

Morphology is a poor predictor of interspecific admixture – the case of two naturally hybridizing newts *Lissotriton montandoni* and *Lissotriton vulgaris* (Caudata: Salamandridae)

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Supplementary material

Supplementary files with newts photos:

- Newts-natural populations.zip
- Newts-reference groups.zip



Figure S1. The example photos collected from natural populations. The scale on the right allows standardization values between photos. Each individual has unique number.

Table S1. Evaluation sheet of qualitative traits of newts. The traits and corresponding scores.

Trait	Variant	Value
Dorsal crest	No crest	0
	Crest, not denticulate	1
	Crest, denticulate	2
Filament on the tail tip	No filament	0
	Pseudo-filament (elongation of the tail tip)	1
	Filament	2
Toe flaps	No toe flaps	0
	Small toe flaps (max. width of flaps = width of finger)	1
	Wide toe flaps	2
Stripe on the lower tail margin	Cream stripe	0
	Blue stripe	2
Color of the palms of the hind legs	Grey to black	0
	In the color of surrounding skin	2
Color of the ventral side of the body	Uniform	0
	Orange/red stripe through the lighter colored belly	2

Spots on the belly	No spots or single small spots on the sides of the body	0
	Small spots	1
	Big spots	2
Spots on the throat	No spots or single small spots on the sides of the body	0
	Small spots	1
	Big spots	2

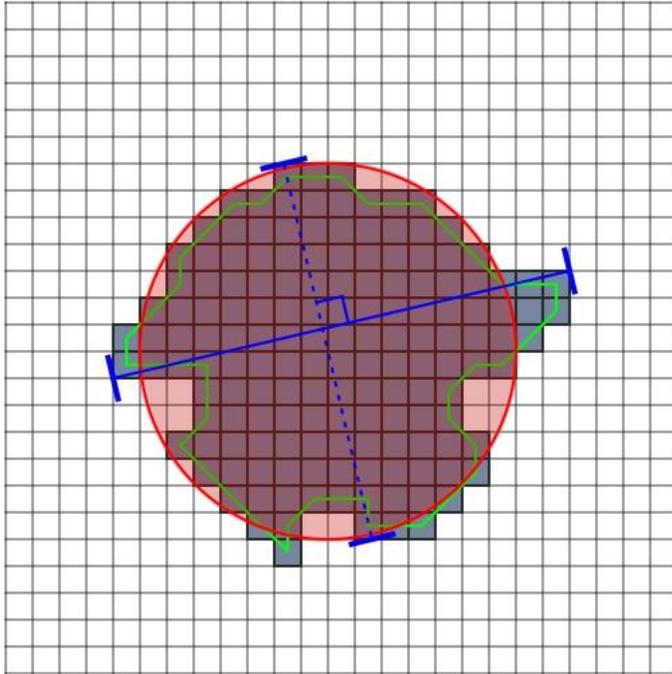


Figure S2. Estimation of the shape of the objects – recognizing spots. Each square represents a pixel, and the irregular shape in the middle is a recognized object. Circularity is the perimeter of a circle with the same area as the object (red) divided by the perimeter of the object (green line). Elongation is estimated by the maximum diameter of the object (solid blue line) and the second maximum diameter, perpendicular to the first one (dashed blue line): the perpendicular diameter is divided by maximum diameter

Table S2. Number of individuals used in measurements. Total number of individuals is the number of individuals used in all measurement except for spots and tail measurements. In the case of specific measurements, some photos were removed due to technical difficulties, e.g. blurry images or bite marks on the tail.

		No. of individuals
Reference groups	Total	112
	Spot measurements	105
	Tail measurements	103 (47 with filament)
Transects	Total	294
		184 – Remetea transect
		110 – Suceava transect
	Spots measurements	283
	Tail measurements	278 (122 with filament)

Table S3. Post-hoc Dunn test of the differences of the index values between all reference groups.

Left: Adjusted P values for multiple comparisons of the differences among the reference groups.

Right: the symbolic representation of the significance of the test. * $P < 0.01$, ** $P < 1 \cdot 10^{-8}$; *** $P < 1 \cdot 10^{-20}$.

	F1 hybrids	L. montandoni	L. v. ampelensis	L. v. vulgaris
F1 hybrids		*	*	**
L. montandoni	2.83E-03		**	***
L. v. ampelensis	4.10E-03	3.69E-10		*
L. v. vulgaris	4.53E-09	1.71E-21	3.48E-03	

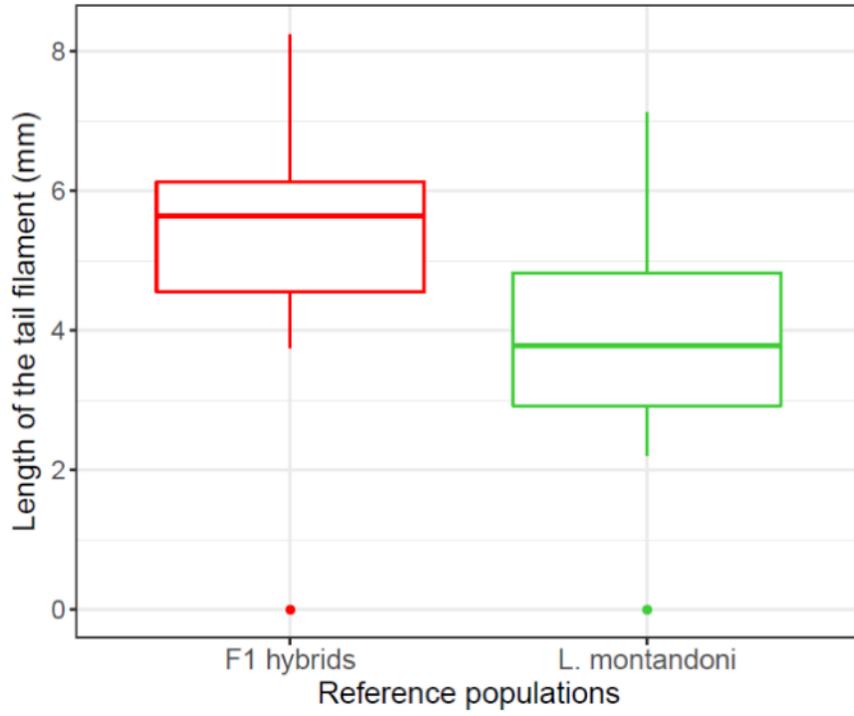


Figure S3. The variation of the length of the tail tip filament within species.

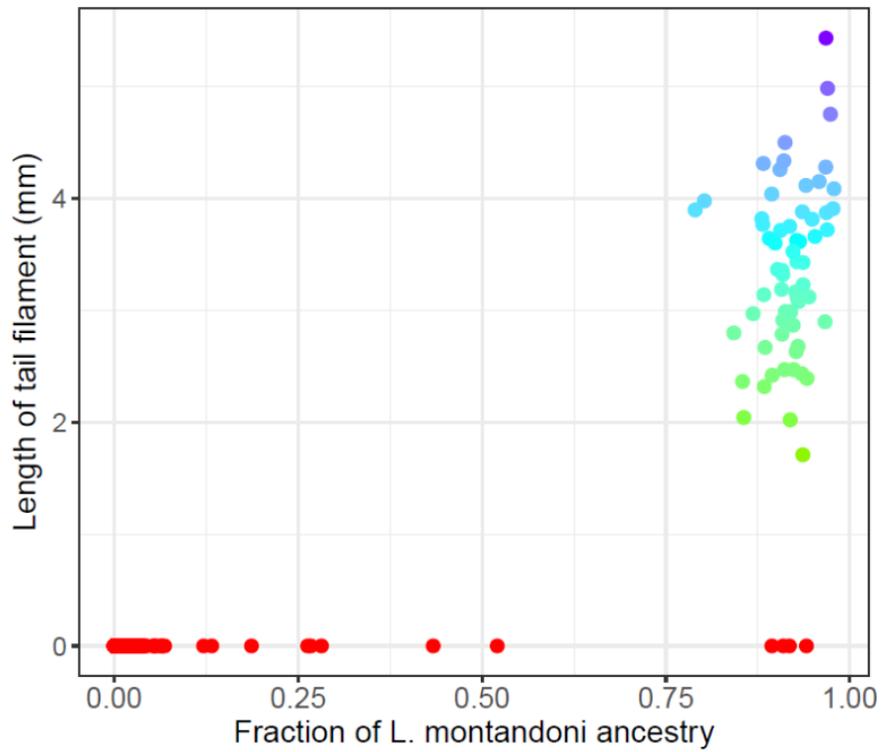


Figure S4. Remetea transect. Length of the tail tip filament. Genetic admixture is a proportion of *L. montandoni* genome in the genome of the individual.