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Betreft : VUB-vorsers ontdekken een voor de wetenschap onbekende kikkerfamilie op het Indisch subcontinent.

“Missing link” in de evolutie van de kikkers ontdekt

Het Indisch subcontinent heeft blijkbaar nog niet al zijn geheimen prijsgegeven. Een jaar na de ontdekking van 100 nieuwe boomkikkers op Sri Lanka, hebben vorsers S.D. Biju en Franky Bossuyt van het labo Ecologie & Systematiek van de Vrije Universiteit Brussel (VUB) een Indische kikker ontdekt die tot een nog onbekende familie behoort. Het is meer dan 75 jaar geleden dat een nieuwe kikkerfamilie ontdekt werd, en de meeste waren reeds door de wetenschap beschreven in de 19^{de} eeuw. Deze ontdekking wordt gepubliceerd in het gezaghebbend vaktijdschrift *Nature* van 16 oktober 2003.

De nieuwe kikker is een echte ‘missing link’ in the evolutie van kikkers. Door DNA-onderzoek hebben de vorsers namelijk aangetoond dat de Indische kikker de nauwste verwant is van vier kikkersoorten die enkel op twee kleine eilanden van de Seychellen voorkomen.

De wetenschap was al tientallen jaren op zoek naar een verklaring waarom die vier soorten op de Seychellen nergens leken te passen in de evolutieve geschiedenis van de moderne kikkers. Gezien de geologische context, werd aangenomen dat de voorouders van deze dieren op het vroegere India-Seychellen-Madagaskar continent geleefd hadden, maar dat hun nakomelingen uitgestorven waren op India en Madagaskar, vermoedelijk al 65 miljoen jaar geleden. Dit blijkt dus niet het geval, en de kikker kan dan ook als een ‘levend fossiel’ beschouwd worden.

Opmerkelijk is dat de Indische kikker geen morfologische gelijkenis meer vertoont met de soorten van de Seychellen. Terwijl deze laatste zuignappen hebben en één van de kleinste kikkersoorten ter wereld (adult 11 mm) bevatten, is de nieuwe ontdekking een gravende kikker van 7 cm groot. Deze soort komt bijna uitsluitend te voorschijn voor de voortplanting tijdens de eerste weken van de moesson, om dan weer diep onder de grond te verdwijnen. Dit verklaart grotendeels waarom deze 100 miljoen jaar oude evolutieve lijn zo lang onopgemerkt gebleven is.

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BIJLAGEN :

In bijlage vindt u het artikel “*New frog family from India reveals an ancient biogeographical link with the Seychelles*”, en het bijhorend “News&Views”-artikel zoals gepubliceerd in het wetenschappelijk tijdschrift *Nature* op 16 oktober 2003.

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New frog family from India reveals an ancient biogeographical link with the Seychelles

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About 96% of the more than 4,800 living anuran species¹ belong to the Neobatrachia or advanced frogs^{2–4}. Because of the extremely poor representation of these animals in the Mesozoic fossil record, hypotheses on their early evolution have to rely largely on extant taxa^{5–7}. Here we report the discovery of a burrowing frog from India that is noticeably distinct from known taxa in all anuran families. Phylogenetic analyses of 2.8 kilobases of mitochondrial and nuclear DNA unambiguously designate this frog as the sister taxon of Sooglossidae, a family exclusively occurring on two granitic islands of the Seychelles archipelago⁸. Furthermore, molecular clock analyses⁹ uncover the branch leading to both taxa as an ancient split in the crown-group Neobatrachia. Our discovery discloses a lineage that may have been more diverse on Indo-Madagascar in the Cretaceous period, but now only comprises four species on the Seychelles and a sole survivor in India. Because of its very distinct morphology and an inferred origin that is earlier than several neobatrachian families¹⁰, we recognize this frog as a new family.

Amphibia L., 1758
 Lissamphibia Haeckel, 1866
 Anura Rafinesque, 1815
 Neobatrachia Reig, 1958
 Nasikabatrachidae fam. nov.
Nasikabatrachus gen. nov.

Nasikabatrachus sahyadrensis gen. et sp. nov.

Etymology. Nasika (Sanskrit) meaning nose, batrachus meaning frog, and Sahyadri, being synonymous for the Western Ghats (the hills along the west coast of the Indian subcontinent).

Holotype. Bombay Natural History Society (BNHS; Mumbai), BNHS 4202, an adult female, snout–vent length 70.1 mm, collected July 2000 by S.D.B. (Fig. 1a).

Type locality. Disturbed secondary forest near a cardamom planta-

tion at Kattappana (09° 45' N, 77° 05' E, altitude approximately 900 m), Idukki district, Kerala, Western Ghats, India.

Diagnosis. The following diagnosis is based solely on the holotype and is thus tentative. A relatively large frog with a bloated general appearance, smooth skin and an overall black coloration dorsally and dark grey ventrally; the head (Fig. 1b) is pointed and short relative to the body; the snout has a distinct white protrusion. The eyes are small with a rounded, horizontal pupil; no apparent tympanum; the forelimbs are short, the hands (Fig. 1c) are rudimentarily webbed, the tips of fingers are rounded, without disks. The hindlimbs are short, feet (Fig. 1d), and the tips of toes are rounded, without disks. A large, white inner metatarsal tubercle is present on both feet (detailed measurements of external morphology are provided as Supplementary Information).

The skeleton (Fig. 1e) is characteristic of a burrowing frog and displays bones with a well-calcified cortical area, a skull with strongly ossified neurocranial and dermal elements (Fig. 1f), a short tibiae and fibulae, strong and short tibiofibular bones, and

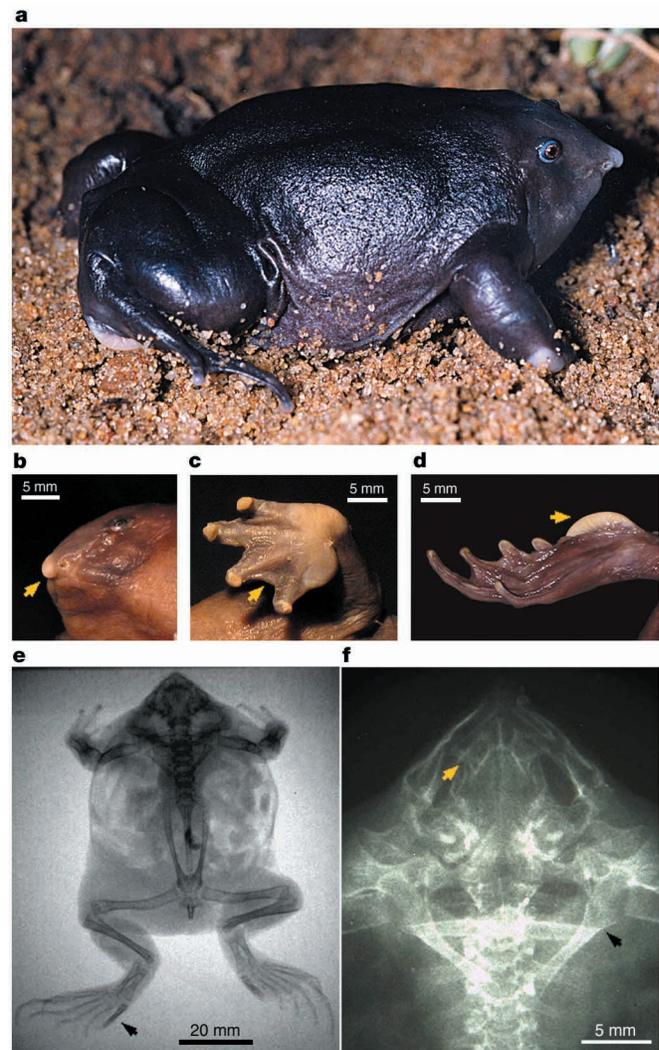


Figure 1 Holotype of *Nasikabatrachus sahyadrensis*. **a**, *Nasikabatrachus sahyadrensis* in life. **b**, Detail of head, showing slender mouth and distinct protrusion on snout. **c**, Detail of hand, showing rudimentary webbing. **d**, Detail of foot showing the large, white inner metatarsal tubercle. **e**, X-ray photograph showing strongly calcified bones. The arrow indicates the prehallux. **f**, X-ray photograph showing strongly ossified skull and pectoral girdle. The yellow arrow indicates the presumed neopalatine bone; the black arrow indicates the coracoid, the lateral end of which is wider than the medial.

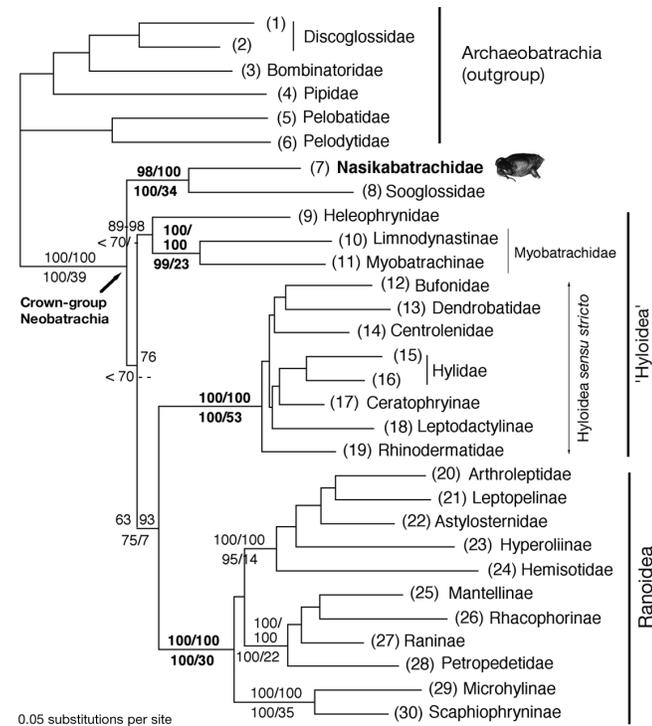


Figure 2 Bayesian consensus phylogram for the analysis of 2,325 bp of DNA. Numbers before (sub)familial names correspond to species as given in the Methods section. Numbers on branches indicate bayesian posterior probabilities and metaGA posterior branch support values (above), respectively, and maximum parsimony bootstrap (10,000 replicates) values and decay indices (below), respectively. The sister group relationship of Nasikabatrachidae with Sooglossidae from the Seychelles is very strongly supported. Although the exact order of early divergences remains tentative, the strong support for several groups (clade support indicated in bold) implies that the Nasikabatrachidae/Sooglossidae lineage is one of the basal-most splits in Neobatrachia.

a well developed and highly calcified prehallux. The following osteological characters were tentatively interpreted from the X-rays: neobatrachian synapomorphies include fusion of the third carpal to other carpals, presence of a neopalatine bone (Fig. 1f) and absence of a parahyoid bone. The pectoral girdle with slender

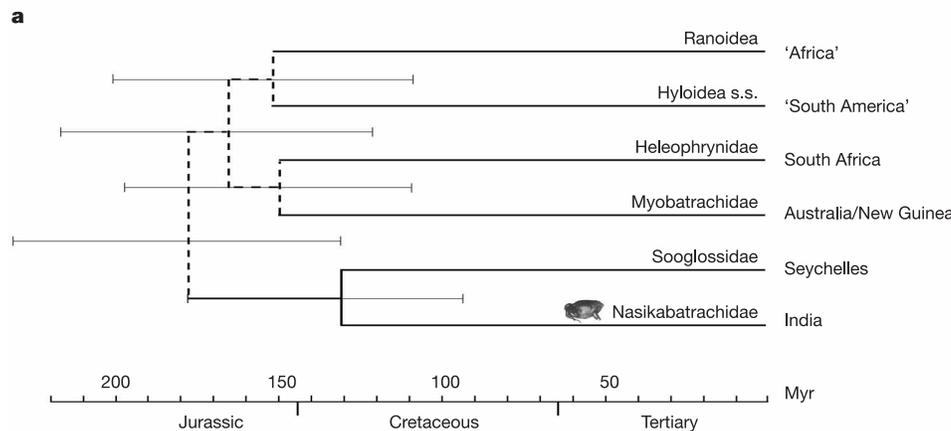


Figure 3 Early evolution of advanced frogs. **a**, Evolutionary tree showing estimates of divergence time for the major lineages, estimated from 1,443 bp of nuclear gene fragments. Analyses were performed on all taxa, but only basal stocks of modern Neobatrachia are shown. Dashed lines indicate uncertain phylogenetic relationships. Thin horizontal lines denote the 95% credibility interval for the corresponding node time. For

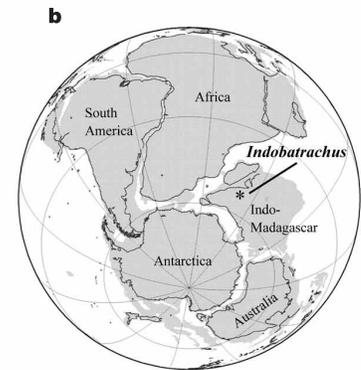
Table 1 Bayesian divergence time estimates

Divergence	Time estimate (Myr ago)
Origin of Ranoidea and Hyloidea s.s.	152 (108, 202)
Origin of Heleophryinae and Myobatrachidae	150 (109, 198)
Origin of Sooglossidae/Nasikabatrachidae lineage	178 (131, 233)
Sooglossidae–Nasikabatrachidae split	131 (93, 177)

See Methods and Supplementary Information for a description of the calibrations used for estimating node times. Numbers in parentheses represent 95% credibility intervals.

coracoids—the lateral end of which is wider than the medial (Fig. 1f)—excludes Nasikabatrachidae from Ranoidea³; a bony element situated at the medio-distal aspect of the tibiale at the level of the third metatarsal, if homologous with the os sesamoides tarsale, links the new family to Sooglossidae³. The combination of the above external and skeletal characters makes Nasikabatrachidae distinct from all anuran families. In particular, the new lineage differs from its sister group Sooglossidae in many aspects, some of the most obvious being the absence of toe disks, a much larger size and the numerous adaptations to a burrowing lifestyle described above.

The phylogenetic position of Sooglossidae has been a point of debate for several decades, and they have been placed variously in Ranoidea¹¹, Hyloidea⁶ or in a trichotomy with the former⁵. Regardless of the optimality criteria used, our mitochondrial DNA, nuclear DNA and combined DNA analyses (see Supplementary Information for analyses of individual genes) strongly support Hyloidea *sensu stricto* and Ranoidea clades, and three additional main lineages: Myobatrachidae, Heleophryinae and the Sooglossidae/Nasikabatrachidae clade (Fig. 2). In the absence of rate constancy, we used a relaxed molecular clock⁹ to estimate their divergence times under different possible topologies (derived from the bayesian posterior probabilities), using multiple calibration points. All analyses resulted in similar dating estimates indicating that the major neobatrachian lineages originated relatively rapidly in the Middle/Late Jurassic and Early Cretaceous periods (Table 1). Around that time, the Gondwanan supercontinent broke up into two landmasses—western Gondwana (Africa and South America) and eastern Gondwana (Australia, Antarctica and Indo-Madagascar)—which rapidly disintegrated further into their respective components¹². These geological events probably isolated the stem group leading to the Nasikabatrachidae/Sooglossidae clade on the Indo-Madagascan fragment of eastern Gondwana (Fig. 3).



each lineage, the current distribution is indicated. Ranoidea and Hyloidea are now wide ranging, but their origin is associated with Africa and South America, respectively⁷. s.s., *sensu stricto*. **b**, Tectonic reconstruction of Gondwana 130.0 Myr ago. The locality of the fossil *Indobatrachus* from the Eocene epoch is indicated with an asterisk.

The endemism of Sooglossidae on the Seychelles has been a constant biogeographical mystery^{5,6,8}. One hypothesis postulates that this family is derived from an extant or extinct ancestral stock on Africa^{11,13}. Alternatively, it has been proposed that Sooglossidae were present on Indo-Madagascar⁶ during its trans-Tethys drift, and subsequently became extinct on India and Madagascar (if they had been present there). The phylogenetic position of Nasikabatrachidae, in combination with our dating estimates, clearly favour the second hypothesis. Furthermore, our analyses indicate that Nasikabatrachidae and Sooglossidae diverged well before the break-up of India and the Seychelles at the Cretaceous/Tertiary boundary (Table 1). Our findings thus uncover the existence of an early stock of advanced frogs, which consisted of at least two major lineages on drifting Indo-Madagascar. It is possible that this assemblage was composed of a much greater diversity during the Cretaceous period on parts of these Gondwanan fragments. Offshoots of this clade may even have existed on Australia and Antarctica, as some tectonic models propose a connection of the latter with Indo-Madagascar until the late Cretaceous period¹⁴.

It has already been suggested that India played a significant role in the passage of amphibians to southeast Asia^{4,15,16}. The phylogenetic pattern revealed here provides independent evidence for this landmass being an important setting for the evolution of advanced frogs. There are no Mesozoic fossil records that testify to the existence of this early assemblage on eastern Gondwana. The only possible palaeontological evidence of a member of this group is *Indobatrachus pusillus* (Owen, 1847) from the Eocene epoch of India. This species has been regarded as a myobatrachid^{4,17,18} or sooglossid^{18,19}, but its osteology is still not completely known¹⁷. Comparison of additional fossil material with extant species of the Nasikabatrachidae/Sooglossidae clade may therefore provide new insights on the phylogenetic position of *Indobatrachus*.

Mesozoic fossils sometimes have important implications for understanding the early history of vertebrate groups^{20,21}. Yet, there are still very few palaeontological findings that have contributed to our knowledge on the origin of advanced frogs. Our discovery of an ancient extant frog lineage in India discloses a clade that significantly adds to the understanding of early neobatrachian biogeography. However, knowledge on how extensively the Indo-Madagascan lineage has radiated (both in the biogeographical and phylogenetic sense) will have to await the recovery of fossils from the Cretaceous period of Gondwanan landmasses. □

Methods

Osteological analyses

In order to perform a preliminary, non-destructive analysis of skeletal characters of the holotype, we made several X-ray photographs. We used a Philips Optimus M200 X-ray system and image intensifier (41 kV, 800 mA). Images were recorded digitally using a Redlake motion Pro high-resolution camera. Furthermore, an MPG 65 generator and a RSN 620 X-ray tube (General Electric) (56 kV, 200 mA) were used to study cranial elements in more detail.

Taxon selection and DNA methods

Our data set includes the following 30 species, sampled from all continental regions (including Madagascar and the granitic Seychelles) and forming a fair representation of the major anuran lineages recognized. Numbers correspond to (sub)familial names in Fig. 2: (1) *Alytes obstetricans boscai*, (2) *Discoglossus pictus*, (3) *Bombina orientalis*, (4) *Pipa pipa*, (5) *Pelobates cultripes*, (6) *Pelodytes punctatus*, (7) *Nasikabatrachus sahyadrensis*, (8) *Nesomantis thomasseti*, (9) *Heleophryne purcelli*, (10) *Limnodynastes salmini*, (11) *Myobatrachus gouldii*, (12) *Bufo melanostictus*, (13) *Dendrobates auratus*, (14) *Centrolene prosoblepon*, (15) *Hyla arenicolor*, (16) *Phrynolias venulosa*, (17) *Ceratophrys ornata*, (18) *Leptodactylus melanonotus*, (19) *Rhinoderma darwini*, (20) *Arthroleptis variabilis*, (21) *Leptopelis kivuensis*, (22) *Trichobatrachus robustus*, (23) *Hyperolius* sp., (24) *Hemisis marmoratus*, (25) *Boophis xerophilus*, (26) *Philautus wynaadensis*, (27) *Meristogenys kinabaluensis*, (28) *Petropedetes cf. parkeri*, (29) *Microhyla ornata*, (30) *Scaphiophryne marmorata*. After preliminary analyses using salamanders as outgroups, Archaeobatrachia (species 1 to 6) were selected as outgroup taxa because of the evidence (osteological and molecular) for monophyly of Neobatrachia (including Nasikabatrachidae).

Two mitochondrial DNA gene fragments—covering part of 12S ribosomal RNA, complete transfer RNA^{Val} and part of 16S rRNA—were sequenced, which together yielded a data matrix of 1,329 base pairs (bp). Additionally, a fragment of the following

nuclear DNA genes was sequenced: exon 1 of rhodopsin, single exon of *Rag1*, and exon 2 of *Cxcr4*, yielding alignments of 315, 555 and 675 bp, respectively. Methods for DNA extraction, amplification (including primers) and sequencing are given elsewhere²². The following primers were developed for this study: Rag1-B, 5'-ATGGGAGATGTGAGTGA RAARCA-3'; Rag1-C, 5'-GGAGATGTTAGTGAAGAARCAAYGG-3'; Rag1-D, 5'-GCTGC ATTTCCRATRTCACATGTG-3'; Rag1-E, 5'-TCCGCTGCATTTCCRATGTGCRCA-3'; and Rag1-F, 5'-CCAATGTCGCAGTGCAGTGCAGCAARGCRT-3'. CXCR4-A, 5'-CTGCTGGGCAT CATTGGRAAYGG-3'; CXCR4-B, 5'-ATCATTGGCAATGGAYTRGT-3'; CXCR4-C, 5'-GTCATGGGCTAYCARAAGAA-3'; CXCR4-D, 5'-AGGACAATGACWGYAATA-3'; CXCR4-E, 5'-AGGACAATGACWGYAAGTA-3'; CXCR4-F, 5'-TTGAATTTGGCCCR AGGAARGC-3'; and CXCR4-G, 5'-AGGCAACAGTGGAARAANGC-3'.

Alignment and phylogenetic analyses

Sequences were aligned using ClustalX 1.64 and ambiguous sections were excluded for subsequent analyses. Phylogenetic analyses were performed using PAUP* 4.0b10 (ref. 23). Plots of transitions and transversions against uncorrected and GTR-corrected pairwise distances indicated that none of the fragments showed saturation. Partition homogeneity tests revealed no significant incongruence among different fragments. Heuristic maximum parsimony searches were executed in 10,000 replicates with all characters unordered and equally weighted. Clade support under maximum parsimony was calculated using decay indices and nonparametric bootstrapping. Appropriate likelihood models were determined using the software Modeltest 3.06 (ref. 24). We also conducted 250 replicated metaGA searches²⁵ using MetaPIGA 1.0.2b, each with strict consensus pruning among four populations, using a HKY + Γ + 1 model (the most parameter-rich model implemented in MetaPIGA) with the T_i/T_c ratio optimized every 200 generations. The 1,000 resulting trees were used to compute a majority-rule consensus tree and calculate posterior branch support values. Bayesian analyses were performed using the software MrBayes 2.01 (ref. 26) under the GTR + Γ + 1 model. Four chains were run simultaneously for 1,000,000 generations and trees were sampled every 100 cycles. Likelihood scores reached stationarity well before 100,000 generations, but to be on the safe side we discarded the first 2,000 trees as the 'burn in'. Hence Bayesian posterior probabilities were estimated as the 50% majority-rule consensus tree of the 8,000 last sampled trees.

Dating estimates

Mean and 95% credibility interval values for node times were estimated from 1,443 bp of nuclear DNA on the consensus phylogram (Fig. 2) using a Bayesian method that allows correlated rate changes between the nodes of a tree⁹. After incorporating in our data set the homologous fragments of the nuclear genes of *Danio rerio*, *Homo sapiens* and *Gallus gallus* (retrieved from GenBank), as well as the caudates *Hynobius formosanus* and *Salamandra salamandra*, we were able to use three calibrations simultaneously: (1) the divergence of amniotes from amphibians at a minimum of 338 Myr ago²⁷; (2) the divergence of diapsids from synapsids at about 310 Myr ago²⁸; and (3) the minimum age of Cryptobranchioidea (164 Myr ago; here represented by the *Hynobius-Salamandra* split)²⁹ (see Supplementary Information).

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Females increase offspring heterozygosity and fitness through extra-pair matings

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Females in a variety of species commonly mate with multiple males, and there is evidence that they benefit by producing offspring of higher genetic quality^{1–3}; however, the nature of these genetic benefits is debated^{1–4}. Enhanced offspring survival or quality can result from intrinsic effects of paternal genes—‘good genes’—or from interactions between the maternal and paternal genomes—‘compatible genes’^{1–5}. Evidence for the latter process is accumulating^{2,6}: matings between relatives lead to decreased reproductive success, and the individual level of inbreeding—measured as average heterozygosity—is a strong fitness predictor^{7–13}. Females should thus benefit from mating with genetically dissimilar males^{2,14}. In many birds, social monogamy restricts mate choice, but females may circumvent this by pursuing extra-pair copulations^{15,16}. Here we show that female blue tits, *Parus caeruleus*, increase the heterozygosity of their progeny through extra-pair matings. Females thereby produce offspring of higher reproductive value, because less inbred individuals have increased survival chances, a more elaborate

male secondary sexual trait (crown colour) and higher reproductive success. The cost of inbreeding may therefore be an important factor driving the evolution of female extra-pair mating.

Previous work suggests that blue tit females gain genetic benefits from mating with multiple males^{17,18}: broods of socially monogamous pairs frequently contain extra-pair young, which are in better condition and are more likely to fledge than their within-pair nest mates¹⁸. So far, the genetic mechanism underlying this fitness advantage is unknown. Individual genetic diversity (heterozygosity) reflects the level of inbreeding and influences survival and fitness in various species^{7–9–13}. High individual heterozygosity reduces the likelihood that recessive deleterious alleles are expressed, or increases the number of potentially useful gene products (for example, at major histocompatibility complex (MHC) genes)⁴. Therefore, mating with individuals carrying dissimilar alleles can be advantageous^{2,14}. If restricted social mate choice leads to pairings of genetically similar individuals, extra-pair copulations provide a mechanism to counteract inbreeding depression by increasing the genetic diversity, and hence fitness, of offspring¹⁶. If female blue tits use this strategy, extra-pair young should be more heterozygous than within-pair young and individual heterozygosity should influence fitness.

We examined genetic parentage, breeding success, and offspring and adult survival in a population of individually marked blue tits breeding in nest boxes in the Viennese Forest, Austria (48°13' N, 16°20' E), from 1998 to 2001. Extra-pair young were more heterozygous than their maternal half-siblings sired by the social father (Fig. 1). This suggests that females are less related to extra-pair fathers than to their social mates. We tested this with all known extra-pair fathers but did not find the expected result (social male, mean relatedness ± standard error of the mean (s.e.m.) = -0.016 ± 0.016; extra-pair males, -0.029 ± 0.014, paired *t*-test, *t* = 0.62, *n* = 96 dyads, *P* = 0.54; 95% confidence interval for the difference in relatedness between female and social/extra-pair male (-0.029, 0.056)). However, 28% of all extra-pair young were sired by unknown males (not found breeding in the study area). Extra-pair young produced by these non-local fathers mainly accounted for the difference in heterozygosity (Fig. 1). Among known extra-pair fathers, close neighbours did not increase offspring heterozygosity, whereas local non-neighbours tended to sire more heterozygous extra-pair young (Fig. 1). Therefore, only non-neighbouring extra-pair males should be less related to the female than her social partner. We failed to find this, but our sample size of broods with known extra-pair fathers is small (local non-neighbours, *n* = 15; non-local males, *n* = 7, both *P* > 0.7). We then tested whether females were generally less related to more distantly breeding males. We measured the distance and calculated the relatedness between all breeding males and females in each of three years. We then averaged relatedness for each of 14 distance classes, ranging from 0 m (social partner) to 1,300 m. In each year, genetic similarity decreased with breeding distance (1998, *r_p* = -0.48, *n* = 13, *P* = 0.096; 1999, *r_p* = -0.63, *n* = 14, *P* = 0.015; 2000, *r_p* = -0.67, *n* = 13, *P* = 0.017; Fisher's combined probability, *P* = 0.003). Thus, a genetic structure in this population enables females to obtain genetically less similar extra-pair partners by copulating with males that breed further away.

Our data show that females increase their offspring's heterozygosity by extra-pair copulations with non-neighbouring males, which accounts for 50% of all extra-pair young (*n* = 385). Extra-pair matings with close neighbours did not lead to increased offspring heterozygosity, but are nevertheless actively pursued by female blue tits (ref. 17 and our own unpublished data). Local extra-pair males were older, larger and sang longer strophes than the cuckolded males in a Belgian population^{17,18}. Similarly, we found here that extra-pair males were older and larger than the social males if they were close neighbours (age in years: social male, mean ± s.e.m. = 1.6 ± 0.1; extra-pair male, 2.0 ± 0.1, Wilcoxon's

The coelacanth of frogs

S. Blair Hedges

A frog that lives in the mountains of southern India is a rare breed indeed: it is a new species that merits the establishment of a new family. Moreover, this is a discovery with considerable biogeographical significance.

The discovery of a living coelacanth in 1938 captured public attention because it represented an ancient lineage of fishes thought to have been extinct for some 80 million years¹. Now, a living amphibian with unusually deep evolutionary roots has been discovered in India. Writing on page 711 of this issue², Biju and Bossuyt describe this odd-looking species of frog, which was collected in the Western Ghats Mountains of southern India. The characteristics that seem strange to a non-herpetologist — a bloated body, stubby limbs, tiny eyes and protruding snout (Fig. 1) — are not uncommon in burrowing frogs. However, its internal anatomy and DNA sequence data show that this species represents a deep branch in the family tree of frogs. Its closest relatives live in the Seychelles, 3,000 kilometres south of India, near Madagascar. Appropriately, the authors place their new species in a new family.

Just how significant is the discovery of another family of frogs? Only 29 families are known, encompassing the approximately 4,800 known species³. Most of these families were named by the mid-1800s, and the last discovery of a species of frog belonging to a new family, as opposed to merely a taxonomic rearrangement, was in 1926 (ref. 3). All others date to the 1700s and 1800s, making this a once-in-a-century find. Moreover, according to fossils and evolutionary 'clocks' devised using molecular data, families of frogs are about as ancient as orders and superorders of mammals, having diverged

from one another during the heyday of the dinosaurs in the Mesozoic era (251–65 million years ago)^{2,4}.

This discovery also draws attention to our incomplete knowledge of biological diversity, even at the higher taxonomic levels. The home of this plump amphibian, the Western Ghats, is one of the eight 'hottest hot spots' of biodiversity in the world⁵, meaning that many species occur there that are found nowhere else. Like most other hot spots, it was a region once covered with tropical forests. But pressures from human activities, such as farming, have reduced the forests to less than 10% of their former extent⁵.

Biologists are racing to survey and discover species in hot spots before they disappear. Unfortunately, fieldwork can be dangerous (diseases, guerrilla wars, venomous animals), and greater efforts are now required to reach unaltered habitats, such as the tops of mountains. Moreover, some governments are afraid of losing their countries' genetic resources, and have been discouraging foreign scientists from collecting plants and animals. To complete a gloomy picture, taxonomy in general has become an unpopular career choice. Nonetheless, extraordinary discoveries such as this frog show that there is an urgent need for more biotic surveys.

Of great interest to biogeographers is the finding that the new species is most closely related to Seychellean frogs of the family



Sooglossidae. Ocean travel by salt-water rafting is not necessary to explain this relationship, because models of continental drift in the Mesozoic place India and the southern land areas together. The southern supercontinent Gondwana began breaking up 160 million years ago, separating a western continent of South America and Africa from an eastern continent of India, Madagascar, the Seychelles, Antarctica and Australia. Thereafter, the eastern continent continued to break apart, losing Antarctica–Australia (130 million years ago), Madagascar (90 million years ago), and finally the Seychelles (65 million years ago) as India continued northwards. India's collision with Asia, 55 million years ago, created the Himalayas^{6–8}. If this geological history is correct, India should have been a 'biotic ferry' with a passenger list of distinctive plant and animal groups that evolved in isolation for tens of millions of years (Fig. 2a).

Figure 1 Star frog: the new species and only member of a newly designated family².

S. D. Biju

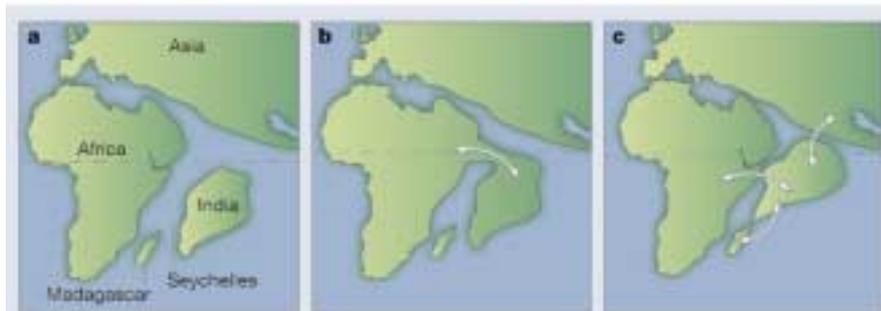


Figure 2 Possible Indian odysseys: different models for the position of India approximately 65 million years ago. a. The standard 'biotic ferry' model showing India isolated by large expanses of water⁶. b. A limited 'biotic (land) bridge' model incorporating a narrow connection (Greater Somalia) with Africa⁷. c. Another biotic bridge model assuming a different longitudinal position for India and showing connections with Madagascar, Africa and Asia⁸. The discovery of the new species of frog in India lends support to a biotic ferry model, but the fossil evidence of other animals favours the existence of land bridges.

Oddly, however, the late Mesozoic fossil record of India does not support a biotic ferry model. Instead, it reveals organisms with close relatives in Africa, South America and Asia^{6,7}, including dinosaurs, lizards, frogs and mammals. Because the geological data allow some flexibility in reconstructing palaeogeography, new models have been proposed that incorporate late Mesozoic land bridges between India and other areas, especially Africa (Fig. 2b,c)^{6,7}.

How does the new species of frog from India bear on these biogeographical models? If it diverged from the Seychellean frogs (sooglossids) as early as molecular clocks indicate, 130 million years ago², continental

breakup would not directly explain its origin — India did not split from the Seychelles until 65 million years later. However, the apparent isolation of Biju and Bossuyt's frog family in India supports the biotic ferry model. Molecular-clock studies of other living groups of plants⁹ and animals^{10,11}, including caecilians (limbless amphibians), also indicate that India developed a unique biota during its northward trek.

But why does the current biota reflect such isolation while the late Mesozoic fossils of India indicate past land connections ('biotic bridges')? Perhaps those bridges were more like chains of islands that allowed some — but not all — groups to disperse, as occurred in the past history of plant and animal interchange between North and South America¹².

The discovery of this remarkable new species adds to growing evidence of past isolation in the biogeographical history of India. Nonetheless, it is unclear why India's Mesozoic partner Madagascar lacks some major groups of vertebrates, such as caecilians and representatives of the new frog family, when evolutionary analyses indicate that

they should have been there in the past. Clearly, there is a need for more fossil collections and investigation of living faunas, and for refined molecular clocks, to better understand how continental drift influenced India's biota. ■

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