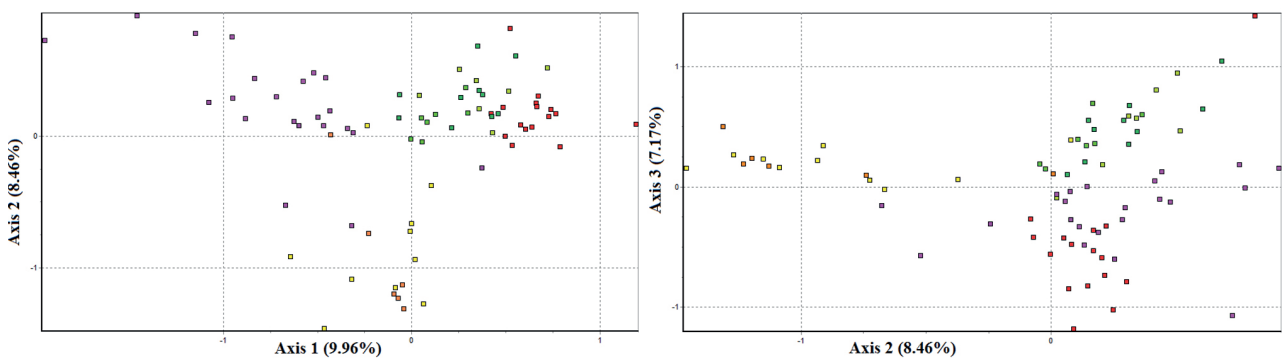


Supplementary Figure S1. STRUCTURE exploratory analysis using different combinations of ancestry and allele frequency models (5 simulations, 100000 iterations, 25000 burn-in): A – admixture and independent; B – no admixture and correlated; C – no admixture and independent; x – axis: *K* number (2–9), y – axis – Delta *K*. All exploratory analysis suggested five clusters as it did the final analysis (see text for details).



Supplementary Figure S2. Factorial Correspondence Analysis (FCA) ordination along the first three axes of 67 individuals of *Salamandra atra* from the Dinarides based on six microsatellite loci. Each label corresponds to a sampling site (from north to south): Gorski Kotar (yellow – Vihoraški put, orange – Samarske stijene), Prenj (light green – Zakantar, dark green – Podotiš, green – Kopilice), Prokletije (pink – Bogičevica, violet – Gozdarevac), Čvrtnica – red. No clear clustering of sampling sites within the same sampling area is inferred. The individuals from Čvrtnica are included for a proper partitioning of variation among the Dinaric population. Axis 2 separates well Gorski Kotar (Northern Dinarides) from the other sampling areas (Central and Southern Dinarides).

Supplementary Table S1. Accession numbers (Acc. No) of the sequences (*cob* and *D-loop*) from public repositories (GenBank) used in this study (courtesy of Crestanello). Hap – Inferred haplotypes (as in Fig. 2 and Table 1). Codes of sampling locations are as in Fig. 1 and Table 1. Collapsed haplotypes from BONATO et al. (2018) are in bold. In the last column, if different, the reference for *cob* is separated from the reference of *D-loop* by a comma: α – BONATO et al. (2018), β – VENCES et al. (2014), γ – STEINFARTZ et al. (2000), δ – this study.

Hap	Code	Acc. No: <i>cob</i>	Acc. No: <i>D-loop</i>	Reference	Hap	Code	Acc. No: <i>cob</i>	Acc. No: <i>D-loop</i>	Reference
H1	18	MN255339	MN255326	δ	H16	16	MN255349	MN255336	δ
H2	18	MN255340	MN255327	δ	H17	16	MN255350	MN255337	δ
H3	18	MN255341	MN255328	δ	H18	1	MG968419	MG968401	α
H4	19	MN255342	MN255329	δ	H19	1, 2	MG968411	MG968401	α
H5	19	MN255343	MN255330	δ	H20	1, 2	MG968418	MG968401	α
H6	23	MN255345	MN255332	δ	H20	1	MG968411	MG968390	α
H7	26, 27	MN255351	MN255338	δ	H21	10, 11, 12, 13	MG968410	AY628440.1	α, γ
H8	20	MN255344	MN255331	δ	H22	12	MG968410	MG968399	α
H9	22	MG968412	MG968391	α	H23	10	KF645910	KT335870	β, γ
H10	22	MG968413	MG968391	α	H24	14, 15	MG968403	KF645583.1	α, β
H11	24	MN255346	MN255333	δ	H25	3	MG968402	MG968400	α
H11	21, 25	MG968412	MG968392	α	H26	8	MG968405	MG968397	α
H12	20, 23, 22	MN255347	MN255334	δ	H27	8, 7, 6	MG968406	MG968397	α
H12	21, 25	MG968415	MG968392	α	H28	6	MG968404	MG968397	α
H12	17	MG968415	MG968393	α	H29	4	MG968409	MG968396	α
H13	24, 22	MN255348	MN255335	δ	H30	5	MG968408	MG968395	α
H13	21, 22, 25	MG968414	MG968394	α	H31	5	MG968407	MG968397	α
H14	9	MG968416	AY628442.1	α, γ	H32	6	MG968407	MG968398	α
H15	9	MG968417	AY628442.1	α, γ					

Supplementary Table S2. PCR conditions and characteristics of the microsatellite loci.

Locus/Forward primer label	PCR option	Allelic range	Number of alleles	Primer conc. (μ M)	PCR thermal profile
SalE6/HEX		252–300	9	0.20	94°C (120 s)
SalE8/HEX	MIX1	135–157	7	0.10	[94°C (40 s) – 60 °C (30 s) – 65°C (40 s) \times 35]
SalE12/TAMRA		160–194	12	0.10	65°C (300 s)
SalE7/HEX		188–220	10	0.08	94°C (120 s)
SalE23/HEX	MIX2	257–323	7	0.20	[94°C (40 s) – 56°C (30 s) – 65°C (40 s) \times 35] 65°C (300 s)
SalE14/TAMRA	Single	219–265	7	0.08	94°C (120 s) [94°C (40 s) – 64°C (30 s) – 65°C (40 s) \times 35] 65°C (300 s)