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On genetic variability in a population of the widespread gecko *Hemidactylus brooki*

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Summary. An electrophoretic investigation of 22 gene loci in a local sample of a widespread and ecologically extremely versatile gecko species has shown a low degree of heterozygosity, as is average in lizards and other vertebrates.

Of the reptilian species whose genic variation has been tested through gel electrophoresis of proteins[1-3], none belong to the tropical family Gekkonidae, the largest lizard family. 3 species of the most prosperous genus of this family, *Hemidactylus brooki, H. mabouia* and *H. turcicus*, are of special interest in the comparison of genetic variability with adaptive strategies between ecological generalists and ecological specialists. Largely through human agency, the 3 *Hemidactylus* species have spread all around the world, and they are to be found in the widest range of habitats from forest to downtown Cairo or São Paulo, from upland savanna to sea-level cliffs, from higher leaves in palm trees to under garbage heaps, etc. No other reptiles have such an ubiquitous distribution, including hundreds of other gekkonid species.

The opportunity having arisen to investigate a sample of 16 individuals (8 adult ♂, 5 adult ♀, 3 young) of *H. brooki* from the coastal town of Port-Gentil, Gabon[4], we have

Table 1. Proteins and their encoding loci examined in *Hemidactylus brooki*. Enzyme commission numbers are in parentheses. Buffer systems as in Selander *et al.*[5]

Proteins	Loci	Active in	With the buffer systems
Lactate dehydrogenases	*Ldh-A*	Liver, kidney, heart, plasma, testis	Continuous Tris-citrate I
(1.1.1.28)	*Ldh-B*	Liver, kidney	Continuous Tris-citrate I
	**Ldh-C*	Testis	Continuous Tris-citrate I
Malate dehydrogenases	*Mdh-1*	Liver	Continuous Tris-citrate II
(1.1.1.37)	*Mdh-2*	Liver, kidney	Continuous Tris-citrate II
Isocitrate dehydrogenases	*Idh-1*	Liver, kidney	Continuous Tris-citrate I
(1.1.1.42)	**Idh-2*	Kidney, heart	Continuous Tris-citrate I
α-Glycerophosphate dehydrogenase (1.1.1.8)	*α-Gpd*	Liver, kidney	Tris-maleate
Phosphoglucomutase (2.7.5.1)	*Pgm*	Liver, kidney, erythrocytes	Tris-maleate
Phosphoglucoisomerase (5.3.1.9)	*Pgi*	Liver, kidney	Tris-maleate
Glutamate oxaloacetate transaminases	*Got-1*	Liver, kidney, heart, testis	Continuous Tris-citrate II
(2.6.1.1)	*Got-2*	Liver, kidney, heart, testis	Continuous Tris-citrate II
Indophenol oxidase	*Ipo*	Liver, kidney	Continuous Tris-citrate II
Esterases	*Est-1*	Kidney	Discontinuous Tris-citrate
(3.1.1.2)	*Est-2*	Liver, kidney, heart, plasma, erythrocytes	Discontinuous Tris-citrate
	Est-3	Liver, kidney	Discontinuous Tris-citrate
	Est-4	Liver, kidney	Discontinuous Tris-citrate
	Est-5	Plasma, erythrocytes	Discontinuous Tris-citrate
Albumine	*Alb*	Plasma	Discontinuous Tris-citrate
General proteins	*Pt-1*	Plasma	Discontinuous Tris-citrate
	Pt-2	Plasma	Discontinuous Tris-citrate
	Pt-3	Plasma	Discontinuous Tris-citrate

Asterisks designate loci not included in heterozygosity and polymorphism computations (see text).

tested allozymic variation, as detectable by starch gel electrophoresis, of 11 classes of enzymes and other proteins, controlled by 22 genes (table 1). Plasma and erythrocyte fractions of blood were used, as well as homogenates of 4 different organs.

4 loci were found to be polymorphic (table 2). Excluding 2 of the monomorphic loci because of insufficient sampling (see below), the average heterozygosity for the sample is 0.052. This falls very close to the 0.047 average found for the lacertilians already examined at 14 loci or more[1]. The lacertilian average is in turn similar to the vertebrate average of 0.049[1].

The amount of polymorphism is found to be 20% when using the 0.01 criterion, but since observed electromorph frequencies cannot be lower than $1/(2\times 16)\simeq 0.03$ with our sample, this is more likely to be a conservative rather than an excessive estimate (An excessive estimate would occur if one of the electromorphs recorded once in our sample happened to be an exceptional allozyme in the population). With the 0.95 criterion, the rate of polymorphism is 15%, a value that seems average among vertebrates[6].

In conclusion, the genetic variability electrophoretically detected in the gekkonid population sampled does not reflect the high gene flow and active diversifying selection suggested by the ecological versatility of *Hemidactylus brooki*. The loci tested in our sample show the low variability typical of vertebrate species. Actually, the absence of variation at loci observed in 8 (*Ldh-C*, only visible in mature males) or 9 geckos (*Idh-2*, controlling a fast denaturating enzyme) suggests that variability may be somewhat lower than estimated[7].

Table 2. Electromorph frequencies at polymorphic loci of the *Hemidactylus brooki* sample of Gabon

Loci	Observed alleles	Frequencies
Idh-1	*1.00*	0.97
	1.40	0.03
a-Gpd	*1.00*	0.67
	1.35	0.33
Est-1	*1.00*	0.80
	1.19	0.20
Est-4	*0.92*	0.04
	1.00	0.88
	1.08	0.08

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7 Technical assistance: Josette Catalan.

Additional chromosome duplication in female meiotic prophase of *Sipyloidea sipylus* Westwood (Insecta, Phasmida), and its absence in male meiosis

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Summary. In the parthenogenetic stick insect *Sipyloidea sipylus*, an additional chromosome duplication takes place in the primary oocytes immediately after pachytene. After duplication, the chromosomes again appear in a pachytene configuration, and oogenesis proceeds with twice the somatic number of chromosomes. Additional duplication does not occur during prophase of primary spermatocytes.

The stick insect *Sipyloidea sipylus* Westwood reproduces by thelytokous parthenogenesis[1]. In first meiotic metaphase, the number of elements equals the somatic number of chromosomes ($2n=80\pm2$). These elements are tetrapartite and consist of 4 chromatids. The 2 meiotic divisions are normal and the somatic number of chromatids enters the pronucleus. The meiosis thus evolves with twice the somatic number of chromosomes[2]. However, it could not be established when and how the chromosomes were doubled. The meiosis of the thelytokous stick insect *Carausius morosus* Br. is rather similar to that of *S. sipylus*[3,4]. With the aid of cytophotometry it could be shown that in the former phasmid the chromosomes are duplicated after pachytene during a stage called pachyreduplication phase[5]. After doubling, they enter anew into a pachytene called tetrapachytene. Moreover it was found that in a (rare) male complete as well as incomplete duplication occurred during zygotene[6]. In order to trace the additional chromosome doubling in *S. sipylus*, cytological and cytophotometrical investigations were carried out on 2 mature ovaries and on a pair of ovotestes.

S. sipylus was bred on leaves of bramble under conditions as described for *C. morosus*[5]. The stock originated from a sample sent by Dr H.K. Van den Bergh (Antwerp) in 1976[1]. An adult male (length 60.5 mm) was obtained from the progeny of females irradiated with 500R of X-rays (11 R/sec). Its morphology conformed to the description given by Urvoy[7]. The 3rd-6th abdominal segments contained a pair of ovotestes: a tube-shaped left testis, with a narrow part at one-third from the distal end from which 2 ovarioles protruded, and a tube-shaped right testis with a narrower distal half from which 7 ovarioles protruded. The ovarioles had a normal morphology (growing oocytes up to 1 mm long). The investigations were carried out on Feulgen stained squash preparations of ovarioles and ovotestes. The slides were made as described before[5,6] (25 min hydrolysis in 5 N HCl at room temp.). The relative quantity of DNA in the nuclei was determined with a Zeiss Scanning Mikroskop-Photometer (Ø diaphragm plug 0.6 µm) at 558 nm.

In the ovary, the end chamber of an ovariole contains oogonia and oocytes in early meiosis[2]. The oocytes are in leptotene, zygotene or pachytene. A bouquet, as developed