

Stripeless tree frogs (*Hyla meridionalis*) with stripes on the Canary Islands

Christophe Dufresnes¹, Laura Gangoso², Nicolas Perrin¹ & Matthias Stöck¹

¹Department of Ecology and Evolution, University of Lausanne, CH-1015 Lausanne, Switzerland

²Department of Conservation Biology, Estación Biológica de Doñana, C.S.I.C., Avda. M(a) Luisa s/n, 41013 Sevilla, Spain

Corresponding author: Christophe Dufresnes, e-mail: christophe.dufresnes@unil.ch

Anurans are known to exhibit a wide array of colour and pattern polymorphisms, including “background” colour and the presence or absence of stripes and spots. Most studies suggest that these traits are heritable (Hoffman & Blouin 2000, O’Neill & Beard 2010), which means that variations can be shaped and influenced by drift, and predatory and sexual selection (e.g., Taylor et al. 2007), in addition to other factors, such as ontogenetic changes, sexual dimorphism, and physiological plasticity (Hoffman & Blouin 2000). In hylid frogs, an array of physiological colour changes has been documented (e.g., Schneider 2009 and references therein). The complex processes that maintain colour polymorphisms in nature allow displaying a large diversity of phenotypes.

Here we focus on the stripeless tree frog *Hyla meridionalis* Boettger, 1874, a widespread anuran distributed around the western Mediterranean basin, from North Africa (Tunisia, Algeria and Morocco) to the Iberian Peninsula, reaching its northern range boundary in southern France and northeastern Italy. Several insular populations also occur on Minorca and the Canary Islands. As indicated by its English vernacular name, the stripeless tree frog is very well distinguishable from other Western Palearctic hylids by having short lateral stripes that typically only reach the forelegs, and are completely absent on the flanks (Arnold & Ovenden 2002, Schneider 2009, Fig. 1h). Here we report on a remarkable exception in several populations from the Canary Islands where individuals display unusually prominent stripes.

Our observations were made on the remote islet of Alegranza (eastern Canary Islands) at a small permanent freshwater pond (the only suitable breeding site for tree frogs; 29°23’5.20” N, 13°31’12.30” W). In September of 2010, we observed about 50 juveniles (ca. 2 cm) with highly polymorphic lateral stripes (Figs. 1a–d), ranging from regular short lines to much more extended flanking stripes, as found, e.g., in *H. arborea*. Besides, all individuals exhibited an unusual brownish background colour that was scattered with large black dots.

In order to ascertain the identity and origin of this isolated population, we sampled buccal cells from three individuals (non-invasive swabs; Broquet et al. 2007), from which we sequenced two mitochondrial markers: cytochrome *b* and 16S rDNA sequences, following the methodology described in Stöck et al. (2008) and Palumbi (1996), respectively. We built a maximum likelihood phylogenetic tree of cytochrome *b* sequences (747 bp aligned) from Alegranza with a subset of those from the study of Stöck et al. (2008), which includes hylids from the entire *H. arborea* group. Interpretation of the tree was straightforward (Figure 2): All three samples from Alegranza unambiguously clustered within the nominal *H. meridionalis* clade, along with other sequences from the neighbouring island of Tenerife and from mainland Morocco. Furthermore, BLAST analysis (Zhang et al. 2000) revealed that our 16S rDNA sequences (543 bp aligned) had the same haplotype as those from Tenerife (GQ916810; Gvozdk et al. 2010) and Fuerteventura (EF566953; Lemmon et al. 2007).

Tree frog populations in the Canaries are assumed to be a result of recent human introduction (Pleguezuelos 2002), which has been confirmed for most islands by phylogenetic studies (Recuero et al. 2007, Stöck et al. 2008). It is unclear whether the first introduction took place when humans arrived from North Africa (some 2500 years ago, Macías 1996), or more recently in connection with the colonization by European settlers (Navarro 2001). Tree frogs have rapidly dispersed since, and are now present on all seven major islands (in addition to Alegranza) of the archipelago (Rodríguez Luengo 2001). Recuero et al. (2007) demonstrated that *H. meridionalis* sequences from the Canaries clustered with those from N-Morocco and NE-Iberia but not with geographically proximate mainland frogs from SW-Morocco (see also Stöck et al. 2008). Our results are thus consistent with previous work, and the Alegranza tree frogs are likely to have originated from the same introduction event(s) as those on neighbouring islands.

How could such phenotypic diversity have then arisen in the archipelago, especially in such a short period of

time? We propose several ideas: The brown “background” colour observed on Alegranza is uncommon, but *H. meridionalis* has been described as exhibiting different colours and spotted patterns (Arnold & Ovenden 2002, Muratet 2008, Schneider 2009). Colour features enable frogs to blend into their environment (homochromy) in order to avoid visual detection by predators (Hoffman & Blouin 2000). Brown morphs might indeed be favoured on Alegranza, where the habitat is homogeneously sub-desertic and composed only of rocks and scrubby vegetation. In contrast, tree frogs from other Canary Islands of-

ten inhabit banana plantations and gardens, and usually display pigmentation that matches this environment (uniform green, Figs. 1e–g), even though with a few exceptions (Schneider 2009 and ref. therein; Mazzei & Pimpellini 2009). Alternatively, stronger genetic drift may be responsible for the unusual colour pattern in this small and isolated population. Green and brown pigmentations only differ in their types of chromatophores (Hoffman & Blouin 2000, Schneider 2009), and various colour morphs are expected to frequently arise within populations over short evolutionary periods.

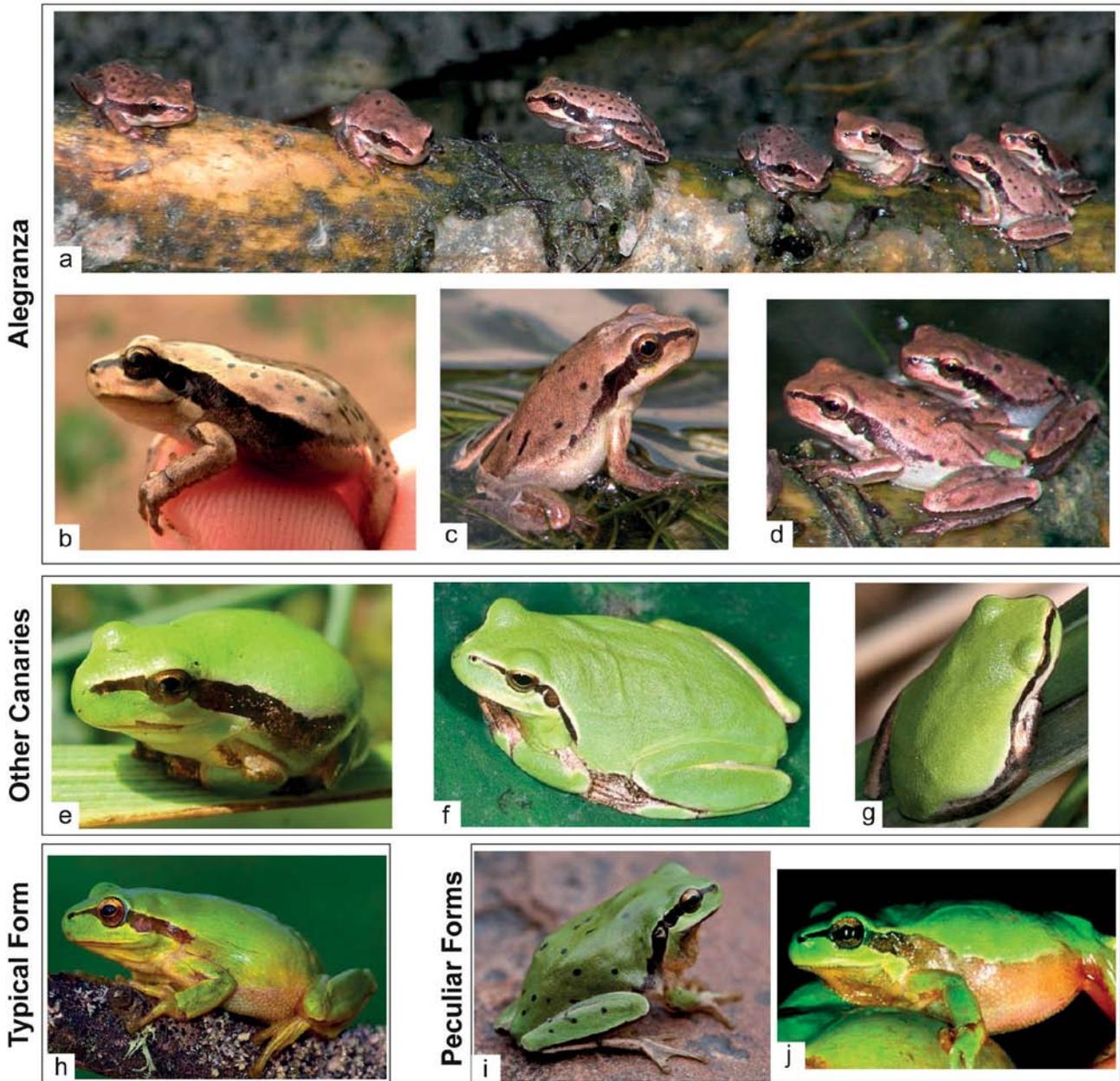


Figure 1. Unusual striped phenotypes amongst tree frogs from the Canary Islands of Alegranza (a–d; note the green colour in a small portion of the back in d), Gran Canaria (e), La Gomera (f) and Lanzarote (g), compared with typical *Hyla meridionalis* (h). Note some similarity with tree frogs of the Anti-Atlas form of *H. meridionalis* (i) and hybrids between *Hyla meridionalis* and *Hyla arborea* (j), which are, however, not closely related to those from the Canaries. Photographs by Christophe Dufresnes (a–d), Paolo Mazzei (f), Miguel Rouco (g), Dini Cortes (h), Frank Deschando1 (i), and adapted from Weimer 2010 (e) and Barbadi1lo & Lapeña 2003 (j).

taxonomic identities have, however, not been confirmed by molecular markers.

Our and most of these observations involve juveniles (but see Figure 1f), suggesting that this unexpected phenotype could be age-related. Striped juveniles can sometimes be found in populations from southern France (P. Geniez, pers. obs.). In addition, physiological colour changes might also cause in part the variation observed. For instance, dorsal dots appear to be physiologically changeable in *H. sarda* (MS pers. obs.).

The occurrence of stripes in few adults along with typically coloured individuals (e.g., on La Gomera, Figure 1f), however, suggests microevolution of skin patterns in the archipelago (e.g., drift, shifts in predatory and sexual selection; Robertson & Robertson 2008, Gomez et al. 2009). In *Eleutherodactylus coqui*, stripe patterns are inherited in a Mendelian manner by “a single autosomal locus, five-allele model, in which all alleles coding for stripes are co-dominant and the allele coding for the unstriped morph is recessive” (O’Neill & Beird 2010). Assuming a similar mode of inheritance in *H. meridionalis*, enhanced drift through multiple founder effects could have led to a fixation of recessive (and elsewhere rare) stripe-coding alleles during the colonisation of the archipelago.

As mtDNA is only maternally transmitted, hybridisation with another tree frog species could still explain the unusual phenotype, but seems to be excluded, as no other hylid has been reported from the Canaries. So far, there is no evidence that striped mainland forms of tree frogs (*H. meridionalis* from the Anti-Atlas, southern Morocco, Bons and Geniez, 1996, Figure 1i), or even *H. meridionalis* × *H. arborea* hybrids (e.g., from Spain, Barbadillo & Lapeña 2003, Fig. 1j) contributed to the peculiar appearance of Canary tree frogs.

Future research might focus on the origin of these unusual phenotypes, especially in adults, and include a more precise reconstruction of tree frog introduction to the islands, for instance by using fast-evolving molecular markers such as microsatellites.

Acknowledgements

We are thankful to the scientific team operating in Aleganza, as well as the photographers who kindly agreed to provide their pictures: Dinis Cortes, Miguel Rouco, Paolo Mazzei, Jorge Rivero Sanchez and Frank Deschando. We also warmly thank Philippe Geniez (CNRS-Montpellier) and Iván Gómez-Mestre (Estación Biológica de Doñana) for their useful comments.

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