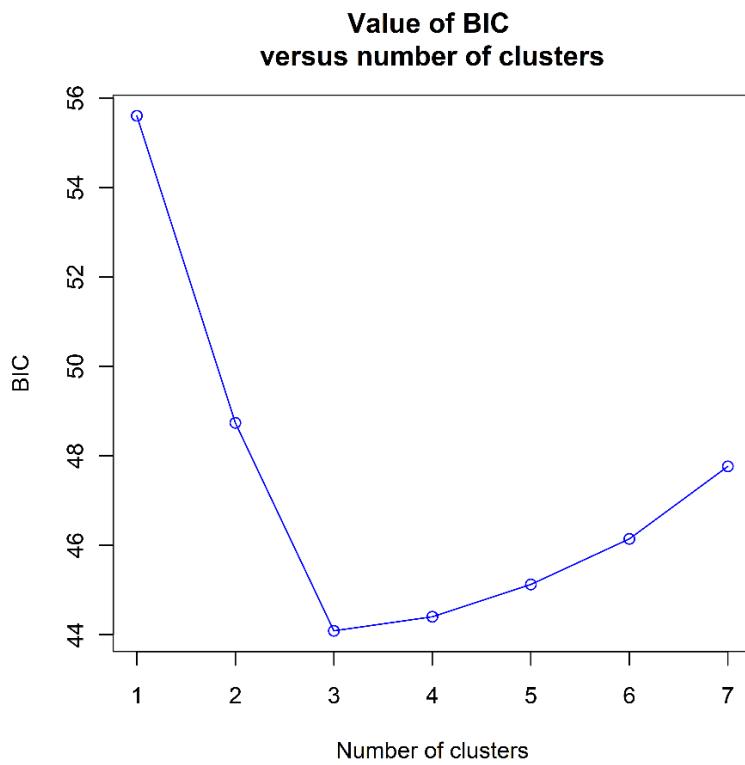


**Fig. S7.** Identification of the optimal number of clusters for 40 *D. portschinskii* calculated by A) STRUCTURE HARVESTER. Delta K values plotted against the number of probable clusters (K); and B) K-means procedure in *adegenet* package. BIC values against the number of probable clusters.

A)



B)



**Fig. S8.** Genetic structure of the species *D. portschinskii* and *D. valentini*, according to the results of clustering in the STRUCTURE program (K=4).

