



# Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards

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## Abstract

**Aim:** Hyper-arid sandy and rocky fields rank among the least biologically diverse habitats of the desert biome, yet knowledge of local biodiversity patterns is also extremely poor. In the Sahara Desert, palaeoclimate oscillations affected the extent of hyper-arid habitats, but it is unclear how these dynamics determined the evolution and distribution of local specialists. Herein, we assessed cryptic diversity, diversification patterns and spatial connectivity within a Sahara-widespread group of dryland-adapted lizards.

**Location:** Sahara-Sahel ecoregions.

**Taxon:** *Acanthodactylus scutellatus* species group.

**Methods:** Inter- and intraspecific phylogenetic structure, divergence times, spatial genetic patterns and cryptic diversity were assessed using nuclear and mitochondrial loci. The effects of topography and land cover on phylogeographic structure and diversity were tested with generalized linear models. Interspecific hybridization was evaluated using 11 microsatellites across the group's major sympatry zone, predicted based on ecological niche models.

**Results:** Species of *Acanthodactylus scutellatus* group exhibit Late Miocene origins, followed by extensive intraspecific divergence throughout the Pliocene. The northern Sahara worked as a major diversification hotspot, harbouring a patchwork of small-ranged, divergent lineages. These lineages are parapatric or sympatric and present concordant nuclear and mitochondrial differentiation, suggesting species status. Genetic connectivity increases in southern latitudes, with wide-ranging lineages spanning from the Red Sea to the Atlantic coast. Within these potential corridors, mountain outskirts and sand fields in the Sahara interior seemingly acted as origins for recent population expansions. Genetic diversity and connectivity are favoured by terrain roughness and soft-sand cover respectively. Three species inhabit the Atlantic Sahara sympatry zone without evidence of gene flow.

**Main conclusions:** Overlooked species-level diversity within a major specialist group of Sahara drylands exposes the recurrent knowledge shortfalls present in hyper-arid

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**Funding information**

National Geographic Society; Mohammed bin Zayed Species Conservation Fund; Fundação para a Ciência e a Tecnologia; European Regional Development Fund

**Handling Editor:** Rayna Bell.

desert environments. Humidity and sandy habitat shifts triggered potential successions of population isolation and re-connectivity, which favoured cladogenesis in northern desert regions and population expansions across southern east-west corridors.

**KEYWORDS**

climatic cycles, gene flow, hidden diversity, lizard, North Africa, phylogeography, sand corridor, speciation, sympatry, xeric

## 1 | INTRODUCTION

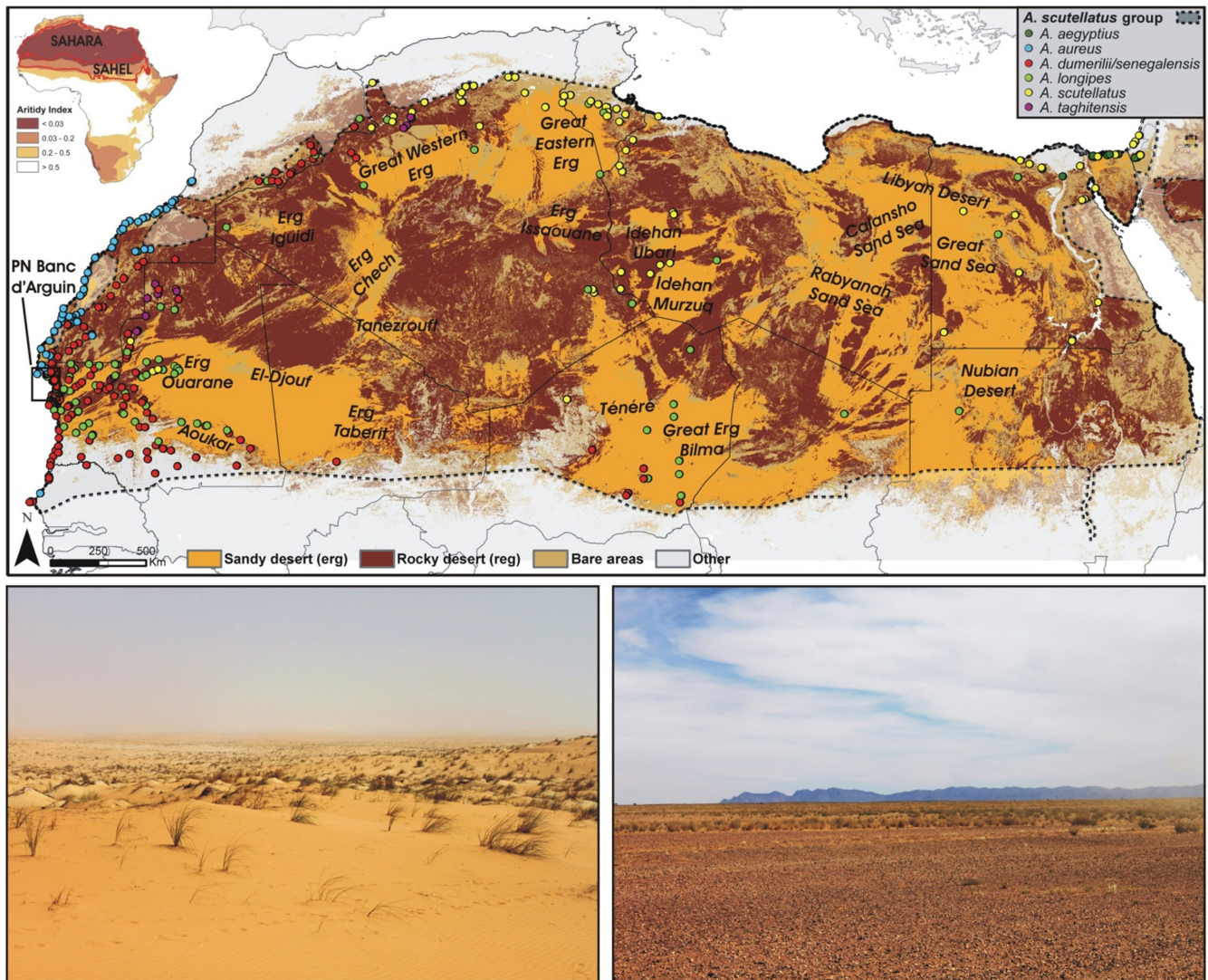
Deserts and arid zones present the lowest species richness among the Earth's biomes (Hughes et al., 2021). Biased by this poor diversity, we tend to perceive desert biomes as vast and homogeneous environments devoid of life, which consequently attract less research and conservation interest (Durant et al., 2012) despite providing key global ecosystems services (e.g., climate regulation [Barkley et al., 2022]). However, many deserts experienced a dynamic geological past (Pepper & Keogh, 2021) that generated high levels of endemism (Šmíd et al., 2021) and unique biodiversity adaptations to aridity (Ward, 2016). The Sahara Desert, together with the neighbouring Sahel (Figure 1), is the largest warm desert on Earth, exhibiting a wide variety of climate and topography (Brito et al., 2014). It spans poor and low developed areas where remoteness, armed conflicts and socio-political instability have undermined surveying and research for decades (Brito et al., 2018). Because of this, Saharan biodiversity is possibly the least known among world deserts (Brito & Pleguezuelos, 2020). Yet, severe anthropogenic (Durant et al., 2014) and climatic (Soulтан et al., 2019) disturbances heighten the urgency to properly catalogue its extant species, understand their biogeographic and evolutionary history and identify priority conservation zones (Brito et al., 2016).

The inventory of Saharan species diversity has long relied on external morphology (e.g., Crochet et al., 2003), which can be misleading given that species' morphology tends to converge due to the harsh desert environments. This has led to a low-resolution taxonomy where distant populations without obvious morphological differences were aggregated under the same unit (e.g., *Mesalina* spp. [Pizzigalli et al., 2021]), thus creating an impression of low biological turnover across the desert. The implementation of molecular tools (reviewed by Brito et al., 2014 but see Velo-Antón et al., 2022) led to the identification of unrecognized diversity within several wide-ranging species (e.g., *Tropicolotes tripolitanus* [Machado et al., 2020]), questioning the presumed homogeneity of the Sahara. However, research efforts are largely biased towards the milder and more accessible areas (mountains [e.g., Liz et al., 2021] and desert margins [e.g., Velo-Antón et al., 2018]; Weiss et al., 2018), while the most xeric habitats (i.e., Aridity Index <0.03 [Ward, 2016]; Figure 1) remain genuinely understudied and perceived as biologically uniform (Brito et al., 2014). These habitats exhibit more geological and ecological diversity than what is often realized (Brito & Pleguezuelos, 2020),

harbouring specialists of a single type of substratum such as sand dunes (*ergs*; e.g., *Scincus* spp. [Šmíd et al., 2020]) or rocky plains (*regs* or *hammadas*; e.g., *Uromastix* spp. [Tamar et al., 2017]). Incomplete knowledge negatively impacts conservation efforts due to biased biodiversity metrics (Brito et al., 2016); thus, phylogeographic studies of wide-ranging xeric species are needed to assess the extent of knowledge shortfalls in the hyper-arid Sahara.

Speciation events and current biodiversity distribution patterns in the Sahara have been influenced by dry/humid cycles since the Late Miocene (Drake et al., 2011). The land cover changes that resulted from climatic oscillations likely elicited contrasting responses from taxa with different ecological requirements (Brito et al., 2014). Mountains are traditionally depicted as refugia and speciation centres for mesic species (e.g., *Agama* spp. [Gonçalves, Pereira, et al., 2018]), but it is unclear how this pattern applies to dryland specialists. These species may have experienced isolation and divergence in xeric lowlands, which were fragmented during green Sahara periods (such as the African Humid Period ~6 kya). However, the climatic cores of xeric habitats could have become too extreme to allow long-term population persistence during arid phases, which would imply that xeric refugia are instead located on the edge of these habitats or on the outskirts of mountain regions. The intermittent expansion and interconnection of sand fields opened opportunities for the dispersal of *erg* specialists, leading to rapid trans-Saharan radiations (e.g. *Scincus* spp. [Šmíd et al., 2020]). No comprehensive assessment exists on the location of these corridors, although the current distribution of some sand-adapted lineages (e.g., *Stenodactylus petrii* [Metallinou et al., 2012]) suggests that they stretched from east to west of the continent throughout southern desert regions, potentially linked to southward desert expansions during arid Sahara phases (e.g., Last Glacial Maximum ~21 kya; Steele, 2007). This contrasts with a widespread pattern of range breaks across northern regions (e.g., *Chalcides* spp. [Carranza et al., 2008]), where humid barriers between xeric habitats (Scerri et al., 2014) likely prompted population fragmentation.

Wide-ranging dryland-adapted taxa with high ecological or morphological variation are ideal to investigate the major drivers of diversification in xeric species. *Acanthodactylus* fringed-toed lizards present such high diversity, holding similar potential for eco-evolutionary studies to *Podarcis* spp. in Europe (Yang et al., 2021), but are still poorly studied. The *A. scutellatus* species group (Boulenger, 1921; hereafter, *Scutellatus* group) comprises



**FIGURE 1** Top: Land cover map of the study area including the three desert-type variables (Bicheron et al., 2009), with main *ergs* indicated in bold. Circles represent samples of *Acanthodactylus scutellatus* group used in the phylogenetic analysis, with species differentiated by colour. The dashed polygon represents the group's range (modified from Roll et al., 2017). The sympatry zone Parc National du Banc d'Arguin targeted in the population genetic analysis is highlighted. Map projection: WGS84. Bottom: Photographs of two hyper-arid habitats, the *erg* Aoukar (left) and the *reg* Gleib el Outat (right) in Mauritania.

seven recognized species (*A. aegyptius*, *A. aureus*, *A. dumerilii*, *A. longipes*, *A. scutellatus*, *A. senegalensis* and *A. taghitensis*) which are abundant and conspicuous across xeric environments of North Africa and the Middle East (Figure 1; Figure S1.1 in Appendix S1; Sindaco & Jeremčenko, 2008), and easily sampled in accessible regions of the hyper-arid Sahara. Most species are linked to sandy habitats, but their ecology varies from the soft-sand specialist *A. longipes* to the more generalist *A. scutellatus*. The only exception is *A. taghitensis*, which only occurs in gravel plains. Despite the group's potential as a study system, baseline knowledge of the species' distributions and phylogenetic relationships is still preliminary (Harris & Arnold, 2000; Psonis et al., 2016; Tamar et al., 2016) or limited to small areas (Velo-Antón et al., 2018). These species show both a high interspecific morphological conservatism and a large amount of intraspecific

variation (Arnold, 1983; Salvador, 1982), which hampers morphological identification and systematics. The occurrence of morphologically intermediate specimens has raised suspicion of interspecific hybridization (Crochet et al., 2003) despite their million-year-old divergence (Tamar et al., 2016). As with many other groups of small vertebrates, distinguishing evolutionary sensible units from geographical variations in morphology requires molecular tools.

The main objective of this study is to understand the biogeographic and ecological drivers of evolutionary diversity in the *Scutellatus* group across the Sahara-Sahel. To do so, we combine ecological niche modelling with phylogenetic and population genetic analyses. First, we examine the distribution of genetic diversity at inter- and intraspecific levels, unveiling a considerable amount of previously unrecognized diversity, to: (1) identify

areas of higher diversity and distinctiveness (i.e., diversification hotspots); and (2) map shared genetic diversity (i.e., recent connectivity). Given palaeogeomodels and allopatric lineage distributions in other sand-dwelling taxa across northern Sahara, we expect multiple diversification hotspots in this region resulting from recurrent fragmentation of xeric habitats. In contrast, we expect widespread connectivity in the south of the Sahara and in the Sahel, where fewer humid barriers among xeric habitats exist as a result of great sand expansion dynamics during the Plio-Pleistocene. Secondly, we (3) investigate the role of speciation in generating evolutionary diversity in the *Scutellatus* group, by examining if recent admixture takes place in an area of sympatry where the number of overlapping evolutionary units is especially large.

## 2 | MATERIALS AND METHODS

### 2.1 | Study region and data collection

Our study area comprises xeric areas of North Africa and adjacent portions of the Middle East (Figure 1). It includes the ecoregions Sahara Desert and parts of the Sahel savannah, as well as neighbouring Mediterranean steppes and dry woodlands in North Africa and the xeric shrublands from Sinai and southern Levant in the Middle East (Dinerstein et al., 2017). For population genetics analyses, we selected an area in coastal Mauritania, the Parc National du Banc d'Arguin (PNBA; Figure 1), where *A. aureus*, *A. dumerilii*, *A. longipes* and *A. senegalensis* are sympatric (Roll et al., 2017; and see Section 3.3) and morphologically intermediate individuals have been reported (Crochet et al., 2003).

For phylogenetic analyses, we used 542 georeferenced tissue samples collected during field expeditions between 2003 and 2019 or acquired from museum collections, representing all the currently accepted species within the *Scutellatus* group (Figure 1; Table S2.1 in Appendix S2). Previously published sequences from additional 124 georeferenced samples were retrieved from GenBank (Tamar et al., 2014; Tamar et al., 2016; Velo-Antón et al., 2018). For ecological modelling, we gathered species' occurrence records from fieldwork, museums and bibliography, totalling 930 observations (Table S2.1). Models targeted all recognized species except for the monophyletic unit made of *A. dumerilii* and *A. senegalensis* (*A. dumerilii/senegalensis* hereafter), following the results of the genetic analyses (see Section 3.1). Observations lacking genetic diagnosis (28%) were only kept if they were located in congruent localities and the taxonomic identification was not dubious. For population genetics, we used a subset of 208 samples from the sympatry zone (Table S2.1). These samples were preliminarily identified based on external morphological characters (scalation and colour pattern; Crochet et al., 2003) and included typical morphotypes for the putative species *A. aureus*, *A. longipes*, *A. dumerilii* and *A. senegalensis*, as well as morphologically intermediate individuals between the latter two taxa.

### 2.2 | Ecological variables

For ecological models, we used multitemporal remote sensing variables derived from preprocessed data of two NASA satellites (dataset MODIS v4; EDENext project). These sources covered the following bands and derived products: middle infra-red (MIR [Jensen, 2007]); day and night time land surface temperatures; normalized difference vegetation index (NDVI [Tucker, 1979]); and enhanced vegetation index (EVI [Huete et al., 1997]). Additionally, we included the eight precipitation-related bioclimatic variables (bio12–bio19); WorldClim 2.0; Fick & Hijmans, 2017) and three desert-specific land cover types (Globcover dataset; Bicheron et al., 2009): *erg*, *reg* and bare-area. All variables were downloaded or upscaled to 30 arc-sec resolution ( $\sim 1 \times 1$  km) and cropped to the study area. Pairwise correlations were assessed based on Spearman's  $R^2 < 0.7$ , selecting a final subset of 18 low-correlated variables (Table S2.2). Extended details in variable selection and processing are given in Text S3.1 in Appendix S3.

### 2.3 | DNA extraction, amplification, sequencing and genotyping

Standard protocols for DNA extraction, amplification and sequencing were followed (see details in Text S3.2). For phylogenetic analyses, two mitochondrial fragments, the 12S ribosomal RNA (12S; 368 base pairs) and the cytochrome-b (Cytb; 377 bp), and the nuclear fragment oocyte maturation factor MOS (C-mos; 468 bp) were targeted. Primers and PCR conditions are given in Tables S2.3 and S2.4 respectively. For population genetic analyses, a selection of 14 microsatellites previously developed for the *Scutellatus* group (Lopes et al., 2015; Table S2.5) was used to genotype the samples from the sympatry zone.

### 2.4 | Phylogenetic inference, divergence dating and lineage delimitation

Sequences were arranged into concatenated mitochondrial (mtDNA;  $n = 555$ ; 745 bp) and cytonuclear (mt-nuDNA;  $n = 482$ ; 1213 bp) datasets (Table S2.1), including samples successfully sequenced for all target markers. Outgroups included representatives of the other two major *Acanthodactylus* clades (Tamar et al., 2016), as well as of the closely related *Mesalina* genus (Table S2.6).

Bayesian Inference (BI) and Maximum Likelihood (ML) analyses were performed with the mt-nuDNA dataset, using BEAST v.1.10.4 (Suchard et al., 2018) and RAXMLGUI (Silvestro & Michalak, 2012) respectively. BEAST was run on the CIPRES gateway (Miller et al., 2010) in two independent runs of  $10^8$  generations, sampling at every  $10^4$ , with unlinked substitution and clock models (Drummond et al., 2006), a constant population size coalescent tree prior (Kingman, 1982) and considering ambiguities in the nuclear partition. For ML analyses,



1000 bootstrap replications were performed. Extended details on the phylogenetic analyses are given in Text S3.3 and Table S2.7. Nodes in the resultant BI and ML trees were considered well supported at posterior probabilities >0.95 and bootstrap values >85 respectively.

The BI phylogenetic inference was time calibrated following the strategy of Tamar et al. (2016). Another mt-nuDNA alignment was produced using representatives of all intraspecific lineages ( $n = 74$ ; Table S2.1) and adding sequences of *Gallotia*, *Psammodromus* and *Podarcis* spp. (Table S2.6). Biogeographic calibration events were the end of the Messinian Salinity Crisis and the ages of the Canary Islands (Table S2.8). Node split times were estimated in BEAST v.1.10.4 (Suchard et al., 2018; see Table S2.7 for detailed settings).

Previously published lineages of *A. aureus* (Velo-Antón et al., 2018) were the baseline threshold to delimit intraspecific lineages within the *Scutellatus* group. Lineages were defined as those reciprocally monophyletic, well-supported clades in the BI mt-nuDNA tree, with splits from sister taxa older than the most recent lineage split within *A. aureus* (1.84 Mya). Our study includes a similar set of genetic markers (excluding cytochrome oxidase I) to those used in the original delimitation (Velo-Antón et al., 2018). Despite its limitations, this strategy works well for assessing intraspecific diversity patterns across the study area, and the general patterns recovered remain consistent when applying more conservative thresholds (e.g. first split within *A. aureus* 3.09 Mya).

Intraspecific haplotype networks were constructed for *C-mos* and the mtDNA marker sequenced for the most samples (12S;  $n = 635$ ; Table S2.1) using Tcs v.1.21 (Clement et al., 2002), with 95% parsimony threshold and visualized using TCSBU (Santos et al., 2015). The nuclear haplotypes were reconstructed for each species using the PHASE implementation in DNASP 5.10.01 (Librado & Rozas, 2009), with  $10^4$  iterations and  $10^3$  of burn-in. Pairwise genetic distances ( $p$ -distances) between species and lineages were calculated on 12S using MEGA v.7 (Tamura et al., 2013), based on Kimura-2 parameter model.

## 2.5 | Spatial interpolations of genetic data

Intraspecific nucleotide diversity was calculated using the mtDNA dataset with 'Pegas' R package (Paradis, 2010). For each species, we measured the pairwise distance between samples and identified the maximum nearest-neighbour distance. This distance was set as a radius of a neighbourhood from which a set of samples was selected to calculate average nucleotide diversity (thus guaranteeing that at least two samples were included in each neighbourhood). To reduce bias due to the different number of samples within the neighbourhood of each location, from the set of haplotypes within the neighbourhood, two of them were iteratively resampled with replacement (1000 replicates) to calculate pairwise nucleotide diversity. Values were averaged across replicates to obtain an estimation of genetic distinctiveness for each mtDNA haplotype in relation to the whole species' diversity. To predict patterns across species' ranges, genetic

distinctiveness was spatially interpolated with the *idw* function of 'phylin' R package (Tarroso et al., 2019), using two spatial grid sizes to account for differences in species' range sizes and sampling: 10x10 km for *A. aegyptius*, *A. aureus*, *A. dumerilii/senegalensis* and *A. taghitensis*; and 50x50 km for *A. longipes* and *A. scutellatus*. Projections were clipped to species' ranges (Roll et al., 2017).

## 2.6 | Landscape drivers of genetic structure and diversity

Generalized linear models (GLMs; Matthiopoulos, 2011) with normal errors were fitted in R to test the effect of different topographic and land cover variables on genetic diversity and connectivity. Two independent approaches were followed, where the response variables were mtDNA haplotype distinctiveness ('diversification model') and diameter of lineage Minimum Convex Polygon (MCP; 'connectivity model') respectively. As predictors for the diversification model, absolute values of altitude and index of terrain roughness (Title & Bemmels, 2018), as well as coverage percentage of *erg*, *reg* and bare-area (Bicheron et al., 2009), were extracted from each haplotype locality, excluding duplicates; for the connectivity model, averages of the same five variables were calculated within MCPs of all lineages using the Zonal Statistics tool of ArcGIS v.10.5 (ESRI, 2006). Additionally, species was included as a predictor in both models, while nearest-neighbour distance and number of lineage samples were also included in the diversification and connectivity models respectively. Model comparisons were performed using different combinations of topographic and land cover predictors based on the Akaike information criterion (AIC; Akaike, 1998), in order to build the best-fitting models including only one topographic and one land cover predictor. Lineages with a sample count <3 were excluded from the connectivity model because it is not possible to construct an MCP for these lineages.

## 2.7 | Ecological niche modelling

For each species, the initial pool of records was tested for spatial clustering to account for potential sampling bias and to avoid model overfitting (Boria et al., 2014) using the *ecospat.mantel.correlogram* function of 'ecospat' R package (Di Cola et al., 2017), and thinned accordingly with 'spThin' (Aiello-Lammens et al., 2015). The final sets contained: 37 records of *A. aegyptius* (minimum distance between records: 7 km); 47 of *A. aureus* (16 km); 82 of *A. dumerilii/senegalensis* (52 km); 77 of *A. longipes* (67 km); 70 of *A. scutellatus* (49 km); and 17 of *A. taghitensis* (18 km).

The contemporary ecological niche of each species was modelled using BIOMOD2 (Thuiller et al., 2021). Detailed procedures are given in Text S3.4. Six algorithms were chosen to reduce the uncertainties associated with modelling techniques (Thuiller et al., 2019). Ten model replicates were run for each of the six algorithms for each species, using 80% of presence data for training.

A final ensemble model was built using model replicates for which the area under the receiver operating characteristic curve (AUC; Fielding & Bell, 1997) was  $>0.7$ . Replicates were weighted proportionally according to predictive performance (Marmion et al., 2009).

Ensemble models were clipped to species' ranges (Roll et al., 2017). Projections of ensemble models were assessed using clamping masks to identify and minimize errors in spatial extrapolations beyond the training range of the models (Elith et al., 2010). Ensemble models were converted to binary (i.e., suitable/unsuitable habitat) using the TSS cut-off threshold. Binary projections between species were overlapped in ArcGIS 10.5 (ESRI, 2006) to infer sympatry zones.

## 2.8 | Microsatellite analyses

Evidence of stuttering, null alleles and allelic dropouts was assessed using MICRO-CHECKER 2.2.3 (Van Oosterhout et al., 2004). Tests for genotypic linkage disequilibrium (LD) and Hardy-Weinberg equilibrium (HWE) were assessed in GENEPOP'007 (Rousset, 2008), with individuals grouped based on the three recovered phylogenetic clades (see Section 3.1). Subsequent sequential Bonferroni corrections were applied in both cases.

Bayesian population clustering analyses were conducted in STRUCTURE 2.3.4 (Pritchard et al., 2000) to estimate the optimal number of clusters, assign individuals to each resultant cluster and infer the differentiation and relationships among clusters (see details in Text S3.5). All genotyped samples were also sequenced for at least one phylogenetic marker except for four cases of failed amplification in *A. aureus*. Potential admixture was examined by assessing concordance between mtDNA and microsatellites species assignment and by examining individual ancestry based on microsatellites clustering. Admixed individuals would indicate contemporary hybridization while cytonuclear discordance in species assignment would suggest past introgression.

## 3 | RESULTS

### 3.1 | Phylogenetic inferences

The phylogenetic mt-nuDNA trees revealed five major, well-supported, monophyletic clades, partially matching with six species of the Scutellatus group (Figure 2; Figures S1.2 and S1.3). *Acanthodactylus aureus*, *A. taghitensis*, *A. longipes* and *A. scutellatus* were recovered as reciprocally monophyletic clades that were largely consistent with the preliminary field identification of the specimens. Samples identified as *A. dumerilii* and *A. senegalensis* were placed together in a single clade. Samples of *A. aegyptius* formed a monophyletic group within *A. longipes*. The relationships between the major clades were strongly supported except for the position of *A. taghitensis*. Divergence estimates indicate that the diversification

of the group started in the Middle Miocene (Figures 2; Figure S1.4) with the basal branching of *A. aureus*  $\sim 16.9$  Mya (95% HPD: 12.7–21.3). All remaining major clades split throughout the Late Miocene. Within major clades, diversification onsets were placed in the Late Miocene (around 7.6–7.9 Mya) for *A. longipes* and *A. scutellatus*, and in the Early Pliocene (4.3–5.1 Mya) for *A. taghitensis* and *A. dumerilii/senegalensis*. Diversification of *A. aureus* started in the Late Pliocene. All major clades presented distinguishable nuclear haplogroups except for *A. dumerilii/senegalensis*, in which some alleles from the intraspecific lineage 'NW Sahara' were embedded within *A. scutellatus* (Figure S1.5).

The five major clades include several lineages with variable range sizes (Figure 2) and degree of genetic differentiation (Figures S1.6 and S1.7a–S1.7c; Table S2.9). The *A. aureus* clade includes three parapatric lineages distributed along the Atlantic Sahara but lacking evidence for nuclear differentiation (concordant with Velo-Antón et al., 2018). Samples of *A. taghitensis* are divided into two allopatric lineages, one from each of the disjoint occurrence areas in Algeria and Mauritania, exhibiting high mtDNA distance and lack of nuclear allele sharing. The *A. longipes* samples form a diverse pan-Saharan complex composed of eight lineages, including *A. aegyptius*, with strongly supported relationships except for the position of lineage 'Grand Western Erg'. Two of these lineages range from the Central Sahara-Sahel to the Red Sea ('E Sahara-Sahel') and Atlantic ('W Sahara-Sahel South') coasts, respectively; two others span over a wide latitudinal axis ('Central Sahara' and 'W Sahara-Sahel Inland'); and all the remaining ones are found in smaller areas across northern Sahara. The three basal lineages of the complex ('Tunisia', 'Grand Western Erg', '*A. aegyptius*') exhibit parapatric distributions relative to adjacent lineages and present remarkable mtDNA distances and private nuclear alleles that are not shared between them or with any other lineage. The *A. scutellatus* clade is another pan-Saharan complex structured in 10 lineages, with mostly unresolved relationships. Among this diversity, one lineage is broadly distributed from Mauritania to Egypt ('Pansaharan'), another from the Central Sahara to the Red Sea ('N Sahara') and the rest show restricted distributions across northern Sahara and the Central Sahara highlands, where they occur mostly in parapatry or even in sympatry. All lineages are separated by several mtDNA mutation steps, whereas four lineages also present private nuclear alleles and two only share one allele. The *A. dumerilii/senegalensis* clade includes four lineages in two main branches, with all relationships resolved except for the split between lineages 'Merzouga' and 'NW Sahara'. One branch is formed by a widespread lineage, spanning over the western Sahara-Sahel throughout the southern distribution of *A. dumerilii* and the entire range of *A. senegalensis*. The other branch is highly diverse, harbouring three seemingly sympatric lineages restricted to a small area on the Moroccan-Algerian border. These lineages exhibit high nuclear differentiation in relation to the other main branch of *A. dumerilii/senegalensis*. Lineage 'Merzouga' is represented by a unique nuclear haplotype that is very distant from those of the other two local lineages. Within lineage 'NW Sahara', one nuclear allele is highly separated from the others, being placed close to lineage 'Merzouga'.

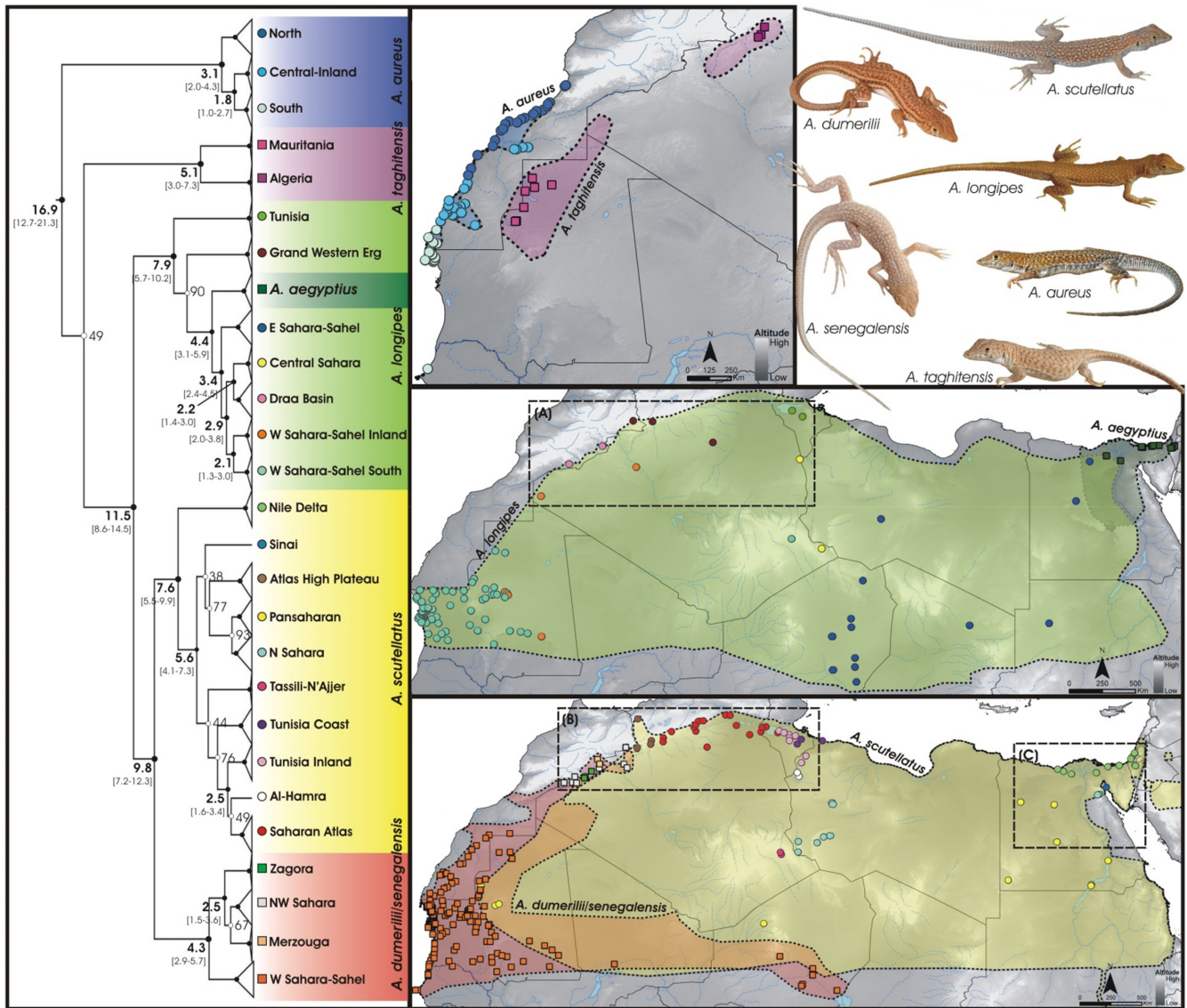


FIGURE 2 Left: Time-calibrated Bayesian mt-nuDNA tree showing species and intraspecific lineages within *Acanthodactylus scutellatus* group, obtained from the concatenation of two mtDNA fragments and one nuclear gene (12S, Cytb, and C-Mos; 1213 bp). Black dots represent supported nodes, with posterior probabilities (pp) > 0.95; white dots represent unsupported nodes, where pp values are indicated at the right. Split times (Mya) are given in bold for supported nodes (95% HPD between brackets). See Figure S1.2 for full sample names. Right: Distribution maps of intraspecific lineages. Dashed rectangles depict small-ranged lineage hotspots zoomed in Figure S1.7. Map projections: WGS84.

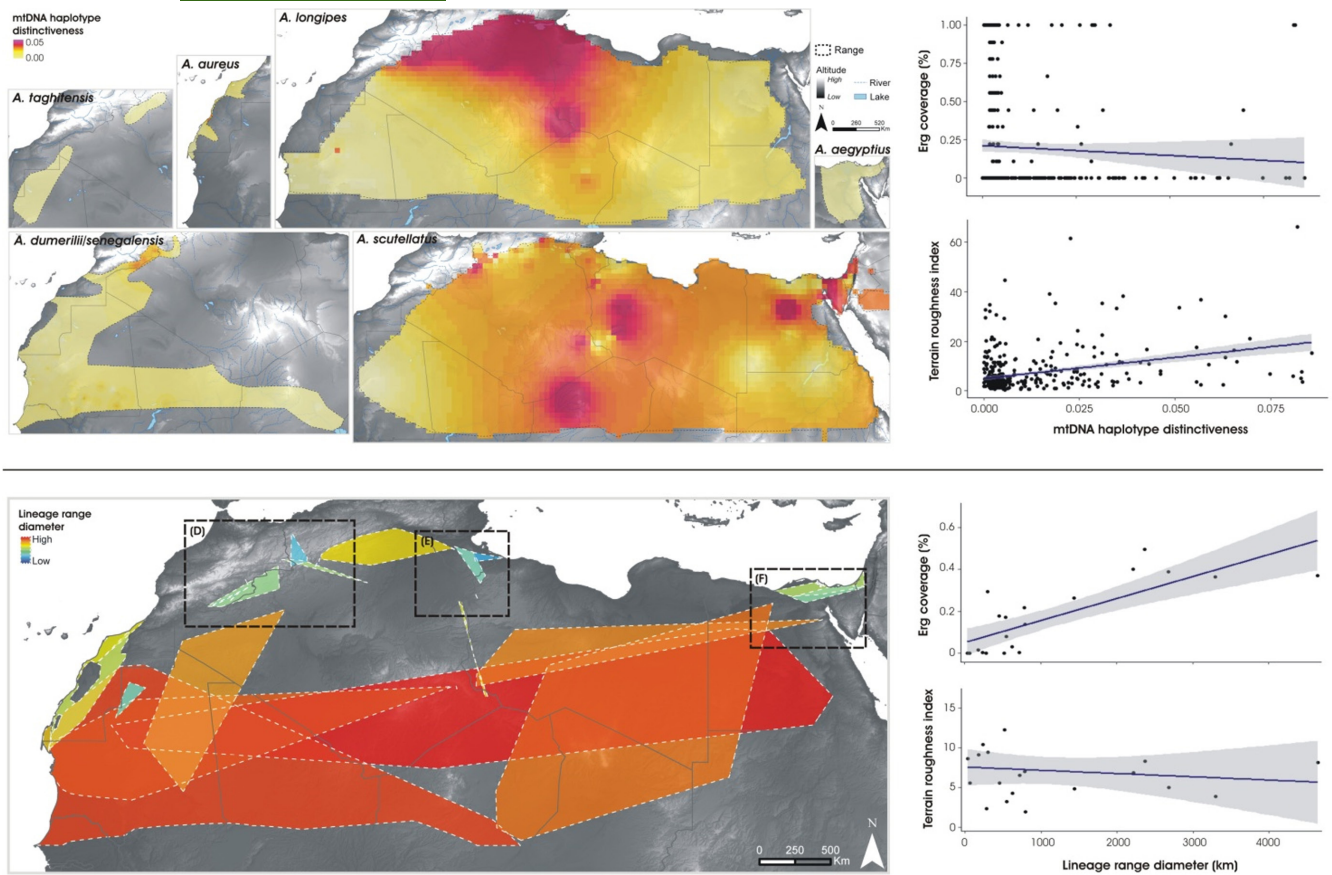
### 3.2 | Patterns and drivers of genetic structure and diversity

Lineage range size increases at lower latitudes, contrasting with higher fragmentation in northern regions (Figure 3; Figures S1.7d–S1.7f). High levels of mtDNA haplotype distinctiveness were found in the north-western Saharan edge for *A. longipes*, *A. scutellatus* and *A. dumerilii/senegalensis* (Figure 3), specifically in areas between the High and Saharan Atlas, the Great Algerian ergs and the chott palaeolakes. Distinctiveness also increased around Ténéré erg (Niger), the Western and Sinai Deserts (Egypt), the Fezzan Mountains and palaeolakes (Libya) and the Tassili-N'Ajjer (Algeria) for *A. scutellatus*; in the Adrar (Mauritania) and Bilma erg (Niger) for *A. longipes*; and around Aouker erg and palaeolakes (Mauritania) for *A. dumerilii/senegalensis*.

The GLMs including *erg* substrate and terrain roughness as predictors presented the lowest AIC to explain variations in lineage range size and haplotype distinctiveness (Table S2.10). Among these predictors, *erg* substrate and terrain roughness positively influence lineage range size and haplotype distinctiveness respectively (Figure 3; Table 1).

### 3.3 | Ecological niche suitability

Ecological niche models achieved good performance (AUC ranged between 0.80 and 0.97; Table S2.11). Species' potential distributions overall matched with their known ranges (Figures S1.8–S1.10). However, *A. longipes* and *A. scutellatus* presented some discrepancies,



**FIGURE 3** Top: Interpolations of mtDNA haplotype distinctiveness for species of *Acanthodactylus scutellatus* group, based on nucleotide diversity of two concatenated markers (12S and Cytb; 745 bp). The linear relationships of haplotype distinctiveness with terrain roughness and soft-sand coverage, at each sampling point, are shown at the right. Bottom: Minimum convex polygons (MCPs) of intraspecific lineages. Dashed rectangles depict small-ranged lineage hotspots zoomed in Figure S1.7. The linear relationships of MCPs' diameter with MCP's average terrain roughness and soft-sand coverage are shown at the right. Grey bands in the regression plots indicate confident intervals (CI: 95%). Map projections: WGS84.

as revealed by the denser concentration of suitable habitats in southern and northern areas of the Sahara respectively. Environmental predictors with the greatest contribution to models varied between species (Table S2.12), but some of those derived from day and night time land surface temperature consistently presented high contribution.

The main sympatry zone was predicted in the western Sahara-Sahel (Figure 4), covering the Atlantic Sahara ecoregion and the Adrar plateau, where up to four species may coexist. Models also predicted high suitability for more than one species in Taberit erg (Mali; *A. longipes* and *A. dumerilii/senegalensis*), the Great Eastern Erg (Algeria; *A. longipes* and *A. scutellatus*) and the Afro-Arabian suture zone (Egypt; *A. aegyptius* and *A. scutellatus*).

### 3.4 | Population genetics and hybridization analysis

All samples from the PNBA sympatry zone were successfully genotyped for 14 microsatellite loci. Evidence of null alleles and

stuttering were revealed in, respectively, nine and six loci across the three clades recovered in the phylogenetic analyses, while no evidence of allelic dropout was found. No heterozygote excess was observed, while eight loci showed heterozygote deficiency across the clades. Two pairs of markers were found to significantly depart from linkage equilibrium. Considering this information, three markers were removed, resulting in a final filtered dataset of 11 markers (Table S2.13).

Delta K and L (K) methods recovered a best-supported number of clusters of  $K = 3$  (Figure S1.11). No further coherent structuring was observed at higher K values. STRUCTURE analyses revealed three genetic clusters matching with the phylogenetic clades *A. aureus*, *A. dumerilii/senegalensis* and *A. longipes* (Figure 4). The pairwise  $F_{ST}$  values confirmed a high degree of genetic partitioning (Table S2.14). The three clusters were also clearly separated in the FCoA (Figure S1.12). No admixed individuals were apparent in the dataset and no differentiation between specimens morphologically identified as *A. dumerilii* or *A. senegalensis* (Table S2.1) was revealed by any analysis.



TABLE 1 GLMs of the effect of topography and soft-sand coverage on (a) mtDNA haplotype distinctiveness ( $n = 421$ ; diversification model) and (b) lineage's range size ( $n = 20$ ; connectivity model) of *Acanthodactylus scutellatus* group

(A) Haplotype distinctiveness	Coefficient	SE	t	p	(B) Lineage range size	Coefficient	SE	t	p
Intercept	$7.1 \times 10^{-4}$	$3.8 \times 10^{-3}$	0.2	0.85	Intercept	-682.7	1080.0	-0.6	0.54
Terrain roughness index	$4.2 \times 10^{-4}$	$8.2 \times 10^{-5}$	5.1	<0.01	Terrain roughness index	-1.2	72.9	0.0	0.99
Erg coverage	$-4.6 \times 10^{-4}$	$2.0 \times 10^{-3}$	-0.2	0.82	Erg coverage	61.23	19.4	3.2	<0.01
Nearest-neighbour distance	$4.5 \times 10^{-3}$	$8.0 \times 10^{-4}$	5.6	<0.01	N of lineage' samples	3.8	4.8	0.8	0.44
<i>A. aureus</i>	$4.6 \times 10^{-3}$	$4.4 \times 10^{-3}$	1.0	0.30	<i>A. aureus</i>	883.6	1093.2	0.8	0.44
<i>A. dumerilii/senegalensis</i>	$2.6 \times 10^{-3}$	$3.9 \times 10^{-3}$	0.7	0.51	<i>A. dumerilii/senegalensis</i>	875.5	1159.3	0.8	0.47
<i>A. longipes</i>	$3.8 \times 10^{-3}$	$4.1 \times 10^{-3}$	0.9	0.35	<i>A. longipes</i>	286.6	1099.7	0.3	0.80
<i>A. scutellatus</i>	$2.0 \times 10^{-2}$	$4.2 \times 10^{-3}$	4.8	<0.01	<i>A. scutellatus</i>	712.3	975.6	0.7	0.48
<i>A. taghitensis</i>	$2.3 \times 10^{-3}$	$7.6 \times 10^{-3}$	-0.3	0.76	<i>A. taghitensis</i>	841.8	1165.6	0.7	0.49

Note: Significant results ( $p < 0.01$ ) are highlighted in bold.

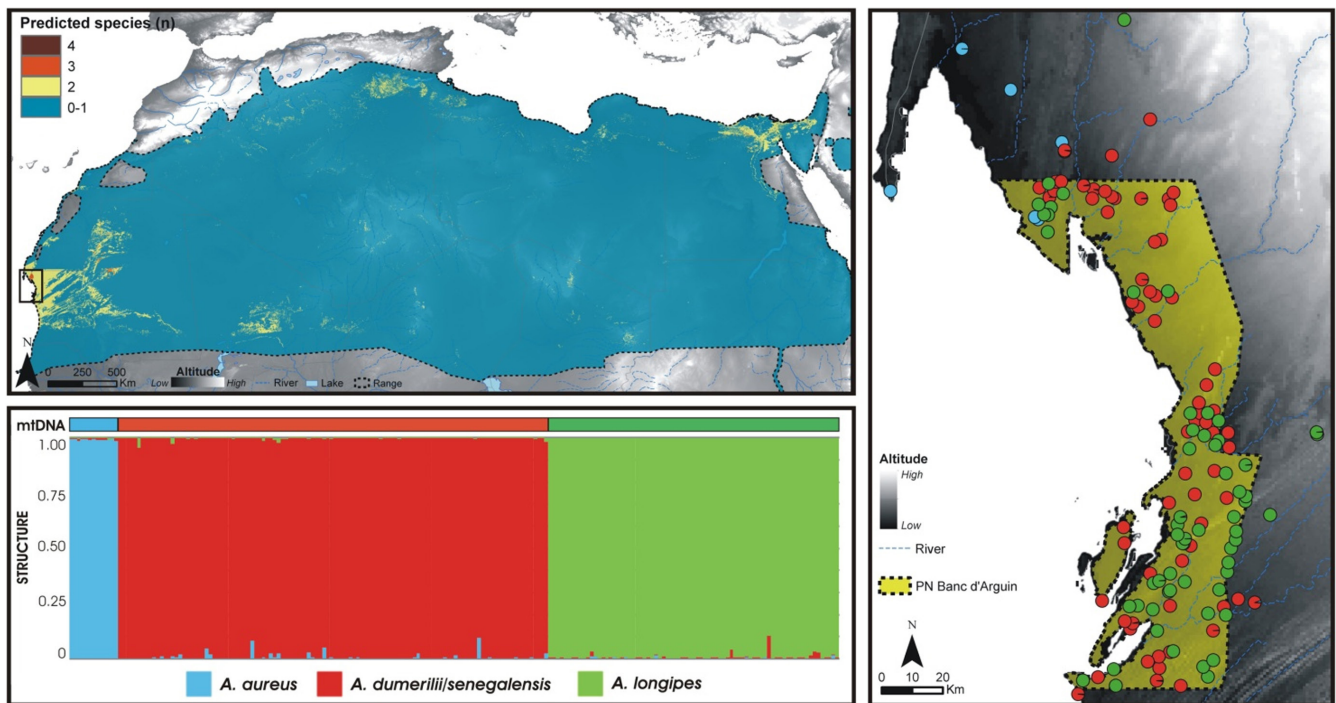


FIGURE 4 Top: Sympatry zones within *Acanthodactylus scutellatus* group, derived from the overlap of binary projections of species' ecological niche models. Right: Population structure of the group in the sympatry zone Parc National du Banc d'Arguin for the optimal number of clusters ( $K = 3$ ), based on 11 microsatellite loci using STRUCTURE. Map projections: WGS84. Bottom: STRUCTURE bar plots of the individual's assignment to each cluster, in relation to mtDNA assignments. Vertical bars represent single individuals.

## 4 | DISCUSSION

### 4.1 | Overlooked species diversity in the hyper-arid Sahara Desert

The amount of diversity uncovered in this work clearly refutes the idea of biological homogeneity in hyper-arid desert habitats, which was

assumed across the Sahara for the *Scutellatus* group due to the lack of morphological differentiation unveiled in early studies (Arnold, 1983; Salvador, 1982). Indeed, our phylogeographic assessment revealed high levels of unrecognized evolutionary diversity: several lineages that are embedded within broader-named species based on current taxonomy diverged before the Pleistocene (Figure 2) and are thus candidates for species-level status (see below). Among these candidate

lineages, only *A. aegyptius* has been formally recognized, based on its distinctive morphology and lack of intergradation in its narrow contact zone with *A. longipes* (Baha el Din, 2007).

The *A. longipes* clade includes two lineages ('Tunisia' and 'Grand Western Erg') which are older and more genetically distinct than *A. aegyptius* (Figure 2; Figure S1.6b; Table S2.9), suggesting that they constitute valid species. Species-level status is supported by private and well-differentiated nuclear haplotypes in relation to those of other closely distributed lineages (Figure S1.7a). Similarly, the *A. scutellatus* clade includes four lineages ('Nile Delta', 'Atlas High Plateau', 'Tassili-N'Ajjer' and 'Tunisia Coast') that point to cryptic species. These lineages show no signs of nuclear admixture in spite of their adjacent or even locally overlapping distributions (e.g. 'Tunisia Coast' lineage; Figures S1.7b and S1.7c). In some cases, their haplotypes appear clearly separated from the rest in the nuclear network ('Nile Delta' and 'Tunisia Coast'), whereas their mtDNA distances reach ~5% ('Nile Delta' and 'Tassili-N'Ajjer'; Table S2.9). Among them, the most evident candidate species is the Miocene-splitting lineage 'Nile Delta' (Figure 2), whose nuclear haplotypes are clearly differentiated from those of the other three co-distributed lineages in the Afro-Arabian suture zone (Figure S1.7c). The high diversity within *A. longipes* and *A. scutellatus* mirrors the patterns recovered in other Sahara-Sahel range-wide species (e.g., *Ptyodactylus togoensis* [Metallinou et al., 2015], *Tropicolotes tripolitanus* [Machado et al., 2020]), although the number of candidate species is much higher in the case of these sand specialists.

The *A. dumerilii/senegalensis* and *A. taghitensis* clades present deep splits with similar timing in the Early Pliocene (Figure 2). The resulting lineages occur in allopatry without evidence of recent contact, given their well-differentiated nuclear haplotypes (Figure S1.6) and high mtDNA distances (Table S2.9). Further studies should assess the extent of reproductive isolation between these allopatric lineages, to determine whether they constitute real speciation events and which underlying processes were involved (e.g., neutral evolution in isolation by distance [Irwin, 2002]).

## 4.2 | Diversification hotspots and drivers of xeric diversity

The northern edge of the Sahara concentrates the highest levels of diversity, harbouring a patchwork of small-ranged endemic lineages consistent across local species (Figure 3; Figures S1.7d–S1.7f). Considering the seemingly parapatric distribution of these lineages, their mtDNA distinctiveness (Figure 3) and crown ages concordant with Saharan dry/humid cycles occurring since the Late Miocene (Figure 2; Zhang et al., 2014), the recovered phylogeographic patterns may be the result of historical episodes of population isolation (Brito et al., 2014). In the north-western side, rivers flowing from the southern foothills of the Saharan Atlas during humid phases could create barriers to gene flow by fragmenting sandy habitats across Algerian ergs (Scerri et al., 2014), like previously suggested for other sand-adapted taxa (e.g., *Chalcides ocellatus* [Beddek et al., 2018]). The increased humidity that allows intermittent north–south dispersal for more mesic species (e.g., *Psammophis schokari* [Gonçalves, Martínez-Freiría, et al., 2018]) may have created barriers to dryland-adapted taxa. An alternative

scenario to barriers is range shifts following climatic fluctuations, triggering genetic differentiation in allopatry (e.g., *Daboia* spp. [Martínez-Freiría et al., 2017]). In the Afro-Arabian suture zone, the observed divergence may also result from a dynamic tectonic history, which has been linked to speciation events and continental translocations of Afro-Arabian fauna (Tejero-Cicuéndez et al., 2022).

In other taxa, lineages endemic to Sahara highlands have highlighted the role of topography and local climate stability in generating diversity (e.g., *Acanthodactylus boskianus* [Liz et al., 2021]). While mountain habitats are far from the ecological optima of xeric species, their refugia may be located in mountain outskirts as a way to avoid the extreme climatic cores of the hyper-arid lowlands. Our models predict the suitability of mountain outskirts and mid-altitude environments for *A. scutellatus* (Figure S1.8), which seems to be able to disperse across mountain barriers (lineage 'Atlas High Plateau'; Figures S1.7b), as well as *A. longipes* (lineage 'Great Western Erg'; Figure S1.7a). These two species and *A. dumerilii/senegalensis* present high genetic variability around mountains areas, as shown by mtDNA haplotype distinctiveness south of the High Atlas, around Saharan Atlas, Fezzan and Adrar (Figure 3), by diverse nuclear haplotypes around the High and Saharan Atlas (Figures S1.7a and S1.7b), and by a seemingly endemic lineage to Tassili-N'Ajjer (Figure 2). We found a positive, significant relationship between terrain roughness and haplotype distinctiveness, supporting the mountain-outskirt xeric refugia hypothesis (Figure 3; Table 1). Nevertheless, conclusions are limited by the biased sampling across the study area, while the observed phylogeographic patterns can also result from long-term population persistence and divergence in the edge of nearby erg habitats, triggered by a favourable combination of environmental drivers (e.g., milder climate, habitat fragmentation). Fine-scale studies assessing diversification and palaeo-range patterns across mountain-erg geographic gradients are needed to further understand xeric refugia.

## 4.3 | Population connectivity and expansions across sand corridors

A pattern of large longitudinal genetic connectivity was recovered across southern latitudes (Figure 3), where lineages of *A. dumerilii/senegalensis*, *A. longipes* and *A. scutellatus* exhibit east–west distributions from Central Sahara-Sahel regions to the Red Sea and Atlantic coasts, including one lineage ('Pansaharan') ranging over an almost complete trans-Saharan axis. Connectivity was significantly favoured by soft-sand substrate (Figure 3; Table 1), which is recovered as a main driver of habitat suitability for range-wide species (e.g., *A. longipes*; Table S2.12). Our findings corroborate the hypothesis of recent longitudinal sand corridors across southern desert regions, previously suggested by lineage distributions from the Central Sahara to the Atlantic coast in other sand-adapted species (e.g., *Mesalina pasteuri*; *M. rubropunctata* [Pizzigalli et al., 2021]; *Stenodactylus petrii*, *S. sthenodactylus* [Metallinou et al., 2012]) and by similar trans-Saharan distributions of xeric species (e.g. *Uromastix dispar* [Tamar



et al., 2017]). These corridors would explain the rapid desert colonization of sand specialists (e.g., *Scincus* spp. [Šmíd et al., 2020]), where intermittent dispersals were potentially followed by climate-induced allopatric diversification in northern latitudes (Brito et al., 2014).

The lack of accurate spatially explicit geological and land cover data for the past hinders inferences on the historical fluctuation of sand corridors and the direction of dispersals. Yet, areas of relatively high mtDNA haplotype distinctiveness within a given lineage distribution would imply long-term local population persistence (Carnaval et al., 2009), while distant areas sharing closely related haplotypes would suggest recent expansion. The *A. dumerilii/senegalensis* lineage 'W Sahara-Sahel south' is a good candidate to explore these patterns, since it is well sampled and associated with presumed xeric corridors (Figure 2). Potential dispersal origins are inferred around the Assaba and Afollé mountains, the Aouker erg and palaeolakes (Mauritania) and Taberit erg (Mali), from where lineage populations expanded north and westwards towards the Atlantic Sahara, and eastwards until the Lake Chad (Figure 3). A similar scenario of dispersal from inland areas may apply to lineage 'Pansaharan' (*A. scutellatus*), which likely expanded from Ténéré erg (Niger) westwards until Mauritania. Likewise, populations of lineage 'E Sahara-Sahel' (*A. longipes*) are distinctive around Bilma erg (Niger), which contrasts with potential areas of recent expansion in Chad and Egypt.

#### 4.4 | Hybridization assessment and systematic clarifications

Population genetic analyses conducted within the main sympatry zone of the *Scutellatus* group (PNBA) indicated no gene flow among the three local species (Figure 4), despite suspicions of interspecific hybridization in the area (Crochet et al., 2003). The range of estimated  $F_{ST}$  values (Table S2.14) and separation of the FCoA clusters (Figure S1.12) is concordant with the deep phylogenetic split observed between these groups. The simplest explanation for the absence of gene flow is a speciation process largely predating the development of the sympatry zone (Figure 2). The area underwent historical climatic and land cover fluctuations, including the intermittent activation of the estuary of the giant Palaeoriver Tamanrasset during humid Sahara phases (Skonieczny et al., 2015), and offers a diverse ecotone (e.g., humidity, sand substrate) for the co-occurrence of closely related species. Ecological segregation between species is supported by different species ecological preferences (Table S2.12).

The genetic structure observed across PNBA supports the synonymy of *A. senegalensis* and *A. dumerilii* suggested by Tamar et al. (2016). Morphological assessments differentiate two local morphotypes, each assigned to an independent species (Table S2.1), based on differences in scalation and colour pattern (i.e., number of longitudinal rows of dorsal and ventral scales, number of femoral pores and presence of vertebral line; Crochet et al., 2003). Our genetic analyses lumped both morphotypes, as well as putative hybrids, into one single nuclear cluster (Figure 4; Figure S1.12). In

addition, samples from the entire range of *A. senegalensis* and the southern range of *A. dumerilii* are integrated within a single mtDNA lineage (Figure 2). Therefore, the two morphotypes co-occurring in coastal Mauritania (Crochet et al., 2003) seem to result from a large morphological plasticity or variability within this single species.

Our results do not support the distribution of *A. dumerilii* as it is currently recognized on its northern range eastwards from Taghit (Algeria) to coastal Libya (Roll et al., 2017). The north-easternmost points where we identified *A. dumerilii* are around Taghit and Béchar (Algeria; Figure 2). Further east, all samples show either *A. scutellatus* or *A. longipes* nuclear haplotypes (Figures S1.7a and S1.7b). Westwards from Taghit, the links between two local lineages of *A. dumerilii/senegalensis* and *A. scutellatus* in the nuclear network (Figure S1.5) raise uncertainties on the identification of these two lineages. Nevertheless, the occurrence of *A. dumerilii* in this region is well supported, according to the mtDNA and nuclear placement of lineage 'Merzouga'. An updated range for *A. dumerilii/senegalensis* is provided in Appendix S4.

#### ACKNOWLEDGEMENTS

We thank BIODESERTS group members and collaborators for their assistance during fieldwork. Paulo Pereira, Sara Lopes and Vanessa Oliveira generated the preliminary genetic datasets used in this study. We thank S. Baha el Din, M. Beddek, A. Benlahrech, W. Böhme, H. in den Bosch, A. Cluchier, E. Didner, M. Geniez, H. Loumassine, P. Lymberakis, O. Peyre, B. Shacham, M. Siol, K. Tamar, J.-F. Trape, J. Viglione and Y. Werner for help with the sample collection. Acknowledgements extended to I. Avella and C. Figueiredo-Vázquez for support during analyses and figure production. This work was funded by Fundação para a Ciência e a Tecnologia - FCT (PTDC/BIA-BEC/099934/2008 and PTDC/BIA-BIC/2903/2012), by FEDER funds through the Operational Programme for Competitiveness Factors - COMPETE (FCOMP-01-0124-FEDER-008917/028276), by AGRIGEN-NORTE-01-0145-FEDER-000007, supported by Norte Portugal Regional Operational Programme (NORTE2020), under the PORTUGAL 2020 Partnership Agreement, through the European Regional Development Fund (ERDF), by National Geographic Society (CRE 7629-04, CRE 8412-08) and by Mohammed bin Zayed Species Conservation Fund (11052709, 11052707, 11052499). AVL, DVG, GVA, PT, SBC and JCB were supported by FCT (SFRH/BD/140348/2018, CEECIND/03848/2020, CEECIND/00937/2018, DL57/2016/CP1440/CT0008, CEECIND/01464/2017 and CEECINST/00014/2018/CP1512/CT0001 respectively). Capture permits were issued by the Haut Commissariat aux Eaux et Forêts (278/2012 and 20/2013/HCEFLCD/DLCDPN/DPRN/CFF) and Ministère de l'Environnement et du Développement Durable de Mauritanie (460/MDE/PNBA). Logistic support for fieldwork was given by P.N. Banc d'Arguin, P.N. Diawling and Université des Sciences, de Technologie et de Médecine de Nouakchott (Mauritania) and Association Nature Initiative and Université Abdelmalek Essaâdi, Tétouan (Morocco).

## FUNDING INFORMATION

National Geographic Society; Mohammed bin Zayed Species Conservation Fund; Fundação para a Ciência e a Tecnologia; European Regional Development Fund.

## CONFLICT OF INTEREST

None.

## DATA AVAILABILITY STATEMENT

GenBank accession numbers and sampling localities are indicated in Table S2.1.

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## BIOSKETCH

**André Vicente Liz** is a Ph.D. candidate at CIBIO-InBIO (University of Porto, Portugal) and Zoological Research Museum Alexander Koenig (Bonn, Germany), and is interested in biogeographic approaches to conservation. His Ph.D. project aims to understand the role of climate-induced dispersal/vicariance as main biodiversity diversification drivers in the Sahara-Sahel desert, based on comparative phylogeography. All authors are interested in the assessment of biodiversity patterns and processes in deserts and arid regions.

**Author contributions:** AVL, DR, DVG and JCB conceived the ideas; AVL, DVG, GVA, JCB, PAC and PG collected the data; AVL, DR, DVG, GVA, PAC, PT and SBC analysed the data; AVL led the writing with inputs from all authors.

## SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

**How to cite this article:** Liz, A. V., Rödder, D., Gonçalves, D. V., Velo-Antón, G., Tarroso, P., Geniez, P., Crochet, P.-A., Carvalho, S. B., & Brito, J. C. (2022). Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards. *Journal of Biogeography*, 00, 1–15. <https://doi.org/10.1111/jbi.14510>

Article reference – “Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards”

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**Supporting Information**

**APPENDIX S1 – Supplementary figures (captions)**

**Figure S1.1** Study area and samples used in this work. The range of *Acanthodactylus scutellatus* group was modified from Roll et al. (2017). Circles represent sampling sites used in the phylogenetic analysis. Main mountains and hydrological features are indicated in bold and italics, respectively. Projection: WGS84.

**Figure S1.2** Bayesian mt-nuDNA phylogeny of *Acanthodactylus scutellatus* group including all haplotypes of the concatenated dataset (12S, Cytb, and C-mos; 1213 bp). Black dots represent supported nodes, with posterior probabilities (pp) >0.95; lower values are shown for species and lineage splits.

**Figure S1.3** Maximum Likelihood mt-nuDNA phylogeny of *Acanthodactylus scutellatus* group including all haplotypes of the concatenated dataset (12S, Cytb, and C-mos; 1213 bp). Black dots represent supported nodes, with bootstrap values > 85; lower values are shown for species and lineage splits.

**Figure S1.4** Time-calibrated Bayesian mt-nuDNA phylogeny of *Acanthodactylus scutellatus* group (12S, Cytb, and C-mos; 1213 bp). Split times (Mya) are given next to the nodes. Horizontal bars represent the 95% HPD. The vertical blue line corresponds to the temporal threshold used to delimit intra-specific lineages (earliest lineage split within *A. aureus*, 1.84 Mya); a more conservative threshold (oldest split, 3.09 Mya) is depicted by a purple line.

**Figure S1.5** Inter-specific nuDNA (C-mos) haplotype network of *Acanthodactylus scutellatus* group. White dots represent mutation steps. Dashed squares depict alleles from the three northern lineages of *A. dumerilii/senegalensis* (Merzouga, NW Sahara, and Zagora). Numbers correspond to samples in Table S2.1.

**Figure S1.6** Intra-specific mtDNA (12S) and nuclear (C-mos) haplotype networks of *Acanthodactylus scutellatus* group. White dots represent mutation steps. Numbers correspond to samples listed in Table S2.1.

**Figure S1.7** Small-ranged lineage hotspots highlighted in Figure 3. Top: (A) *Acanthodactylus longipes* in north-western Sahara; (B) *A. dumerilii/senegalensis* and *A. scutellatus* in north-western Sahara; and (C) *A. scutellatus* in the Afro-Arabian suture zone. Maps show the distribution of nuDNA (C-mos) haplotypes for intra-specific lineages. White dots in the haplotype networks represent mutation steps. Allele numbers correspond to samples in Table S2.1. The time-calibrated phylogenetic trees (mt-nuDNA; 1213 bp) depict each lineage's positions within the main group clades (in dashed squares). Bottom: (D) Transition between the Saharan Atlas and the Great Western Erg; (E) Transition between Chott paleolakes and the Great Eastern Erg; and (F) Afro-Arabian suture zone. Black asterisks depict individual lineages. Projection: WGS84.



**Figure S1.8** Ecological niche models for species of *Acanthodactylus scutellatus* group, clipped to the species' ranges (modified from Roll et al., 2017). Projection: WGS84.

**Figure S1.9** Binary maps of habitat suitability for species of *Acanthodactylus scutellatus* group, derived from the ensemble models and TSS cut-off thresholds. Projection: WGS84.

**Figure S1.10** Clamping mask implementation on the ecological niche models for species of *Acanthodactylus scutellatus* group. Species' observations and model calibration areas are represented. Projection: WGS84.

**Figure S1.11** STRUCTURE HARVESTER graphic outputs of Delta (K) and Mean L(K), based on microsatellite analyses of *Acanthodactylus scutellatus* group in the sympatry zone Parc National du Banc d'Arguin.

**Figure S1.12** The two first axes of the Factorial Correspondence Analyses (FCoA) run on individual genotypes of *Acanthodactylus scutellatus* group from the Parc National du Banc d'Arguin sympatry zone. The lack of overlap among clusters with homogeneous species identity indicates lack of gene-flow.

Figure S1.1

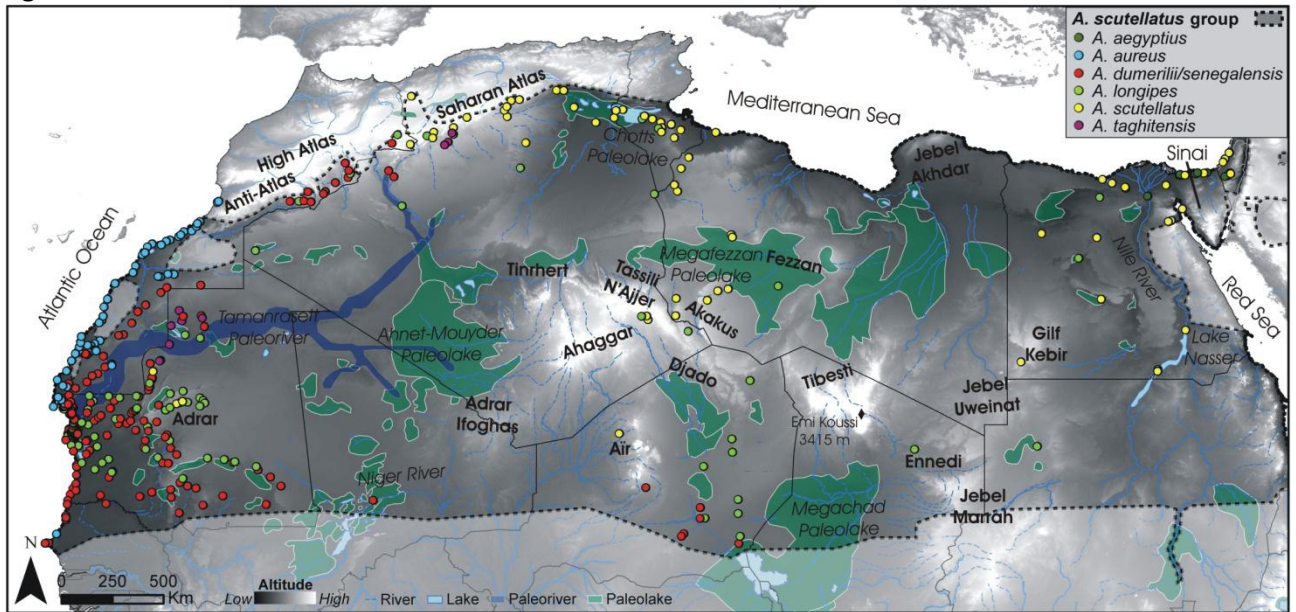


Figure S1.2

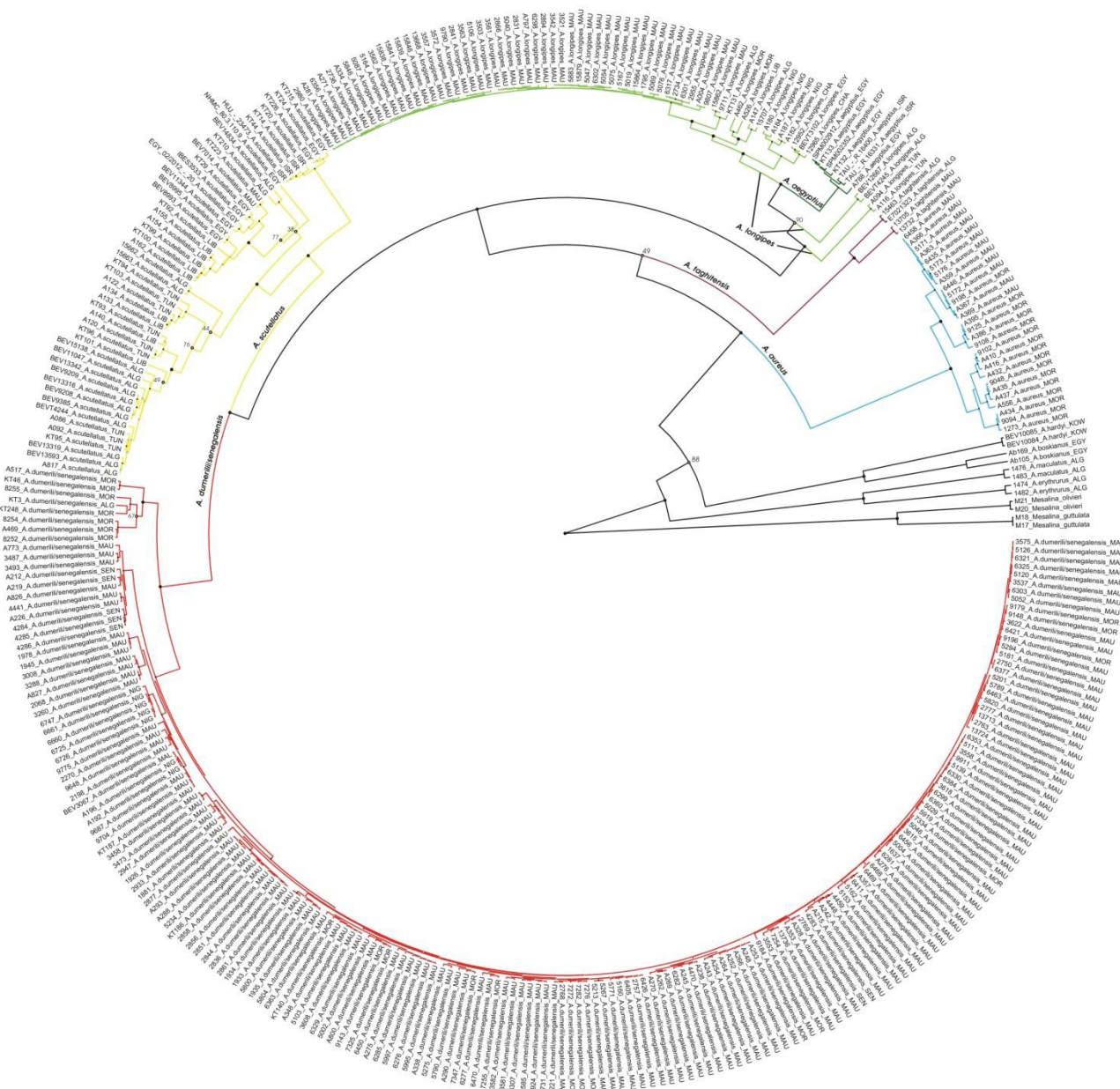


Figure S1.3

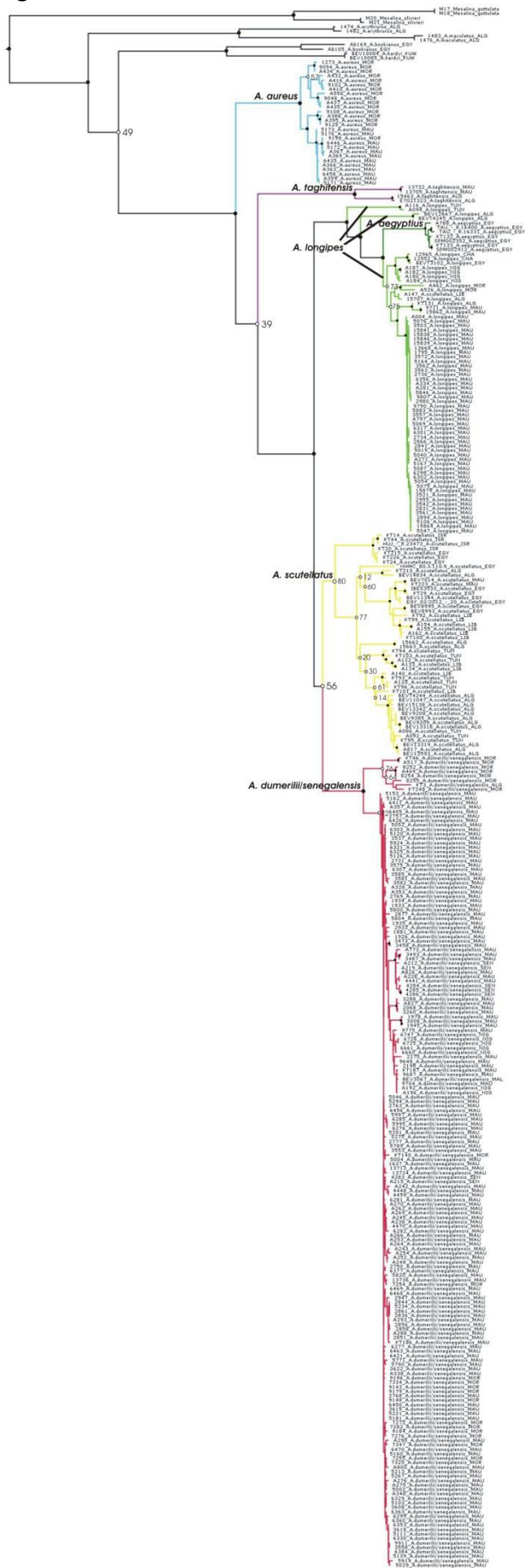


Figure S1.4

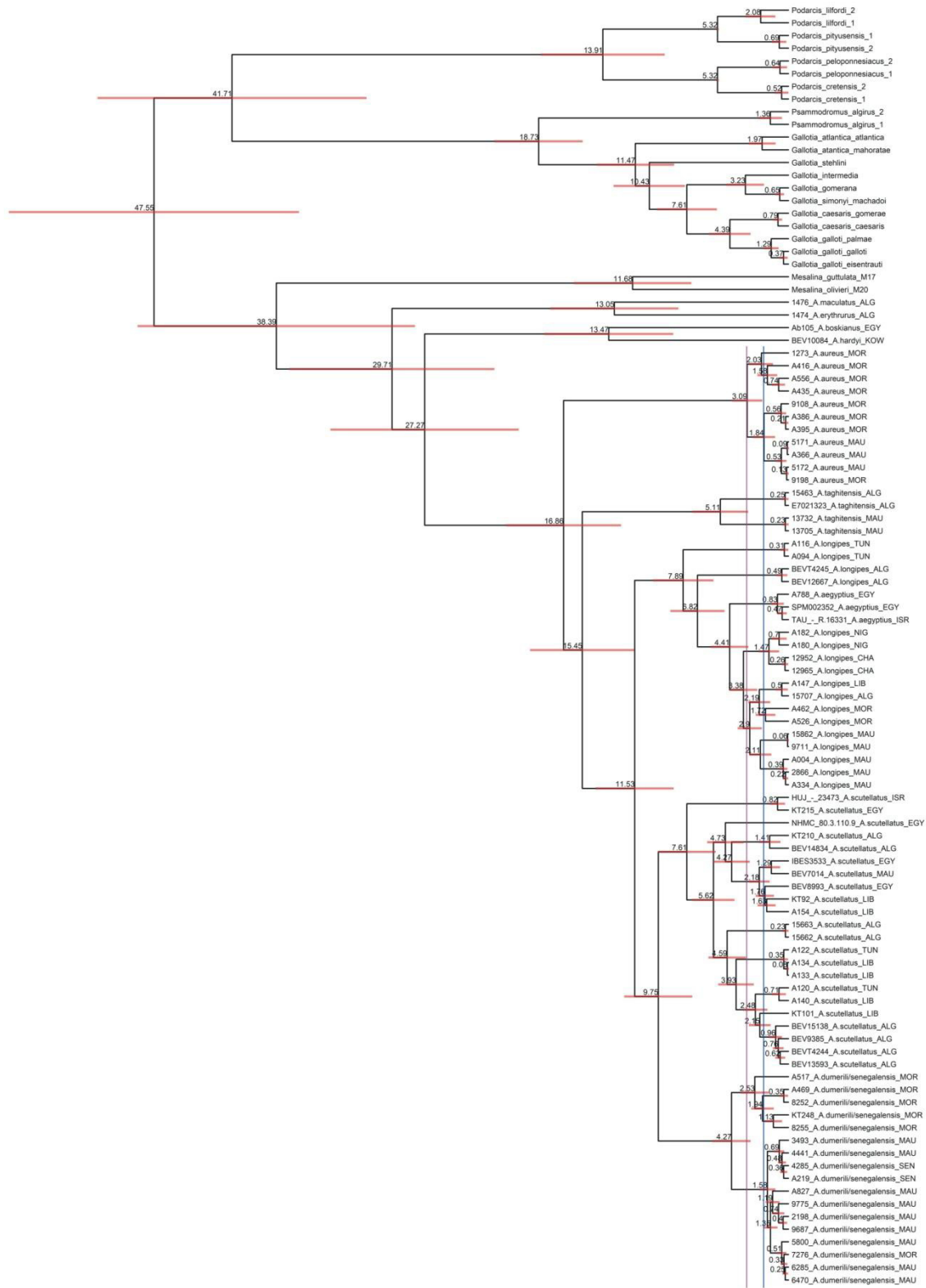


Figure S1.5

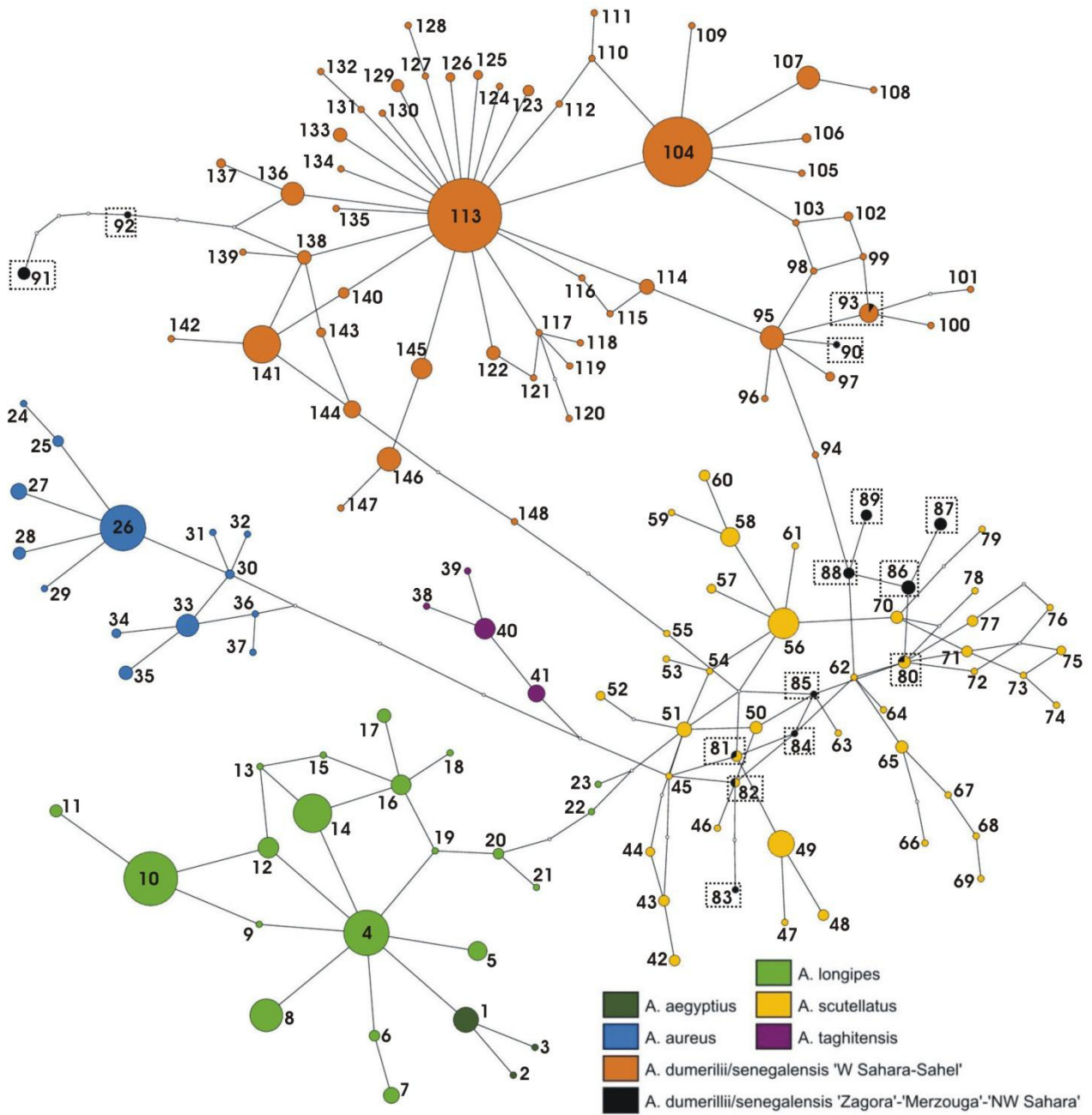


Figure S1.6

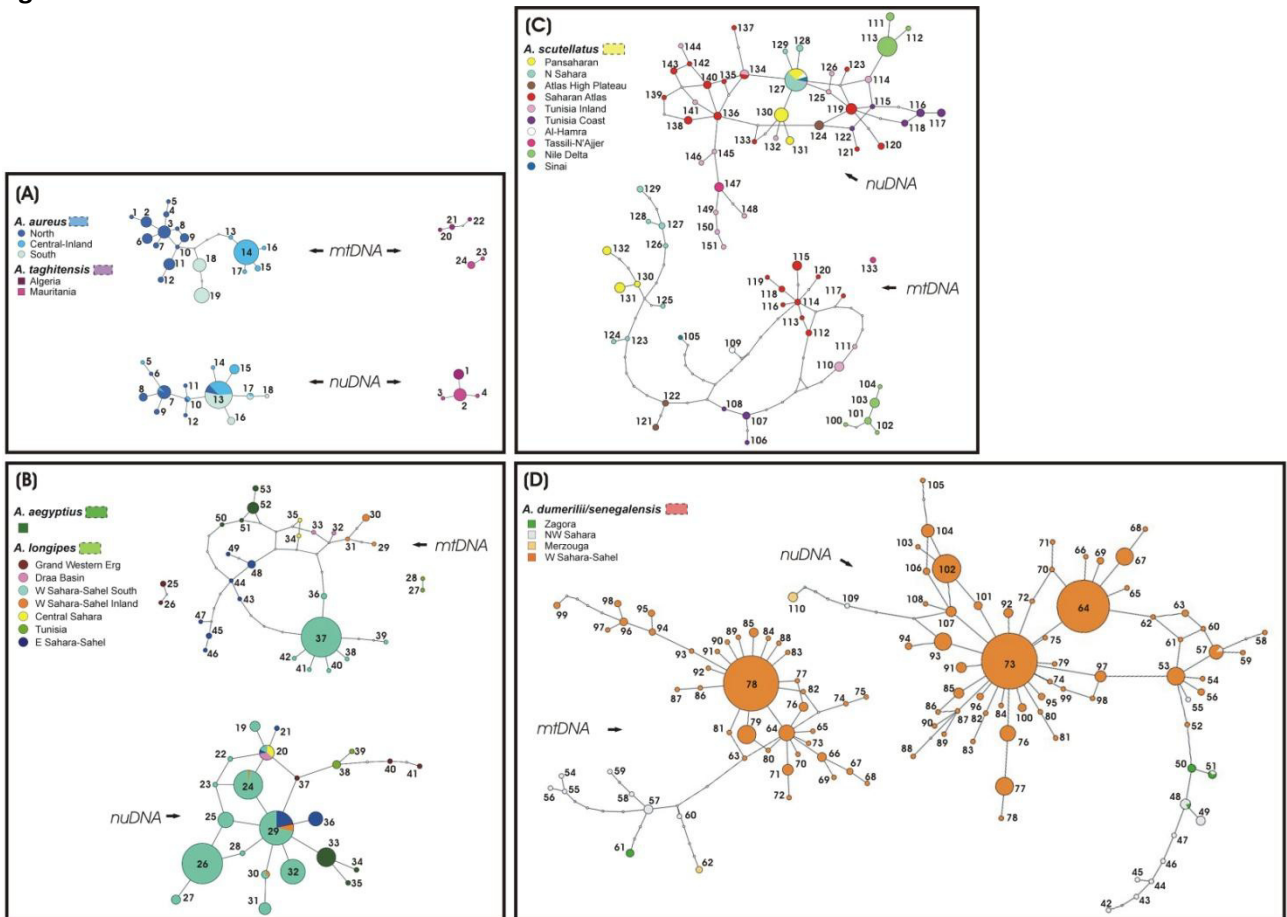


Figure S1.7

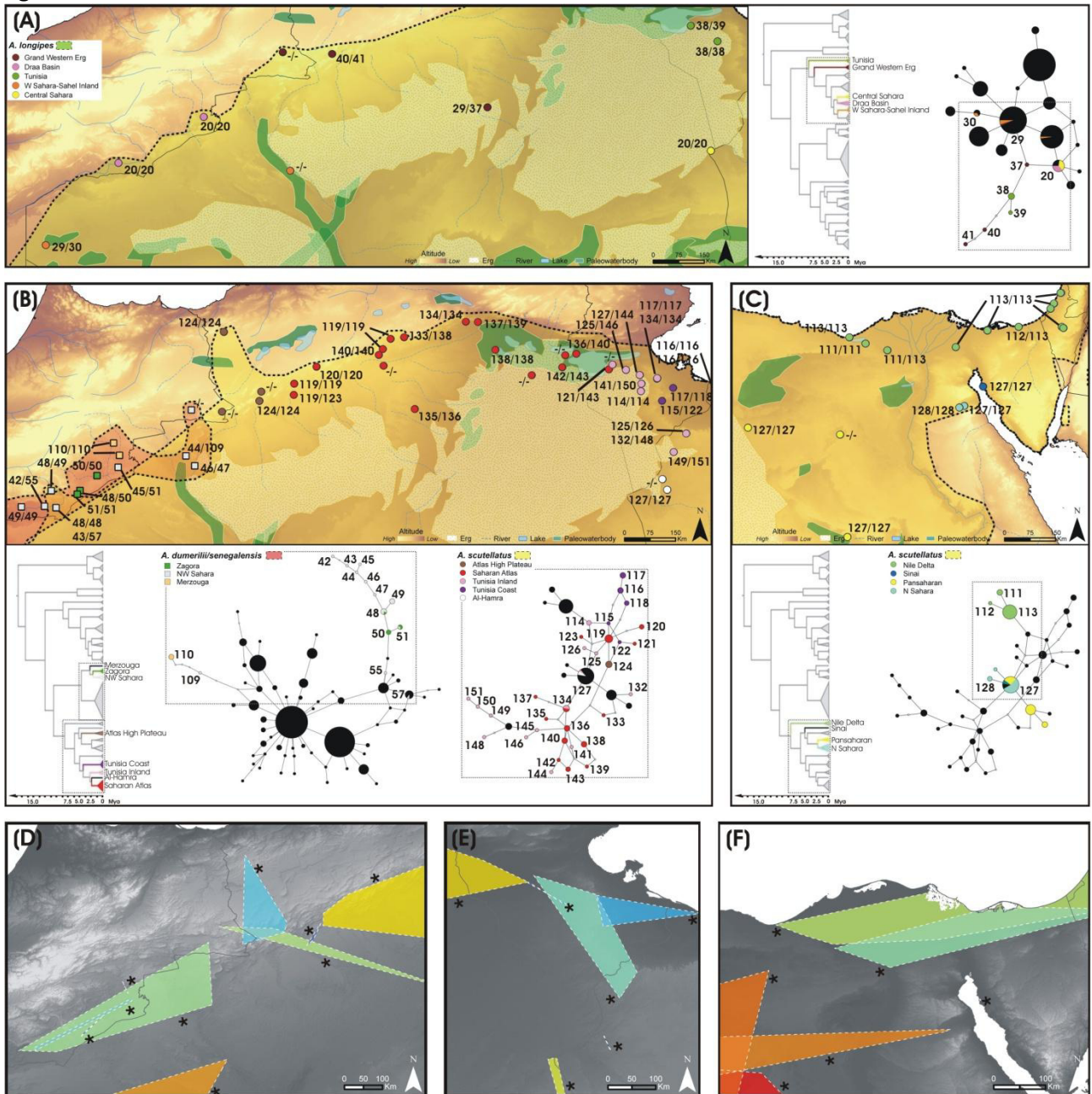




Figure S1.8

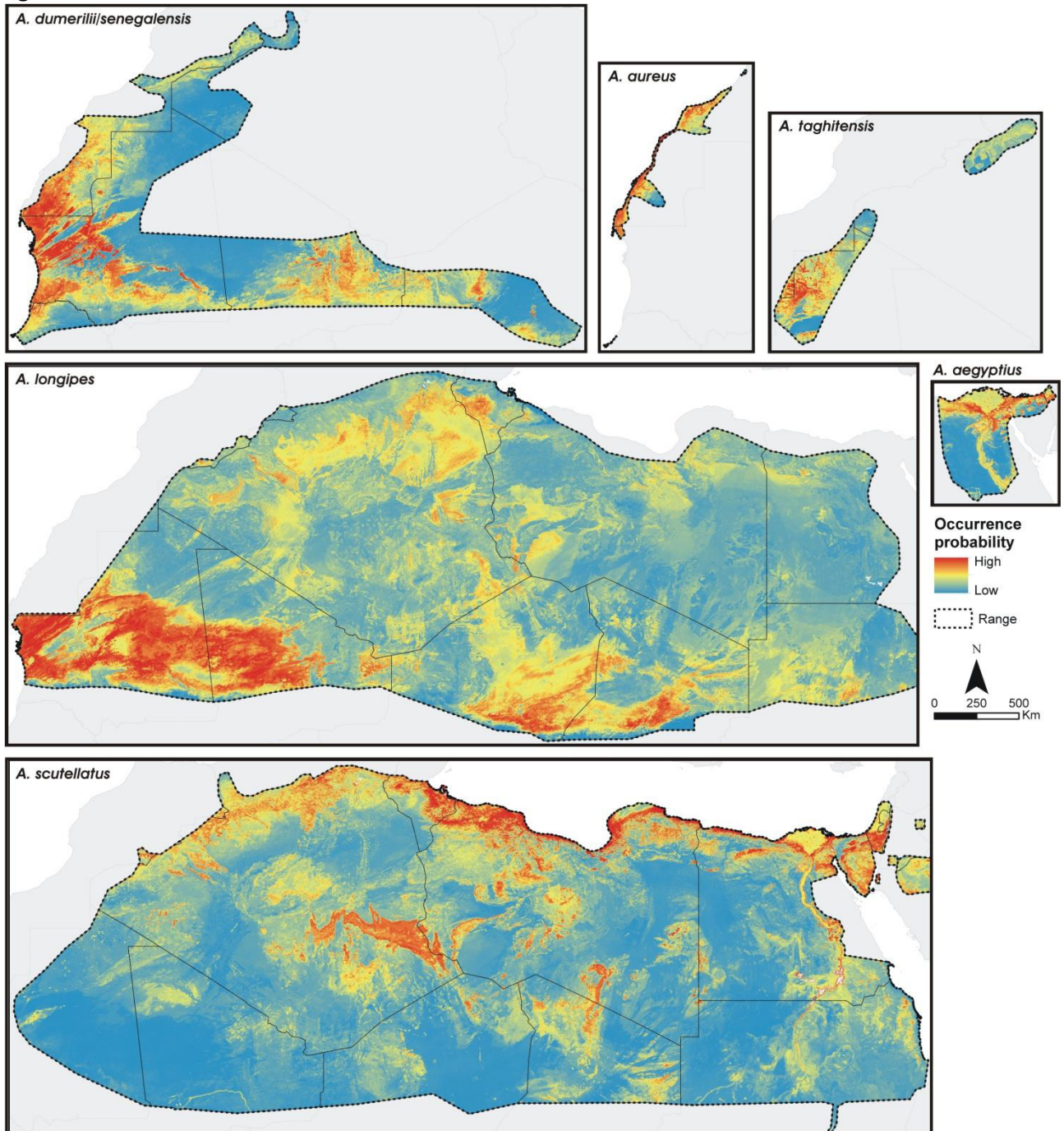


Figure S1.9

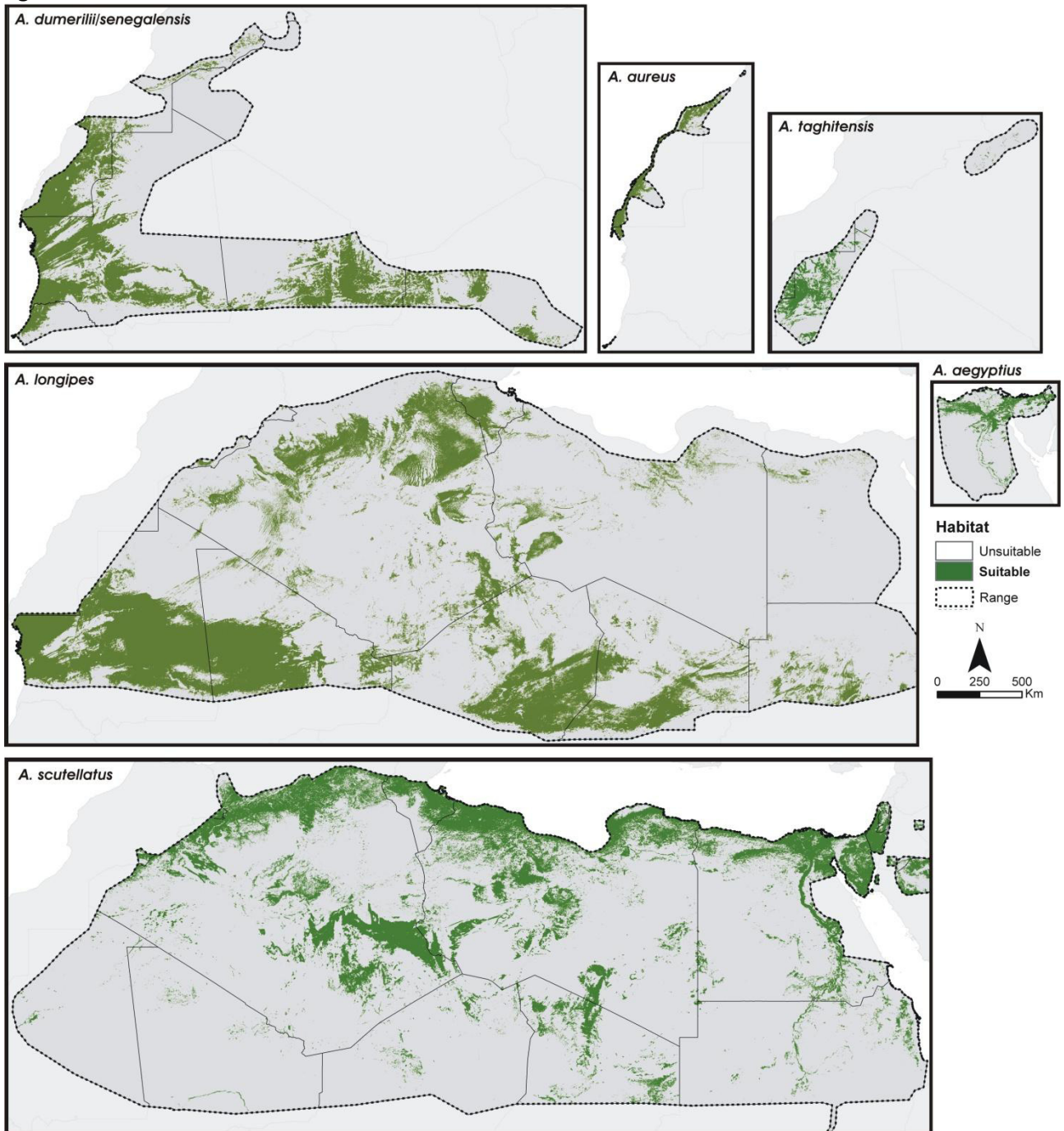


Figure S1.10

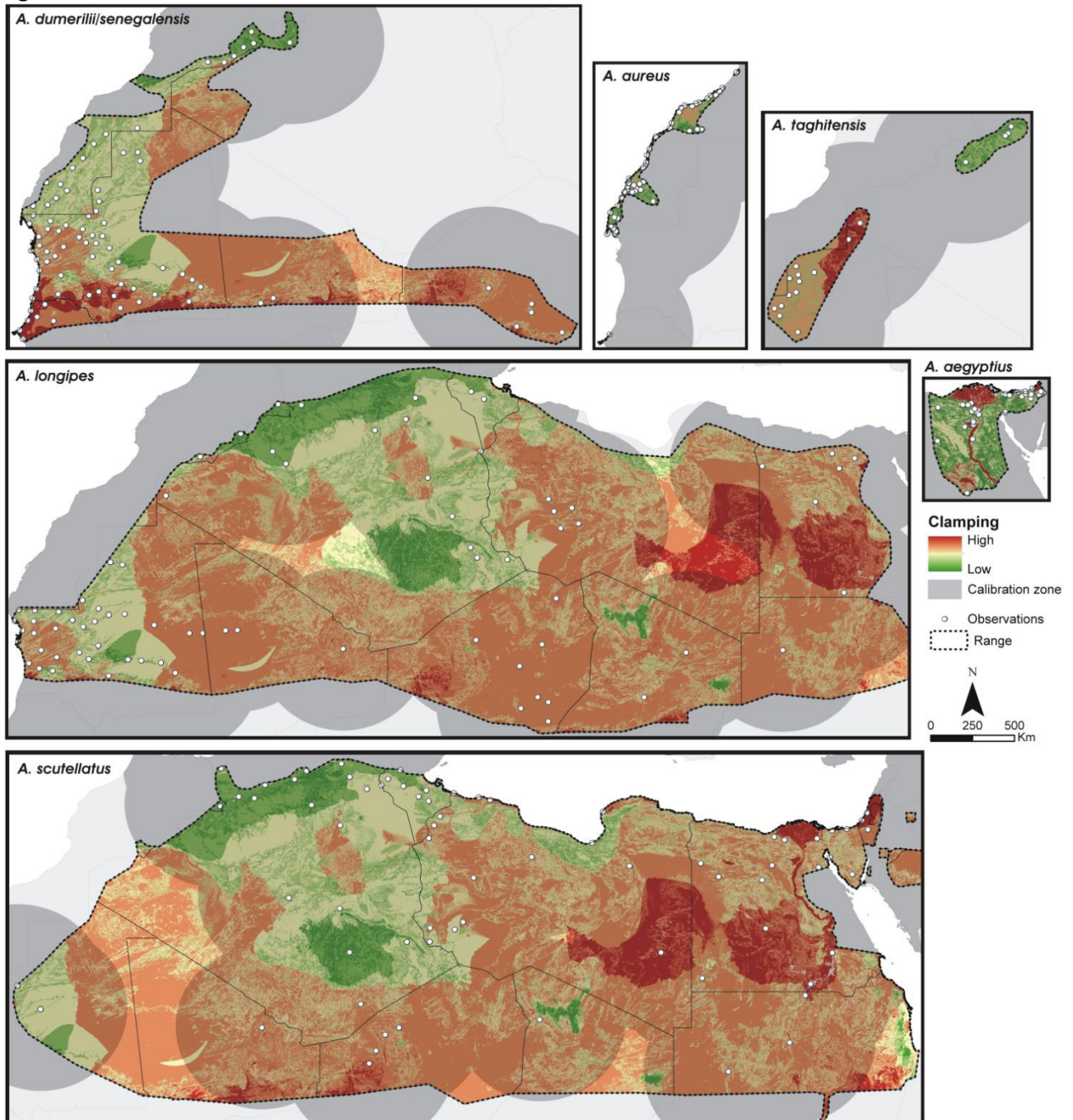


Figure S1.11

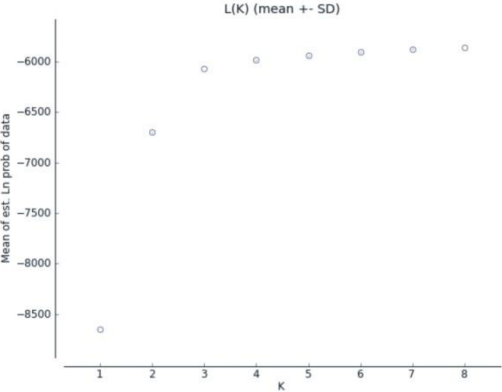
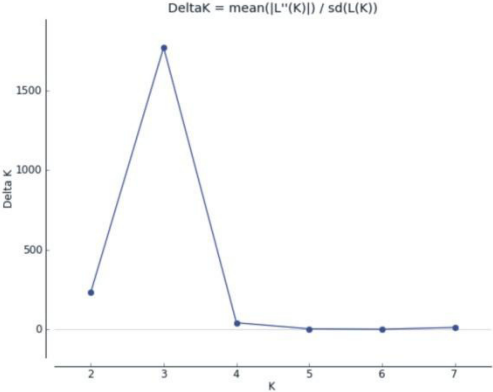
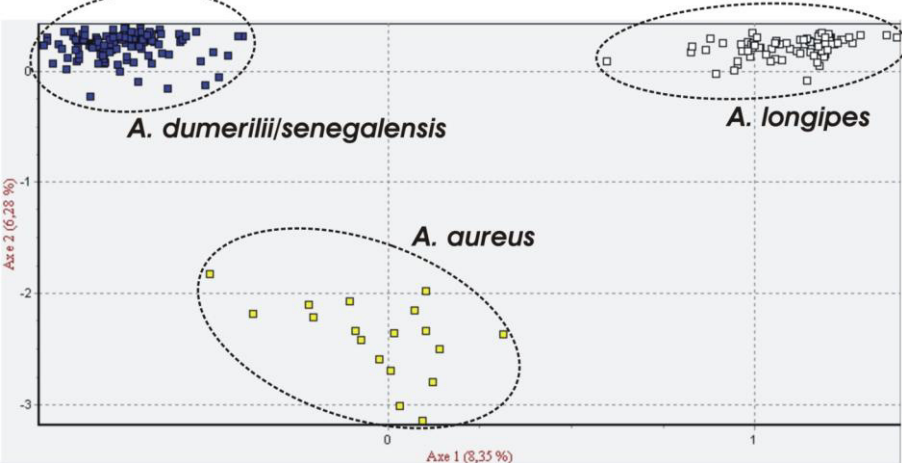


Figure S1.12



Article reference – “Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards”

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**Supporting Information**

**APPENDIX S2 – Supplementary tables (captions)**

**Table S2.1** Samples of *Acanthodactylus scutellatus* group used in this study. The first and second sheets list the specimens and observations included in the genetic and ecological modelling analyses, respectively. Newly produced sequences are highlighted in bold.

**Table S2.2** Environmental variables included in the ecological niche models.

**Table S2.3** Primers for the sequenced gene fragments of mtDNA and nuDNA.

**Table S2.4** PCR conditions for the sequenced gene fragments of mtDNA and nuDNA, and genotyped microsatellite markers.

**Table S2.5** Characteristics of the 11 microsatellite loci used in the final dataset.

**Table S2.6** Outgroups and taxa used in the time-calibration of the phylogenetic tree. Newly produced sequences are highlighted in bold.

**Table S2.7** Details of the phylogenetic analyses. The number of samples included in each dataset is shown between brackets (ingroups only). Uclد refers to relaxed uncorrelated lognormal clock. Priors not mentioned in the table were left as default.

**Table S2.8** Biogeographic events used to time-calibrate the phylogenetic inference.

**Table S2.9** Mean 12S pairwise genetic distances (p-distances) among species and intra-specific lineages.

**Table S2.10** Generalized Linear Models exploring correlations between different sets of topographic and land-cover predictors and (A) mtDNA haplotype distinctiveness (n = 421) or (B) lineages' range sizes (n = 20). For each group of predictors, the best-fitting model is highlighted in bold.

**Table S2.11** Metrics measuring the performance of the ensemble models and threshold values used to generate the binary maps.

**Table S2.12** Importance of environmental predictors (mean ± SD) in the ecological niche models. Full variable names are given in Table S2.2. The three most important variables in each case are highlighted in bold. The number replicates passing the threshold of TSS > 0.7 is shown between brackets.

**Table S2.13** Observations of heterozygote deficiency (Hdef) and null alleles (Nall) in *Acanthodactylus aureus*, *A. dumerilii/senegalensis*, and *A. longipes* from the Parc National du Banc d'Arguin sympatry zone. Significant values after Bonferroni correction are marked with an asterisk (\*). Two asterisks indicate observations of stuttering (\*\*).

**Table S2.14** Pairwise  $F_{ST}$  values based on microsatellites for the three identified genetic clusters from the Parc National du Banc d'Arguin sympatry zone. (+) indicate significance ( $\alpha=0.05$ ).

**Table S2.1**

*--- Uploaded as a separate .xlsx file ---*



**Table S2.2** Environmental variables included in the ecological niche models.

Code	Source	Meaning of derive variable
ED1503_bio7	MODIS V4 Band 03 Synoptic Months: Middle Infra-Red	Annual Range of Middle Infra-Red
ED1503_bio10	MODIS V4 Band 03 Synoptic Months: Middle Infra-Red	Mean Middle Infra-Red of Highest Quarter
ED1503_bio11	MODIS V4 Band 03 Synoptic Months: Middle Infra-Red	Mean Middle Infra-Red of Lowest Quarter
ED1514_bio1	MODIS V4 Band 14 Synoptic Months: Normalised Difference Vegetation Index	Annual Mean of Normalized Difference Vegetation Index (NDVI)
ED1514_bio7	MODIS V4 Band 14 Synoptic Months: Normalised Difference Vegetation Index	Annual Range of Normalized Difference Vegetation Index (NDVI)
ED1515_bio7	MODIS V4 Band 15 Synoptic Months: Enhanced Vegetation Index	Annual Range of Enhanced Vegetation Index (EVI)
ED150708_bio1	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Annual Mean Temperature
ED150708_bio2	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Mean Diurnal Range (Mean of monthly (max temp - min temp))
ED150708_bio3	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Isothermality (BIO2/BIO7) (* 100)
ED150708_bio4	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Temperature Seasonality (standard deviation *100)
ED150708_bio5	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Maximum Temperature of Highest Month
ED150708_bio6	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Minimum Temperature of Lowest Month
bio12	Worldclim	Annual Precipitation
bio14	Worldclim	Precipitation of Driest Month
bio17	Worldclim	Precipitation of Driest Quarter
200	Globcover	Bare Areas
201	Globcover	Consolidated Bare Areas (hardpans, gravels, bare rock, stones, boulders)
202	Globcover	Non-consolidated Bare Areas (sandy desert)

References: MODIS V4 dataset from the EDENext project ([www.edenextdata.com](http://www.edenextdata.com)); Worldclim dataset from Fick and Hijmans, 2017 (<https://www.worldclim.org/data/worldclim21.html>); Globcover dataset from Bicheron et al., 2009 ([http://due.esrin.esa.int/page\\_globcover.php](http://due.esrin.esa.int/page_globcover.php)).

**Table S2.3** Primers for the sequenced gene fragments of mtDNA and nuDNA.

Gene	Primers	DNA strand	Sequence 5'- 3'
12S	12Sa	Forward	AAACTGGGATTAGATACCCCACTAT
	12Sb	Reverse	GAGGGTGACGGGCGGTGTGT
Cytb	Gludg	Forward	TGACTTGAARAACCAAYCGTTG
	Cytb2	Reverse	CCCTCAGAATGATATTTGTCCTCA
C-mos	Lsc1-F	Forward	CTCTGGKGGCTTTGGKKCTGTSTACAAGG
	Lsc2-R	Reverse	GGTGATGGCAAANGAGTAGATGTCTGC

**Table S2.4** PCR conditions for the sequenced gene fragments of mtDNA and nuDNA, and genotyped microsatellite markers.

Gene	Amplification step	Temperature	Duration	Nº of cycles
12S	Initial denaturation	94 °C	5 minutes	1
	Denaturation	94 °C	30 seconds	35
	Annealing	56 °C	40 seconds	
	Extension	72 °C	60 seconds	
	Final extension	72 °C	5 minutes	1
Cytb	Initial denaturation	94 °C	5 minutes	1
	Denaturation	94 °C	30 seconds	35
	Annealing	49 °C	45 seconds	
	Extension	72 °C	90 seconds	
	Final extension	72 °C	5 minutes	1
C-mos	Initial denaturation	94 °C	5 minutes	1
	Denaturation	94 °C	30 seconds	35
	Annealing	57 °C	45 seconds	
	Extension	72 °C	70 seconds	
	Final extension	72 °C	5 minutes	1
MP1	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	59-55 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	54 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	
MP2	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	57-53 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	53 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	
MP3	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	58-54 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	54 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	
MP4	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	55-51 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	51 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	

**Table S2.5** Characteristics of the 11 microsatellite loci used in the final dataset.

Locus	Repeat	Primer sequence (5'- 3')	Multiplex	Ta	Dye
Ac1	(ATAC) <sub>8</sub>	F: CTGTGGTATATCCCCTGCCA R: GGTGGCTTCTCCACAGCTATT	1	58/54 °C	FAM
Ac5	(AAC) <sub>15</sub>	F: GTTGCTCAACTGCTCCTCC R: AGTGTCTGTGCACAACCAG	1	58/54 °C	VIC
Ac8	(TTG) <sub>11</sub>	F: GACATCTGAAGGCAGCCCTA R: GGTGTAGCCTGGAGCAGAA	1	58/54 °C	NED
Ac13	(AAC) <sub>14</sub>	F: TCCATGGGGTCACAAAGAGT R: TCTCCAGCACTTATCTGATGC	2	58/54 °C	FAM
Ac14	(CAA) <sub>10</sub>	F: TTAAGTGGCAATGTGTTGCAT R: TCCCACATGGTGGGTTACTT	2	58/54 °C	VIC
Ac19	(AAC) <sub>14</sub>	F: TCATTTCACTTCAAACCTGTGG R: ACTGATGTTGGGTTTGGAGC	2	58/54 °C	PET
Ac20	(GTT) <sub>11</sub>	F: ATGCATAAGTACGAAAAGGGGA R: TCTACAGAGAAAGAGAAATAACAACAA	2	58/54 °C	PET
Ac32	(TTC) <sub>15</sub>	F: TAGTCCGTAACCTTGTGGGTCA R: TTCTCAGACAACAGACACCCA	3	58/54 °C	FAM
Ac36	(TGT) <sub>9</sub>	F: GTCACGTTGATTGCATTGCT R: GCCAACTGGGAAACCTAGC	3	58/54 °C	VIC
Ac43	(CAA) <sub>13</sub>	F: AGCTTTGTACGTTCTTTGC R: CCAGAGAAAACACATATGCAAGC	4	55/51 °C	FAM
Ac45	(CAA) <sub>10</sub>	F: AGGCAATGGAAGACAGGGA R: GCCTACAGTTTGTGCATAGGG	4	55/51 °C	VIC

**Table S2.6** Outgroups and taxa used in the time-calibration of the phylogenetic tree. Newly produced sequences are highlighted in bold.

ID	Taxon	Source	Country	Local	12S GB	Cytb GB	C-mos GB	mt-nuDNA tree	mt-nuDNA dating
10084	<i>Acanthodactylus hardyi</i>	<b>This study</b>	Kuwait	Sabah Al-Ahmed Natural Reserve	<b>OP218993</b>	<b>OP220505</b>	<b>OP220960</b>	X	X
10085	<i>Acanthodactylus hardyi</i>	<b>This study</b>	Kuwait	Al-Abraq to Al-Khabari road	<b>OP218994</b>	<b>OP220506</b>	<b>OP220961</b>	X	X
1474	<i>Acanthodactylus erythrurus</i>	<b>This study</b>	Algeria	PN Theniet el Had: Kaf Sahchine	<b>OP219005</b>	<b>OP220047</b>	<b>OP220548</b>	X	X
1476	<i>Acanthodactylus erythrurus</i>	<b>This study</b>	Algeria	Dar Chioukh - 40 km Nord Est Djelfa	<b>OP219006</b>	<b>OP220048</b>	<b>OP220549</b>	X	X
1482	<i>Acanthodactylus erythrurus</i>	<b>This study</b>	Algeria	Medrissa - 60 km Sud Tiaret	<b>OP219007</b>	<b>OP220049</b>	<b>OP220550</b>	X	X
1483	<i>Acanthodactylus maculatus</i>	<b>This study</b>	Algeria	Medrissa - 60 km Sud Tiaret	<b>OP219008</b>	<b>OP220050</b>	<b>OP220551</b>	X	X
Ab105	<i>Acanthodactylus boskianus</i>	Tamar et al., 2014	Egypt	Serabit el Khadim - Gebel Raqaba	KJ567672	KJ567768	KJ547966	X	X
Ab169	<i>Acanthodactylus boskianus</i>	Tamar et al., 2014	Egypt	Sidi Brani	KJ567729	KJ567813	KJ548015	X	X
M17	<i>Mesalina guttulata</i>	Tamar et al., 2016	Israel	4 km W. to Arad	KX296984	KX297187	KX297735	X	X
M18	<i>Mesalina guttulata</i>	Tamar et al., 2016	Israel	Hirbet Nizana	KX296985	KX297188	KX297736	X	X
M20	<i>Mesalina olivieri</i>	Tamar et al., 2016	Israel	Hirbet Mamshit	KX296987	KX297191	KX297738	X	X
M21	<i>Mesalina olivieri</i>	Tamar et al., 2016	Israel	Ramat Hovav	KX296988	KX297190	KX297739	X	X
Gatat1	<i>Gallotia atlantica atlantica</i>	Arribas et al., 2006	Spain	Lanzarote	AY151915	AY151836	AY151999	X	X
Gatma1	<i>Gallotia atlantica mahoratae</i>	Arribas et al., 2006	Spain	Fuerteventura	AY151916	AY151837	AY152000	X	X
Gcaca1	<i>Gallotia caesaris caesaris</i>	Arribas et al., 2006	Spain	El Hierro	AY151922	AY151843	AY152006	X	X
Gcago1	<i>Gallotia caesaris gomerae</i>	Arribas et al., 2006	Spain	La Gomera	AY151921	AY151842	AY152005	X	X
Ggo1	<i>Gallotia bravoana</i>	Hernández et al., 2001	Spain	La Gomera	AJ272395	AJ272396		X	X
Ggae1	<i>Gallotia galloti eisentrauti</i>	Arribas et al., 2006	Spain	Tenerife	AY151918	AY151839	AY152002	X	X
Ggaga1	<i>Gallotia galloti galloti</i>	Arribas et al., 2006	Spain	Tenerife	AY151919	AY151840	AY152003	X	X
Ggapa1	<i>Gallotia galloti palmae</i>	Arribas et al., 2006	Spain	La Palma	AY151920	AY151841	AY152004	X	X
Gin1	<i>Gallotia intermedia</i>	Arribas et al., 2006	Spain	Tenerife	AY151923	AY151844	AY152007	X	X
Gsima1	<i>Gallotia simonyi machadoi</i>	Arribas et al., 2006; Carranza et al., 1999	Spain	El Hierro	AY151924	AF101219	AY152008	X	X
Gst1	<i>Gallotia stehlini</i>	Arribas et al., 2006	Spain	Gran Canaria	AY151917	AY151838	AY152001	X	X
Pcr1	<i>Podarcis cretensis</i>	Kapli et al., 2013; Poulakakis et al., 2003	Greece	Crete		AF486216	KF003242	X	X
Pcr2	<i>Podarcis cretensis</i>	Kapli et al., 2013; Poulakakis et al., 2003	Greece	Crete		AF486218	KF003244	X	X
Pli1	<i>Podarcis lilfordi</i>	Brown et al., 2008	Spain	Menorca	EF694766	EF694810	EF679323	X	X
Pli2	<i>Podarcis lilfordi</i>	Brown et al., 2008	Spain	Cabrera	EF694764	EF694805	EF679302	X	X
Ppe1	<i>Podarcis peloponnesiacus</i>	Kapli et al., 2013; Poulakakis et al., 2005	Greece	Peloponnese		AY896121	KF003245	X	X
Ppe2	<i>Podarcis peloponnesiacus</i>	Kapli et al., 2013; Poulakakis et al., 2005	Greece	Peloponnese		AY896124	KF003246	X	X
Ppi1	<i>Podarcis pityusensis</i>	Brown et al., 2008	Spain	Ibiza	EF694768	EF694814	EF679324	X	X
Ppi2	<i>Podarcis pityusensis</i>	Brown et al., 2008	Spain	Espardell	EF694769	EF694815	EF679325	X	X
Pal1	<i>Psammodromus algirus</i>	Arribas et al., 2006	-	-	AY151914	AY151835	AY151998	X	X
Pal2	<i>Psammodromus algirus</i>	Harris et al., 1998	Morocco	S. of Tizi Chika, High Atlas	AF080308	AF080309		X	X

**Table S2.7** Details of the phylogenetic analyses. The number of samples included in each dataset is shown between brackets (ingroups only). Priors not mentioned in the table were left as default.

Phylogenetic analysis	Dataset ( <i>N</i> tips)	Partition	Length	Nucleotide substitution model	Clock model	Tree model	Run Specifications
<b>Bayesian Inference</b>	mt-nuDNA haplotypes (338)	<i>12S</i>	368	GTR+I+G; estimated bf	Ucld	Coalescent: Constant Size. Random starting tree	2 runs; 10 <sup>8</sup> generations; 10 <sup>4</sup> sampling frequency; 10% burn-in
		<i>cytb</i>	377	GTR+I+G; estimated bf	Ucld		
		<i>C-mos</i>	468	HKY+I+G; equal bf	Strict		
<b>Maximum Likelihood</b>	mt-nuDNA haplotypes (338)	<i>12S</i>	368	GTR+I+G; estimated bf			
		<i>cytb</i>	377				
		<i>C-mos</i>	468				
<b>Bayesian Inference (splits dating)</b>	mt-nuDNA (74 + 21 samples used for time-calibrating)	<i>12S</i>	371	GTR+I+G; estimated bf	Ucld	Speciation: Yule Process Random starting tree	2 runs; 10 <sup>8</sup> generations; 10 <sup>4</sup> sampling frequency; 10% burn-in
		<i>cytb</i>	377	GTR+I+G; estimated bf	Ucld		
		<i>C-mos</i>	468	HKY+I+G; equal bf	Strict		

Abbreviations: Ucld refers to relaxed uncorrelated lognormal clock; bf refers to base frequencies.

**Table S2.8** Biogeographic events used to time-calibrate the phylogenetic inference.

Event	Period	Value	Taxa
Fragmentation of Balearic Islands	End of the Messinian Salinity Crisis	5.32 ± 0.05	<i>Podarcis pityusensis</i> – <i>Podarcis lilfordi</i>
Isolation of Greece from Peloponnesus	End of the Messinian Salinity Crisis	5.32 ± 0.05	<i>Podarcis cretensis</i> – <i>Podarcis peloponnesiacus</i>
Origin of Fuerteventura and Lanzarote	Age of the Canary Islands	18 ± 2	<i>Gallotia</i> spp. – <i>Psammodromus algirus</i>
Origin of La Gomera	Age of the Canary Islands	6 ± 3	<i>Gallotia galloti</i> – <i>Gallotia caesaris</i>
Origin of La Palma	Age of the Canary Islands	1 ± 0.5	<i>Gallotia galloti palmae</i> – ancestor of <i>Gallotia galloti galloti</i> & <i>Gallotia galloti eisentrauti</i>
Origin of El Hierro	Age of the Canary Islands	0.8 ± 0.2	<i>Gallotia bravoana</i> – <i>Gallotia simonyi machadoi</i>
Origin of El Hierro	Age of the Canary Islands	0.8 ± 0.2	<i>Gallotia caesaris caesaris</i> – <i>Gallotia caesaris gomerae</i>

**Table S2.9** Mean 12S pairwise genetic distances (p-distances) among species and intra-specific lineages.

SPECIES									
	<i>A. aegyptius</i>	<i>A. aureus</i>	<i>A. dumerilii/senegalensis</i>	<i>A. longipes</i>	<i>A. scutellatus</i>	<i>A. taghitensis</i>			
<i>A. aegyptius</i>									
<i>A. aureus</i>	0.077								
<i>A. dumerilii/senegalensis</i>	0.040	0.076							
<i>A. longipes</i>	0.016	0.087	0.048						
<i>A. scutellatus</i>	0.040	0.079	0.052	0.049					
<i>A. taghitensis</i>	0.091	0.080	0.094	0.101	0.095				
LINEAGES									
<i>A. taghitensis</i>	Mauritania								
Mauritania									
Algeria	0.040								
<i>A. aureus</i>	North		Central-Inland						
North									
Central-Inland	0.015								
South	0.010	0.015							
<i>A. dumerilii/senegalensis</i>	Zagora	NW Sahara		Merzouga					
Zagora									
NW Sahara	0.018								
Merzouga	0.019	0.024							
W Sahara-Sahel	0.018	0.022	0.022						
<i>A. longipes</i>	Tunisia	Great Western Erg	Aegyptius	E Sahara-Sahel	Central Sahara	Draa Basin	W Sahara-Sahel Inland		
Tunisia									
Great Western Erg	0.040								
Aegyptius	0.034	0.026							
E Sahara-Sahel	0.044	0.032	0.013						
Central Sahara	0.040	0.021	0.011	0.016					
Draa Basin	0.037	0.027	0.008	0.016	0.006				
W Sahara-Sahel Inland	0.039	0.028	0.015	0.020	0.011	0.011			
W Sahara-Sahel South	0.042	0.028	0.015	0.016	0.011	0.014	0.019		
<i>A. scutellatus</i>	Nile Delta	Sinai	Atlas High Plateau	Pansaharan	N Sahara	Tassili-N'Ajjer	Tunisia Coast	Tunisia Inland	Saharan Atlas
Nile Delta									
Sinai	0.045								
Atlas High Plateau	0.031	0.023							
Pansaharan	0.042	0.042	0.029						
N Sahara	0.042	0.044	0.028	0.016					
Tassili-N'Ajjer	0.040	0.040	0.031	0.048	0.049				
Tunisia Coast	0.037	0.020	0.010	0.029	0.028	0.032			
Tunisia Inland	0.048	0.025	0.020	0.033	0.033	0.031	0.013		
Saharan Atlas	0.046	0.028	0.024	0.036	0.037	0.036	0.019	0.019	
Al-Hamra	0.040	0.023	0.020	0.031	0.033	0.028	0.014	0.017	0.018



**Table S2.10** Generalized Linear Models exploring correlations between different sets of topographic and land-cover predictors and (A) mtDNA haplotype distinctiveness (n = 421) or (B) lineages' range sizes (n = 20). For each group of predictors, the best-fitting model is highlighted in bold.

(A) diversification model	Model	Comparison	Predictors	df	AIC
	<i>Mod1</i>	Topography	Hapl. disct. ~ x(Altitude) + x(TRI) + nearest + sp	10	-2464.4
<i>Mod2</i>	Topography	Hapl. disct. ~ x(Altitude) + nearest + sp	9	-2458.6	
<b><i>Mod3</i></b>	<b>Topography</b>	<b>Hapl. disct. ~ x(TRI) + nearest + sp</b>	<b>9</b>	<b>-2445.5</b>	
<i>Mod1</i>	Land-cover 1	Hapl. disct. ~ x(Erg) + x(Reg) + x(BA) + nearest + sp	11	-2424.1	
<b><i>Mod2</i></b>	<b>Land-cover 1</b>	<b>Hapl. disct. ~ x(Erg) + x(Reg) + nearest + sp</b>	<b>10</b>	<b>-2424.7</b>	
<i>Mod3</i>	Land-cover 1	Hapl. disct. ~ x(Erg) + x(BA) + nearest + sp	10	-2425.5	
<i>Mod4</i>	Land-cover 1	Hapl. disct. ~ x(Reg) + x(BA) + nearest + sp	10	-2425.8	
<b><i>Mod1</i></b>	<b>Land-cover 2</b>	<b>Hapl. disct. ~ x(Erg) + nearest + sp</b>	<b>9</b>	<b>-2419.4</b>	
<i>Mod2</i>	Land-cover 2	Hapl. disct. ~ x(Reg) + nearest + sp	9	-2426.4	
<i>Mod3</i>	Land-cover 2	Hapl. disct. ~ x(BA) + nearest + sp	9	-2425.1	
<b>FINAL</b>		<b>Hapl. disct. ~ x(TRI) + x(Erg) + nearest + sp</b>	<b>10</b>	<b>2443.5</b>	

(B) connectivity model	Model	Comparison	Predictors	df	AIC
	<i>Mod1</i>	Topography	Diameter ~ x(Altitude) + x(TRI) + n + sp	10	349.6
<i>Mod2</i>	Topography	Diameter ~ x(Altitude) + n + sp	9	348.4	
<b><i>Mod3</i></b>	<b>Topography</b>	<b>Diameter ~ x(TRI) + n + sp</b>	<b>9</b>	<b>347.8</b>	
<i>Mod1</i>	Land-cover 1	Diameter ~ x(Erg) + x(Reg) + x(BA) + n + sp	11	335.7	
<i>Mod2</i>	Land-cover 1	Diameter ~ x(Erg) + x(Reg) + n + sp	10	334.7	
<b><i>Mod3</i></b>	<b>Land-cover 1</b>	<b>Diameter ~ x(Erg) + x(BA) + n + sp</b>	<b>10</b>	<b>333.9</b>	
<i>Mod4</i>	Land-cover 1	Diameter ~ x(Reg) + x(BA) + n + sp	10	346.2	
<b><i>Mod2</i></b>	<b>Land-cover 2</b>	<b>Diameter ~ x(Erg) + n + sp</b>	<b>9</b>	<b>334.8</b>	
<i>Mod3</i>	Land-cover 2	Diameter ~ x(BA) + n + sp	9	345.3	
<b>FINAL</b>		<b>Diameter ~ x(TRI) + x(Erg) + n + sp</b>	<b>10</b>	<b>336.8</b>	

**Table S2.11** Metrics measuring the performance of the ensemble models and threshold values used to generate the binary maps.

Species	TSS				AUC		
	TSS	Sensitivity	Specificity	Threshold	AUC	Sensitivity	Specificity
<i>A. aegyptius</i>	0.926	97.143	95.416	0.584	0.986	97.143	95.486
<i>A. aureus</i>	0.967	100.000	96.625	0.575	0.992	100.000	96.695
<i>A. dumerilii/senegalensis</i>	0.850	97.436	87.504	0.457	0.963	97.436	87.744
<i>A. longipes</i>	0.813	98.701	82.570	0.472	0.952	98.701	82.940
<i>A. scutellatus</i>	0.795	95.714	83.759	0.466	0.941	95.714	84.209
<i>A. taghitensis</i>	0.967	100.000	96.689	0.568	0.991	100.000	96.729



		GAM	GBM	GLM	ANN	CTA	Maxent	Ensemble
		(9)	(10)	(10)	(10)	(10)	(10)	(59)
<i>A. scutellatus</i>	ED1503_bio7	0.42 ± 0.17	0.05 ± 0.03	0.00 ± 0.00	0.31 ± 0.17	<b>0.10 ± 0.21</b>	0.08 ± 0.10	0.20 ± 0.26
	ED1503_bio10	<b>0.66 ± 0.10</b>	0.02 ± 0.01	0.03 ± 0.07	0.42 ± 0.32	0.04 ± 0.09	0.02 ± 0.05	0.19 ± 0.29
	ED1503_bio11	0.53 ± 0.11	<b>0.15 ± 0.10</b>	<b>0.20 ± 0.40</b>	<b>0.56 ± 0.32</b>	<b>0.80 ± 0.29</b>	0.08 ± 0.10	<b>0.38 ± 0.36</b>
	ED1514_bio1	0.14 ± 0.06	0.03 ± 0.01	0.01 ± 0.02	0.05 ± 0.05	0.02 ± 0.05	0.14 ± 0.10	0.06 ± 0.08
	ED1514_bio7	0.27 ± 0.06	0.01 ± 0.00	0.05 ± 0.08	0.09 ± 0.08	0.01 ± 0.04	0.03 ± 0.04	0.08 ± 0.10
	ED1515_bio7	0.34 ± 0.04	0.05 ± 0.04	0.06 ± 0.12	0.08 ± 0.08	0.02 ± 0.06	0.18 ± 0.15	0.12 ± 0.14
	ED150708_bio1	<b>0.74 ± 0.10</b>	0.01 ± 0.01	0.01 ± 0.03	0.48 ± 0.36	0.01 ± 0.03	0.05 ± 0.10	0.21 ± 0.32
	ED150708_bio2	0.61 ± 0.26	0.03 ± 0.01	0.00 ± 0.00	0.34 ± 0.26	0.02 ± 0.05	0.10 ± 0.21	0.18 ± 0.28
	ED150708_bio3	0.55 ± 0.19	0.03 ± 0.02	0.05 ± 0.14	0.11 ± 0.15	0.00 ± 0.01	0.10 ± 0.16	0.13 ± 0.22
	ED150708_bio4	0.55 ± 0.13	<b>0.12 ± 0.04</b>	<b>0.42 ± 0.48</b>	<b>0.70 ± 0.24</b>	0.02 ± 0.04	<b>0.46 ± 0.25</b>	<b>0.37 ± 0.34</b>
	ED150708_bio5	0.62 ± 0.20	0.01 ± 0.01	0.00 ± 0.00	0.30 ± 0.23	0.03 ± 0.09	0.02 ± 0.05	0.16 ± 0.26
	ED150708_bio6	<b>0.62 ± 0.13</b>	0.05 ± 0.02	<b>0.07 ± 0.12</b>	<b>0.54 ± 0.31</b>	0.04 ± 0.13	0.07 ± 0.08	<b>0.23 ± 0.29</b>
	bio12	0.20 ± 0.05	<b>0.10 ± 0.05</b>	0.02 ± 0.07	0.15 ± 0.13	0.06 ± 0.13	<b>0.24 ± 0.14</b>	0.13 ± 0.13
	bio14	0.13 ± 0.05	0.00 ± 0.00	0.00 ± 0.00	0.03 ± 0.04	0.00 ± 0.00	0.21 ± 0.28	0.06 ± 0.14
	bio17	0.20 ± 0.05	0.01 ± 0.01	0.00 ± 0.00	0.06 ± 0.06	<b>0.11 ± 0.14</b>	0.18 ± 0.27	0.09 ± 0.15
	200	0.35 ± 0.06	0.02 ± 0.02	0.02 ± 0.03	0.01 ± 0.02	0.02 ± 0.06	0.12 ± 0.09	0.08 ± 0.13
	201	0.37 ± 0.09	0.00 ± 0.00	0.00 ± 0.00	0.02 ± 0.03	0.02 ± 0.06	0.04 ± 0.04	0.07 ± 0.14
202	0.45 ± 0.16	0.06 ± 0.02	0.05 ± 0.14	0.01 ± 0.02	0.01 ± 0.04	<b>0.38 ± 0.21</b>	0.15 ± 0.22	
<i>A. taghitensis</i>		GAM	GBM	GLM	ANN	CTA	Maxent	Ensemble
		(9)	(10)	(8)	(10)	(6)	(10)	(53)
	ED1503_bio7	0.81 ± 0.20	0.04 ± 0.02	0.00 ± 0.00	<b>0.79 ± 0.13</b>	0.00 ± 0.00	0.09 ± 0.14	0.25 ± 0.36
	ED1503_bio10	0.72 ± 0.23	0.15 ± 0.07	0.07 ± 0.17	0.61 ± 0.23	0.13 ± 0.22	0.01 ± 0.02	0.26 ± 0.32
	ED1503_bio11	0.68 ± 0.27	0.04 ± 0.02	0.00 ± 0.00	<b>0.82 ± 0.14</b>	0.01 ± 0.04	0.00 ± 0.00	0.22 ± 0.35
	ED1514_bio1	0.58 ± 0.25	<b>0.17 ± 0.08</b>	<b>0.22 ± 0.33</b>	0.23 ± 0.14	<b>0.45 ± 0.42</b>	<b>0.27 ± 0.05</b>	<b>0.33 ± 0.29</b>
	ED1514_bio7	0.62 ± 0.30	0.01 ± 0.01	0.02 ± 0.06	0.27 ± 0.09	0.03 ± 0.09	0.02 ± 0.05	0.15 ± 0.26
	ED1515_bio7	0.45 ± 0.27	0.01 ± 0.01	0.00 ± 0.00	0.25 ± 0.05	0.02 ± 0.06	0.00 ± 0.00	0.11 ± 0.21
	ED150708_bio1	0.81 ± 0.23	0.00 ± 0.00	0.00 ± 0.00	0.79 ± 0.10	0.04 ± 0.08	0.00 ± 0.00	0.24 ± 0.37
	ED150708_bio2	<b>0.92 ± 0.17</b>	0.13 ± 0.04	<b>0.38 ± 0.43</b>	0.59 ± 0.24	0.06 ± 0.14	0.00 ± 0.00	<b>0.32 ± 0.39</b>
	ED150708_bio3	<b>0.90 ± 0.19</b>	<b>0.22 ± 0.06</b>	0.00 ± 0.00	0.51 ± 0.25	0.10 ± 0.16	0.12 ± 0.03	0.29 ± 0.34
	ED150708_bio4	0.83 ± 0.25	0.03 ± 0.02	0.02 ± 0.04	0.76 ± 0.19	0.04 ± 0.13	0.00 ± 0.00	0.24 ± 0.38
	ED150708_bio5	0.86 ± 0.15	0.16 ± 0.06	0.03 ± 0.08	0.75 ± 0.26	<b>0.28 ± 0.28</b>	<b>0.25 ± 0.07</b>	<b>0.36 ± 0.34</b>
	ED150708_bio6	0.90 ± 0.15	0.01 ± 0.01	0.00 ± 0.00	<b>0.78 ± 0.16</b>	0.00 ± 0.00	0.01 ± 0.01	0.24 ± 0.39
	bio12	0.59 ± 0.26	0.16 ± 0.04	0.08 ± 0.15	0.42 ± 0.26	0.08 ± 0.13	0.11 ± 0.04	0.23 ± 0.25
	bio14	0.39 ± 0.26	0.00 ± 0.00	0.01 ± 0.04	0.20 ± 0.20	0.00 ± 0.00	0.08 ± 0.06	0.11 ± 0.19
	bio17	0.70 ± 0.24	0.05 ± 0.03	0.17 ± 0.32	0.37 ± 0.17	0.03 ± 0.08	0.13 ± 0.03	0.23 ± 0.29
200	0.88 ± 0.12	0.00 ± 0.00	0.01 ± 0.03	0.02 ± 0.03	0.07 ± 0.14	0.01 ± 0.03	0.17 ± 0.33	
201	<b>0.96 ± 0.06</b>	0.05 ± 0.04	<b>0.37 ± 0.26</b>	0.09 ± 0.11	<b>0.19 ± 0.29</b>	0.07 ± 0.06	0.29 ± 0.36	
202	0.84 ± 0.11	<b>0.21 ± 0.08</b>	0.09 ± 0.21	0.04 ± 0.04	0.13 ± 0.20	<b>0.36 ± 0.09</b>	0.29 ± 0.30	

**Table S2.13** Observations of heterozygote deficiency (Hdef) and null alleles (Nall) in *Acanthodactylus aureus*, *A. dumerilii/senegalensis*, and *A. longipes* from the Parc National du Banc d'Arguin sympatry zone. Significant values after Bonferroni correction are marked with an asterisk (\*). Two asterisks indicate observations of stuttering (\*\*).

Locus	<i>A. aureus</i>		<i>A. dumerilii/senegalensis</i>		<i>A. longipes</i>	
	Hdef	Nall	Hdef	Nall	Hdef	Nall
Ac1						
Ac5				*		
Ac8			*			
Ac13			*	**		
Ac14						
Ac19					*	**
Ac20						
Ac32			*	**		
Ac36						
Ac43			*	**		
Ac45						

**Table S2.14** Pairwise  $F_{ST}$  values based on microsatellites for the three identified genetic clusters from the Parc National du Banc d'Arguin sympatry zone. (+) indicate significance ( $\alpha=0.05$ ).

	<i>A. aureus</i>	<i>A. dumerilii/senegalensis</i>	<i>A. longipes</i>
<i>A. aureus</i>		+	+
<i>A. dumerilii/senegalensis</i>	0.267		+
<i>A. longipes</i>	0.371	0.277	

**Article reference – “Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards”**

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**Supporting Information**

**APPENDIX S3 – Supplementary texts**

**Text S3.1 Ecological variables (extended details).**

The heterogeneity of desert landscapes is poorly represented in land-cover maps (Campos and Brito, 2018). To minimize this issue, for ecological models we used primarily multi-temporal remote sensing variables, derived from pre-processed monthly variables from MODIS sensors of two NASA satellites (EDENext project; data set MODIS v4). These sources provide non-interpolated continuous measurements for the target temporal resolution, and covered the following bands and derived products: middle infra-red [MIR; indicating the water content of the surface (Jensen, 2007)]; day and night time land surface temperatures; normalized difference vegetation index [NDVI (Tucker, 1979)]; and enhanced vegetation index [EVI (Huete et al., 1997)]. Annual and seasonal variations were computed with the ‘dismo’ (Hijmans and Etten, 2012) and ‘raster’ (Hijmans et al., 2012) R packages, using temporal snapshots analogue to bioclimatic predictors [for details, see Ahmadzadeh et al. (2016)]. Additionally, we included the eight precipitation-related bioclimatic variables (bio12–bio19) for current climatic conditions from WorldClim 2.0 (Fick and Hijmans, 2017) and three desert-specific land-cover variables derived from the Globcover dataset (Bicheron et al., 2009): bare areas, consolidated bare areas (*regs*), and non-consolidated bare areas (*ergs*). The land-cover predictors were produced by upscaling the original variable (~300×300 m) to 30 arc-sec resolution (~1×1 km) and calculating the pixel percentage of the target land-cover type at the new scale. All remaining variables were downloaded at 30 arc-sec resolution and cropped to the study area. The complete set of variables describes seasonal changes in environmental conditions in terms of temperature, precipitation, humidity, and vegetation structure, while controlling for the substrate type. Pairwise correlations were assessed based on Spearman’s  $R^2 < 0.7$ , selecting a final subset of 18 low-correlated variables (Table S2.2). The absence of spatial artefacts in the final variables was verified.

**Text S3.2 DNA extraction, amplification, sequencing, and genotyping (extended details).**

Genomic DNA extractions were performed from ethanol-preserved tissues using QIAGEN’s EasySpin Kit and stored at -20°C prior to amplification. The success of DNA extractions was evaluated by electrophoresis on 0.8% agarose gels stained with Gel Red, in TBE 0.5x buffer.

All samples were amplified and sequenced for two mitochondrial fragments, the 12S ribosomal RNA (12S; 368 base pairs) and the cytochrome-b (Cytb; 377 bp), and the nuclear fragment oocyte maturation factor MOS (C-mos; 468 bp). Polymerase chain reactions (PCRs) were performed in 10 µl reaction volumes comprising 5 µl of MyTaq (MyTaq™ Mix; Bioline), 3 µl of ultrapure water, 0.5 µl of forward and reverse primers, and 1 µl of template DNA. Primers and PCR conditions are given in Tables S2.3 and S2.4, respectively. PCR products were cleaned with ExoSAP, and the purification and sequencing for the forward strand was outsourced to MacroGen Inc., NL (<https://www.macrogen-europe.com/>). Chromatograms were verified in GENEIOUS PRO v.4.8.5 (Drummond et al., 2010) and sequences were aligned using MAFFT v.7 (Kato and Standley, 2013). Gene alignments were proofread and the absence of stop codons in coding regions was verified. Topological incongruences between markers were checked by inferring Neighbour-Joining trees for each marker in MEGA v.7 (Tamura et al., 2013).

A set of 22 microsatellites previously developed for the *Scutellatus* group (Lopes et al., 2015) was used to genotype the samples from the sympatry zone. Of those, 14 amplified consistently, were polymorphic, and showed less than 40% of missing data for the target taxa (see Table S2.5 for the final set of markers). PCRs were performed in 10 µl reaction volumes comprising 5 µl of Master Mix, 3 µl of ultrapure water, 1 µl of primer mix, and 1 µl of template DNA. Loci were combined into four multiplexes using varying amounts of primer concentrations (Table S2.4). Microsatellites PCR products were later separated by capillary electrophoresis on an automatic sequencer ABI3130xl Genetic Analyzer (AB Applied Biosystems), using 1 µl of amplification product and 10 µl of formamide + 75-400 (-250) LIZ NEW size standard. Allele calling was performed in GENEMAPPER v4.0 (Applied Biosystems, 2005) and manually checked twice.

### **Text S3.3 Phylogenetic inference (extended details).**

The best-fit models of molecular evolution were inferred in the mt-nuDNA dataset using PARTITIONFINDER v1.1.1 (Lanfear et al., 2012), implementing partitions schemes by gene and the parameters linked branch lengths, mrbayes models, BIC model selection criterion, and greedy search scheme. Bayesian Inference (BI) analyses were performed in BEAST v.1.10.4 (Suchard et al., 2018), after collapsing haplotypes with FABOX (Villesen, 2007). BEAST was run on the CIPRES gateway (Miller et al., 2010) in two independent runs of  $10^8$  generations, sampling at every  $10^4$ , with unlinked substitution and clock models (Drummond et al., 2006), a constant population size coalescent tree prior (Kingman, 1982), and considering ambiguities in the nuclear partition (manually editing the .xml file to Ambiguities = true). Detailed settings are given in Table S2.7. The convergence of chains and Effective Sample Sizes higher than 200 for all parameters was verified using TRACER v.1.7.1 (Rambaut et al., 2018). Log and tree files of the independent runs were combined using LOGCOMBINER and the subsequent maximum clade credibility summary tree with posterior probabilities for each node, using mean values, was obtained using TREEANNOTATOR (both from the BEAST package). The resulting trees were visualised and edited with FIGTREE v.1.4.3 (Rambaut, 2016). To complement the BI assessment, Maximum Likelihood (ML) analyses were performed in the mt-nuDNA dataset using RAXMLGUI (Silvestro and Michalak, 2012). A bootstrapping tree was built based on 1,000 rapid bootstrap replications, GTR+G+I substitution model and rates, and a nearest-neighbour interchange heuristic method. BI and ML nodes were considered supported if they received a posterior probability > 0.95 or bootstrap support > 85 respectively.

### **Text S3.4 Ecological niche modelling (extended details).**

Three regression-based (GAM, generalized additive models, GBM, generalized boosting models; and GLM, generalized linear models) and three machine learning-based (ANN, artificial neural networks; CTA, classification tree analysis; and MAXENT.Philipps, maximum entropy) algorithms were chosen to reduce the uncertainties associated with modelling techniques (Thuiller et al., 2019). All models were run using default parameters. Background areas for each species were limited by a radial buffer of 500 km from presence records, to avoid excessive biases towards regions with no occurrence when selecting pseudo-absences (Anderson and Raza, 2010). As pseudo-absences, 10,000 random points were sampled randomly from the buffer area, with a minimum distance of 10 km from presence records (Barbet-Massin et al., 2012).

Ten model replicates were run for each of the six algorithms for each species, and each of them was subsequently rescaled using a binomial GLM (an internal routine from the biomod2 package to make the



single models comparable). Presence data for each model replicate were selected randomly by cross-validation, using 80% of data for training. Individual model replicate performance was evaluated using true skill statistic (TSS) metric (Allouche et al., 2006) and the area under the receiver operating characteristic curve (AUC; Fielding & Bell, 1997). Across all potential models, only those with AUC scores > 0.7 were combined in a final ensemble model, weighted proportionally according to predictive performance (Marmion et al., 2009). The contributions of the environmental variables to the ensemble models by algorithm were evaluated by averaging the relative contribution to individual model replicates.

### **Text S3.5 Microsatellite analyses (extended details).**

Bayesian clustering analyses were conducted using STRUCTURE 2.3.4 (Pritchard et al., 2000). The admixture model was used, assuming correlated allele frequencies, and without incorporation of sampling localities. Ten runs were carried out for each K value, from 1 to 8 (exceeding the number of intra-specific lineages detected with the phylogenetic analyses), with an initial burn-in of 200,000 iterations and additional  $10^6$  iterations after the burn-in. STRUCTURE HARVESTER v.0.6.94 (Earl, 2012) was used to estimate the optimal number of clusters (K) through the examination of  $\ln p(X|K)$  as well as the  $\Delta K$  (Evanno et al., 2005; Pritchard et al., 2000). The results were averaged across runs using CLUMPP v.1.1.2 (Jakobsson and Rosenberg, 2007). Genetic differentiation ( $F_{ST}$ ) among the resultant clusters were computed in ARLEQUIN (Excoffier and Lischer, 2010) using the Weir and Cockerham's estimator  $\Theta$ , performing 10,000 permutations to test for significance. Factorial Correspondence Analyses (FCoA) on individual genotypes were run in GENETIX (Belkhir et al., 2004) using default options, to visualize the relationships among clusters.

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**Supporting Information**

**APPENDIX S4 – Supplementary files (captions)**

**File S4.1** Updated range for *Acanthodactylus dumerilii/senegalensis* in format .shp.

**File S4.1**

*--- Uploaded as a separate ZIP file ---*













OBSERVATION CODE		TAXONOMY	SOURCE		SPATIAL REFERENCE			
Source	Museum	Species	Source	Reference	Country	Local	Lat	Long
A788		<i>Acanthodactylus aegyptius</i>	CIBIO - genetics		Egypt	10km NW of Cairo	30.08	31.18
A790		<i>Acanthodactylus aegyptius</i>	CIBIO - genetics		Egypt	Wadi Natroun	30.42	30.22
A791		<i>Acanthodactylus aegyptius</i>	CIBIO - genetics		Egypt	Al Arish	31.12	33.80
SPM002352(42)		<i>Acanthodactylus aegyptius</i>	CIBIO - genetics		Egypt	Zerenuk, N. Sinai (Zaraniq)	31.07	33.30
SPM002912		<i>Acanthodactylus aegyptius</i>	CIBIO - genetics		Egypt	N Sinai - 17 km NW to Bir Qatia	31.01	32.58
TAU - R.16331	TAU - R.16331	<i>Acanthodactylus aegyptius</i>	CIBIO - genetics		Israel	Ashelim	30.99	34.72
TAU - R.16400	TAU - R.16400	<i>Acanthodactylus aegyptius</i>	CIBIO - genetics		Israel	Bir Mashash sands	31.10	34.81
KT132		<i>Acanthodactylus aegyptius</i>	Paper - genetics	Tamar et al., 2016	Egypt	5.5 km NW. to Bir Qatia, Sinai	30.99	32.70
KT133		<i>Acanthodactylus aegyptius</i>	Paper - genetics	Tamar et al., 2016	Egypt	17 km NW. to Bir Qatia, Sinai	31.04	32.62
KT135		<i>Acanthodactylus aegyptius</i>	Paper - genetics	Tamar et al., 2016	Egypt	Zaraniq, Sinai	31.11	33.39
KT10		<i>Acanthodactylus aegyptius</i>	Paper - genetics	Tamar et al., 2016	Israel	Bir Mashash sands	31.07	34.85
KT37		<i>Acanthodactylus aegyptius</i>	Paper - genetics	Tamar et al., 2016	Israel	Ashelim	30.97	34.70
KT277	TAU - R.16161	<i>Acanthodactylus aegyptius</i>	Paper - genetics	Tamar et al., 2016	Israel	Shivta junction	30.94	34.60
15746	BEV 8984	<i>Acanthodactylus aegyptius</i>	CIBIO - observ		Egypt	Cairo, 32km W of (192km from Alexandria)	30.08	30.90
iNat25531526		<i>Acanthodactylus aegyptius</i>	GBIF - observ		Israel	HaDarom	31.14	34.68
BMNH1987.2332	BMNH1987.2332	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Arish, North Sinai	31.10	33.67
BMNH1987.2334	BMNH1987.2334	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Arish, North Sinai	31.10	33.67
BMNH1987.2335	BMNH1987.2335	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Arish, North Sinai	31.10	33.67
BMNH1987.2336	BMNH1987.2336	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Arish, North Sinai	31.10	33.67
BMNH1987.2337	BMNH1987.2337	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Arish, North Sinai	31.10	33.67
BMNH1987.2338	BMNH1987.2338	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Arish, North Sinai	31.10	33.67
BMNH1987.2339	BMNH1987.2339	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Arish, North Sinai	31.10	33.67
SMB34	SMB34	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	25km S.W. El Arish, North Sinai	30.93	33.65
SMB35	SMB35	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	33km S.W. El Arish, North Sinai	30.86	33.62
SMB38	SMB38	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	40km S.W. El Arish, North Sinai	30.83	33.59
FMNH269502	FMNH269502	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	17km S. El Arish, North Sinai	31.00	33.82
SMB41	SMB41	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	44km S.E. El Arish, North Sinai	30.86	34.09
SMB36	SMB36	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	10km SW Bir El Abd, North Sinai	30.93	32.93
SMB65	SMB65	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Sad el Rawafa, North Sinai	30.75	34.12
SMB66	SMB66	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Sad el Rawafa, North Sinai	30.75	34.12
SMB67	SMB67	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Sad el Rawafa, North Sinai	30.75	34.12
SMB68	SMB68	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Sad el Rawafa, North Sinai	30.75	34.12
FMNH269503	FMNH269503	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Sad el Rawafa, North Sinai	30.75	34.12
SMB70	SMB70	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Arish, North Sinai	31.15	33.81
SMB71	SMB71	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Arish, North Sinai	31.15	33.81
SMB77	SMB77	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Massaid, North Sinai	31.12	33.72
SMB78	SMB78	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	5 km S.E. El Gorah, North Sinai	30.98	34.14
SMB125	SMB125	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Rafah Beach, North Sinai	31.31	34.20
SMB8247	SMB8247	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Zaranik, North Sinai	31.07	33.30
SMB8322	SMB8322	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Zaranik, North Sinai	31.07	33.30
SMB8355	SMB8355	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Zaranik, North Sinai	31.07	33.30
SMB8508	SMB8508	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Zaranik, North Sinai	31.07	33.30
SMB10612	SMB10612	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Zaranik, North Sinai	31.07	33.30
SMB10721	SMB10721	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Zaranik, North Sinai	31.07	33.30
SMB10824	SMB10824	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Zaranik, North Sinai	31.07	33.30
SMB37	SMB37	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	10 km E. of Suez, North Sinai	29.99	32.69
SMB42	SMB42	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	10 km E. of Suez, North Sinai	29.99	32.69
SMB11136	SMB11136	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	N.W. Cairo, Western Desert	30.10	30.87
BMNH97.10.28.303	BMNH97.10.28.303	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Giza, Western Desert	29.97	31.13

BMNH97.10.28.312	BMNH97.10.28.312	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Giza, Western Desert	29.97	31.13
FMNH78889	FMNH78889	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	1 km W. El Birigat, Beheira, Western Desert	30.49	30.79
SMB8509	SMB8509	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Natrun, Western Desert	30.40	30.32
BMNH1910.6.3.8	BMNH1910.6.3.8	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Natrun, Western Desert	30.40	30.32
BMNH1910.6.3.9	BMNH1910.6.3.9	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Natrun, Western Desert	30.40	30.32
SMB8563	SMB8563	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11055	SMB11055	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11056	SMB11056	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11110	SMB11110	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11111	SMB11111	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11330	SMB11330	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11331	SMB11331	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11342	SMB11342	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
SMB11343	SMB11343	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
FMNH205942	FMNH205942	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
FMNH269501	FMNH269501	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis, Western Desert	30.25	28.94
FMNH68848	FMNH68848	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bir Victoria, Western Desert	30.39	30.61
FMNH68849	FMNH68849	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Abu Rawash, Western Desert	30.03	30.83
FMNH68857	FMNH68857	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Abu Rawash, Western Desert	30.03	30.83
FMNH78890	FMNH78890	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Abu Rawash, Western Desert	30.03	30.83
FMNH82874	FMNH82874	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Abu Rawash, Western Desert	30.03	30.83
FMNH109736	FMNH109736	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Abu Rawash, Western Desert	30.03	30.83
FMNH78872	FMNH78872	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Birqash, Western Desert	30.17	30.99
FMNH78873	FMNH78873	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Birqash, Western Desert	30.17	30.99
FMNH63975	FMNH63975	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Mansuriya, Western Desert	30.12	30.95
FMNH68850	FMNH68850	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Mansuriya, Western Desert	30.12	30.95
FMNH78874	FMNH78874	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Mansuriya, Western Desert	30.12	30.95
FMNH78875	FMNH78875	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Mansuriya, Western Desert	30.12	30.95
FMNH78876	FMNH78876	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Mansuriya, Western Desert	30.12	30.95
FMNH78877	FMNH78877	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	El Mansuriya, Western Desert	30.12	30.95
FMNH78883	FMNH78883	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Giza Pyramids, Western Desert	29.98	31.13
FMNH78886	FMNH78886	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Giza Pyramids, Western Desert	29.98	31.13
FMNH78887	FMNH78887	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Giza Pyramids, Western Desert	29.98	31.13
FMNH78888	FMNH78888	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Giza Pyramids, Western Desert	29.98	31.13
BMNH129.9.1.20	BMNH129.9.1.20	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Sakkara, Western Desert	29.85	31.22
BMNH97.10.28.313	BMNH97.10.28.313	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Fayoum, Western Desert	29.28	30.91
FMNH58700	FMNH58700	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Kom Oshim, Fayoum, Western Desert	29.52	30.89
FMNH77992	FMNH77992	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Kafr Mahfuz, Fayoum, Western Desert	29.45	30.91
FMNH77994	FMNH77994	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Kafr Mahfuz, Fayoum, Western Desert	29.45	30.91
FMNH78002	FMNH78002	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Kafr Mahfuz, Fayoum, Western Desert	29.45	30.91
SMB73	SMB73	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Rayan, Western Desert	29.20	30.38
SMB249	SMB249	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Rayan, Western Desert	29.20	30.38
SMB11137	SMB11137	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Rayan, Western Desert	29.20	30.38
SMB11138	SMB11138	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi El Rayan, Western Desert	29.20	30.38
FMNH164680	FMNH164680	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164681	FMNH164681	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164682	FMNH164682	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164683	FMNH164683	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164684	FMNH164684	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164685	FMNH164685	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164686	FMNH164686	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43

FMNH164687	FMNH164687	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164688	FMNH164688	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164689	FMNH164689	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164691	FMNH164691	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164692	FMNH164692	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164693	FMNH164693	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164694	FMNH164694	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164695	FMNH164695	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164696	FMNH164696	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH164697	FMNH164697	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Wadi Muwellig, Western Desert	29.17	30.43
FMNH152628	FMNH152628	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Beni Mazar, Minya, Western Desert	28.49	30.87
SMB126	SMB126	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
SMB127	SMB127	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
SMB128	SMB128	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
SMB11089	SMB11089	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
SMB11094	SMB11094	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
BMNH1998.61	BMNH1998.61	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
FMNH167866	FMNH167866	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
FMNH167883	FMNH167883	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
FMNH167884	FMNH167884	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Bahariya oasis, Western Desert	28.38	28.91
SMB10516	SMB10516	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Egypt	Ghouita Temple, Khargah Oasis, Western Desert	25.47	30.56
MCZ96825	MCZ96825	<i>Acanthodactylus aegyptius</i>	Paper - observ	Baha El Din, 2007	Israel	Treibe, Negev		
1273		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Tarfaya, N of	27.98	-12.71
5171		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, central 2	20.72	-16.62
5172		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, central 2	20.72	-16.62
5173		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, W side 1	20.73	-16.63
5176		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, W side 3	20.76	-16.62
6435		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PNBA: Sebket Dbâdeb et Teintâne, W margin	20.79	-16.55
6443		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	Kerekchet et Teintâne, Western face	20.78	-16.63
6446		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PNBA: Kerekchet et Teintâne, Western face	20.81	-16.62
6448		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PNBA: Kerekchet et Teintâne, Western face	20.81	-16.62
6449		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PNBA: Kerekchet et Teintâne, central	20.82	-16.59
6458		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	PNBA: Kerekchet et Teintâne, central	20.80	-16.57
6477		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Mauritania	Kerekchet et Teintâne, extreme N	20.94	-16.55
7245		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Laasallien	26.64	-11.73
7308		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Raglamhoun	23.71	-15.00
7309		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Raglamhoun	23.71	-15.00
7310		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Tayart Labwir, SE of	23.58	-15.23
7322		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Glayb Al Faj	23.48	-15.39
7326		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Khanfrat Al Faj	23.35	-15.42
7327		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Khanfrat Al Faj	23.35	-15.42
7335		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Hfor An-Naçrani, W of	23.17	-15.48
7339		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Oued Hawl	23.10	-15.57
7340		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Oued Hawl	23.10	-15.57
7344		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Oued Hawl	23.13	-15.64
7345		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Oued Hawl	23.13	-15.64
7346		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Oued Hawl	23.13	-15.64
7361		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Sebkha Imlili	23.28	-15.92
9048		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Plage Blanche	28.97	-10.60
9094		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Tarfaya, 20km S of	27.84	-12.91
9100		<i>Acanthodactylus aureus</i>	CIBIO - genetics		Morocco	Ait Kanawin	25.54	-14.67

9101		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Ait Kanawin	25.54	-14.67
9102		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Ait Kanawin	25.54	-14.67
9108		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Chtoukane	24.78	-14.87
9111		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Oued Lakra, S of	24.61	-14.92
9112		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Oued Lakra, S of	24.61	-14.92
9125		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Sebkha Imlili, NW of	23.42	-15.91
9135		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Atf	23.51	-15.55
9139		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Oum Al Fissan	23.29	-15.20
9145		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Graret Ouchfegt	23.26	-15.17
9198		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Ghrad Al 'Angra	21.67	-16.45
9205		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Krikchet	21.72	-16.64
9920		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Chtoukane	24.79	-14.86
9999		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Derraman	22.61	-14.47
10620		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Sidi Moussa	29.81	-9.83
10624		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Tafnidilt	28.55	-10.96
10625		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Douira, N of	28.52	-11.30
10633		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Oued Chebeika	28.30	-11.53
10634		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laareig	28.15	-11.91
10635		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Sidi Akhfennir	28.09	-12.08
10636		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Leirane	27.93	-12.29
10638		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Douira, S of	28.37	-11.44
10640		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayounne, S of	27.00	-13.44
10641		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bojador, N of	26.24	-14.33
13265	BEV T3700	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco		26.64	-12.01
13266	BEV 10874	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco		26.53	-12.34
13267	BEV 10875	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco		26.54	-12.44
13268	BEV 10846	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco		26.54	-12.44
A011	BEV 10708	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Fort Guerguerat, 70km N of	21.98	-16.88
A359		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 70km S of	21.10	-16.70
A363	BEV 10712	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 70km S of	21.10	-16.70
A366	BEV 10715	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 40km S of	21.22	-16.84
A367	BEV 10716	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 40km S of	21.22	-16.84
A369	BEV 10718	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 40km S of	21.22	-16.84
A371	BEV 10720	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Mauritania	Blanc, cape, 4km N of	20.80	-17.05
A376	BEV 10725	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Fort Guerguerat, 70km N of	21.98	-16.88
A377	BEV 10726	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Fort Guerguerat, 70km N of	21.98	-16.88
A379	BEV 10728	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Fort Guerguerat, 70km N of	21.98	-16.88
A380	BEV 10729	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Fort Guerguerat, 70km N of	21.98	-16.88
A381	BEV 10730	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Fort Guerguerat, 70km N of	21.98	-16.88
A382		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 240km S of crossroad for	22.37	-16.47
A383	BEV 10731	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 240km S of crossroad for	22.37	-16.47
A385	BEV 10733	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 240km S of crossroad for	22.37	-16.47
A386	BEV 10734	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 190km S of crossroad for	22.82	-16.25
A387	BEV 10735	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 190km S of crossroad to	22.82	-16.25
A388	BEV 10736	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 190km S of crossroad to	22.82	-16.25
A389	BEV 10737	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 190km S of crossroad to	22.82	-16.25
A391	BEV 10739	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 190km S of crossroad to	22.82	-16.25
A393		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 140km S of crossroad to	23.13	-16.08
A394		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	El Argoub, 2km N of	23.63	-15.85
A395	BEV 10740	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 20km N of	23.89	-15.82
A396	BEV 10741	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 20km N of	23.89	-15.82

A397	BEV 10742	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 20km N of	23.89	-15.82
A398	BEV 10743	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 20km N of	23.89	-15.82
A399	BEV 10744	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 20km N of	23.89	-15.82
A400	BEV 10745	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 20km N of	23.89	-15.82
A401		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad for	24.50	-15.03
A402		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A403	BEV 10746	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A404	BEV 10747	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A405	BEV 10748	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A406	BEV 10749	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A407	BEV 10750	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A408	BEV 10751	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A409	BEV 10752	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Dakhla, 100km N of crossroad to	24.50	-15.03
A410	BEV 10753	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Boujdour, 110km S of	25.20	-14.83
A411	BEV 10754	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bojador, 110km S of	25.20	-14.83
A412	BEV 10755	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bojador, 110km S of	25.20	-14.83
A413	BEV 10756	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bojador, 110km S of	25.20	-14.83
A414	BEV 10757	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bojador, 110km S of	25.20	-14.83
A416	BEV 10759	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A417	BEV 10760	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A418	BEV 10761	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A419	BEV 10762	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A420	BEV 10763	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A421	BEV 10764	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A422	BEV 10765	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A423	BEV 10766	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 70km S of	26.71	-13.55
A425	BEV 10767	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A426	BEV 10768	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A427	BEV 10769	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A428	BEV 10770	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A429	BEV 10771	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A430	BEV 10772	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A431	BEV 10773	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A432	BEV 10774	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Laayoune, 40km N of (in litoral dune field)	27.50	-13.14
A434		<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Sebkhla Oum Db, NW margin of	27.59	-13.02
A435	BEV 10775	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	25km S of Aoreora	28.74	-10.74
A436	BEV 10776	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 25km S of	28.74	-10.74
A437	BEV 10777	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 15km E of; Plage Blanche	28.87	-10.70
A438	BEV 10778	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 15km E of; Plage Blanche	28.87	-10.70
A439	BEV 10779	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 15km E of; Plage Blanche	28.87	-10.70
A440	BEV 10780	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 15km E of; Plage Blanche	28.87	-10.70
A441	BEV 10781	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 15km E of; Plage Blanche	28.87	-10.70
A442	BEV 10782	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 15km E of; Plage Blanche	28.87	-10.70
A443	BEV 10783	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Aoreora, 15km E of; Plage Blanche	28.87	-10.70
A556	BEV 10784	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bou Soun	29.85	-9.77
A558	BEV 10786	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bou Soun	29.85	-9.77
A559	BEV 10787	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bou Soun	29.85	-9.77
A560	BEV 10788	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bou Soun	29.85	-9.77
A561	BEV 10789	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Morocco	Bou Soun	29.85	-9.77
A765	ZFMK 17430	<i>Acanthodactylus aureus</i>	CIBIO - genetics	Senegal	M'boro-sur-mer	15.18	-16.92
1637		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Zmeila el Beida, 2km W of	21.67	-12.80

1812		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Dâyet et Teila	19.72	-12.87
1881		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Terjît, 15km S of	20.17	-13.07
1926		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Aoueloul crater, 30km SE of	20.13	-12.50
1933		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oued Oûl Moûssa	19.56	-12.05
1934		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oued Oûl Moûssa	19.56	-12.05
1935		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oued Oûl Moûssa	19.56	-12.05
1945		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Eydh Kerim	18.98	-11.90
1978		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Rachid, 25km SE of	18.69	-11.62
2068		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tâmcheppet, 10km SW of	17.20	-10.77
2198		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Gleib Mari Tarecha	16.86	-9.58
2270		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oumm Mgheirît	16.46	-10.46
2731		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, 5km N of Oûdei el Ghassâl	19.61	-16.03
2743	BEV 10511	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, NE of El Mounâne	20.10	-16.18
2750		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Dlô Matai	20.28	-16.10
2757	BEV 10512	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, dunes NW of N-Tâbiyât	20.49	-16.27
2758		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, floodplain SE of Tachekché	20.54	-16.31
2763		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, N of Baie d'Arguin	20.81	-16.46
2768		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne	20.81	-16.57
2769		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne	20.81	-16.57
2777		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, 5km NW of El Kerekchi well	20.78	-16.32
2779		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, 5km NE of El Kerekchi well	20.78	-16.24
2836		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tîgjafât, 5km S of	20.05	-14.19
2844		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tiberguent well	20.27	-14.10
2851	BEV 10594	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oum Khzâma	20.52	-13.61
2856		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Touâma	20.60	-13.54
2858	BEV 10513	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Guellâbet 'Alla	20.62	-13.45
2861		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	El Mokhanza	20.68	-13.41
2877		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oued Jraif	20.86	-12.42
2933		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Jâlet Atîl	19.76	-13.43
2947		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Lekoueiriyât	19.31	-13.00
2951		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tâmkarkart	18.98	-13.06
2992	BEV 10595	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Inikhâne	18.31	-12.23
3008	BEV 10596	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Iguevane II, 20km NW of	18.29	-11.99
3260	BEV 10819	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tarhad Rhiz N'Dégué	17.14	-11.89
3270		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tarf Mendjoura, dunes on basis of plateaux	17.45	-11.47
3288	BEV 10820	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Boumedeit, towards Bou Blei'îne	17.29	-11.14
3314	BEV 10597	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oued Guérou	16.79	-11.86
3458		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Gueltet Thor, 10km S of	17.03	-12.71
3473		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Poleti	16.84	-13.25
3487		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	El Ferghailiya well, 10km SW of	17.68	-14.60
3493		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tidemmallîne well, 5km NW of	17.94	-14.45
3537		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Tâfrajoût	19.45	-16.23
3553		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Tifegtene, 2km SW of	19.40	-16.40
3558		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Nouâmghâr, 15km NE of	19.38	-16.44
3575		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aleib et Talah, 12km SW of	19.59	-16.23
3581		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aghoueinît	19.52	-16.35
3582		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aghoueinît	19.52	-16.35
3585		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aghoueinît	19.53	-16.34
3594	BEV 10514	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Tidra island	19.60	-16.43
3599		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Teichott, 2km N of	19.56	-16.40
3608	BEV 10585	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, louïk, crossroad to	19.89	-16.23

3615	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Râs Tafarît, 16km E of	20.09	-16.11
3618	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Adeim el Marrâr	20.05	-16.06
3622	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Grâret Zra	20.09	-16.06
4282	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	Saint-Louis Peninsula	15.97	-16.51
4283	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	Saint-Louis Peninsula	15.97	-16.51
4284	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	Dakar	14.79	-17.36
4285	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	Dakar	14.79	-17.36
4286	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	Dakar	14.79	-17.36
4441	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Oumm el Kcheb	17.36	-16.08
4448	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Aftoût es Sâhel	17.18	-16.20
4459	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Aftoût es Sâhel	16.92	-16.32
4470	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Argoui Tichilit	16.67	-16.42
4477	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Chott Boul, 13km S of	16.49	-16.45
5002	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 140km NE of	19.02	-15.15
5004	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Akjoujt, 40km SW of	19.53	-14.68
5029	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Khatt en Negued	19.27	-15.61
5046	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Afreighilât 1	19.51	-16.11
5052	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Oûdei el Ghassâl, 1km N of	19.58	-16.07
5103	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Oûl el Qâdi	19.90	-16.07
5111	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Agreigrât, 1km E of	19.97	-16.19
5120	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aguilâl, 1km W of	20.15	-16.17
5126	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aguilâl 1	20.13	-16.16
5135	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aguilâl 4	20.15	-16.14
5139	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Oued Nouaffer 3	20.16	-16.10
5153	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Ouein Zidîne	20.66	-16.26
5158	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Amgheououas es Sâhli	20.78	-16.39
5160	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Amgheououas es Sâhli	20.78	-16.40
5162	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Amgheououas es Sâhli, 3km NW of	20.80	-16.42
5181	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, central 3	20.78	-16.59
5201	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tijirît 2	20.19	-15.25
5213	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Sebkhet Nich	20.32	-15.07
5221	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Ichkrâne el Khader	20.41	-14.96
5234	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Boû el Gra', 2km W of	20.73	-14.55
5249	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Gleibât Ajayât, 4km NW of	21.06	-14.37
5267	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Çtel Ogmâne, 12km SW of	20.98	-15.42
5275	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Imkebdene, N extreme	20.53	-15.57
5293	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Ouein Zidîne	20.74	-16.18
5294	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, El Kerekchi, 5km W of	20.76	-16.23
5298	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, El Kerekchi, 8km NE of	20.80	-16.22
5771	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Châr, valley	21.53	-12.86
5789	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Châr, 10km N of	21.68	-12.83
5790	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Châr, 10km N of	21.68	-12.83
5800	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Açâbet Châr	21.99	-12.71
5804	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tâjâlet el Gara	22.07	-12.70
5820	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Zouérat, 17km NE of	22.84	-12.33
5827	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Guelb Atomai	22.70	-12.78
5833	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tâjâlet el Gara	22.06	-12.71
5834	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tâjâlet el Gara	22.06	-12.71
5919	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 100km NE of	18.88	-15.45
5923	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Tidra island, northern half	19.82	-16.37
5924	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Tidra island, northern half	19.77	-16.37

5995	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Nouâmghâr, 2km E of	19.37	-16.49
5997	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Nouâmghâr, 2km E of	19.37	-16.49
6276	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Agneitîr	19.35	-16.20
6277	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Agneitîr	19.35	-16.20
6281	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Agneitîr	19.37	-16.27
6282	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Agneitîr	19.37	-16.27
6285	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Agneitîr	19.40	-16.26
6288	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Tâfrâjoût, 2km W of	19.44	-16.27
6289	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Tâfrâjoût, 2km W of	19.44	-16.27
6297	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Tâfrâjoût, 4km W of	19.42	-16.30
6299	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Chriffiya	19.51	-16.27
6303	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Toueïgueret, 1km SW of	19.59	-16.33
6307	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Tîla, 4km NW of	19.54	-16.37
6315	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kôra, 1km NW of	19.68	-16.29
6321	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Ackenjeïl	19.66	-16.26
6325	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Ackenjeïl, 4km NE of	19.72	-16.20
6329	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Mdeinet Taouadouaddît	19.76	-16.17
6330	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Mdeinet Taouadouaddît	19.76	-16.17
6331	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Mdeinet Taouadouaddît	19.76	-16.17
6347	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Grâret Agoueïfa	19.83	-16.14
6353	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Taguïlâlet Jreik	19.79	-16.21
6360	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Taguïlâlet Jreik, 2km W of	19.91	-16.16
6363	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Taguïlâlet Jreik, 2km W of	19.98	-16.10
6364	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Taguïlâlet Jreik, 2km W of	19.98	-16.10
6375	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Oued Nouaffer, 2km S of	20.08	-16.13
6376	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Oued Nouaffer, 2km S of	20.08	-16.13
6377	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Oued Nouaffer	20.12	-16.13
6378	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Oued Nouaffer	20.12	-16.13
6384	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Aguilâl	20.10	-16.17
6390	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Dlo' Matai	20.18	-16.15
6391	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Dlo' Matai	20.18	-16.15
6394	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Dlo' Matai	20.23	-16.12
6405	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Jerf el Oûstâni, 4km E of	20.42	-16.28
6410	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Îmgoûtene, 2km E of	20.46	-16.33
6411	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Îmgoûtene, 3km NE of	20.48	-16.34
6415	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Îmgoûtene, 7km NE of	20.51	-16.29
6416	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Oued ech Chibka	20.49	-16.23
6421	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Ouein Zidîne	20.65	-16.28
6426	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Sebkheth Dbâdeb et Teintâne, 8km SE of	20.74	-16.42
6431	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Sebkheth Dbâdeb et Teintâne, 4km E of	20.78	-16.46
6433	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Sebkheth Dbâdeb et Teintâne, 2km E of	20.82	-16.49
6445	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, Western face	20.81	-16.62
6450	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.82	-16.59
6453	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.82	-16.59
6456	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.80	-16.57
6457	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.80	-16.57
6460	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.83	-16.57
6461	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.83	-16.57
6462	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.83	-16.57
6463	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.83	-16.57
6468	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.83	-16.55



6469		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.83	-16.55
6470		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Kerekchet et Teintâne, extreme N	20.92	-16.54
6473		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Kerekchet et Teintâne, extreme N	20.92	-16.54
6474		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Kerekchet et Teintâne, extreme N	20.92	-16.54
6660		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Nguigmi, 60km N of	14.75	13.16
6661		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Nguigmi, 60km N of	14.75	13.16
6725		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Termit, Madaranga	15.87	11.45
6726		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Termit, Madaranga	15.87	11.45
6747		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Termit, Nourou Nga	16.34	11.46
6764		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Tasker, 8km N of	15.20	10.73
6769		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Tasker, 8km S of	15.08	10.63
7254		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Tiglatatin, W of	26.05	-12.06
7255		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Legcheinat	25.83	-12.32
7272		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued Awlettiss, SE of	25.28	-12.99
7276		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued Zbayra	24.99	-13.33
7282		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued Clayina	24.49	-13.60
7293		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued Tindkine	23.97	-13.97
7301		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Raim Ould Ad-Dlile	23.94	-14.18
7325		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Khanfrat Al Faj	23.35	-15.42
7334		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Hfor An-Naçrani, W of	23.17	-15.48
7347		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued Hawl	23.13	-15.64
8252		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Amerdou Bou Tazoult	30.28	-5.07
8254		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Talmaidert	30.68	-4.62
8255		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Taouz, W of	30.90	-4.07
9141		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Graret Ouchfegt	23.26	-15.17
9142		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Graret Ouchfegt	23.26	-15.17
9143		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Graret Ouchfegt	23.26	-15.17
9144		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Graret Ouchfegt	23.26	-15.17
9148		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Zmoul at Teha	23.02	-14.86
9153		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued Aj Jenna	22.68	-14.49
9168		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Lahraycha	22.54	-14.79
9171		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Adrar Souttouf	22.25	-15.10
9179		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Koudyat Laghnam	22.16	-15.34
9184		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Galb Ska'dwiyat	21.88	-15.57
9191		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued El Melah	21.62	-16.08
9196		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	Oued Archane	21.82	-16.37
9648		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nebyet el Dris el Abiad	16.48	-7.68
9687		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Tarf Tagouraret	17.69	-7.49
9704		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Kerkour	18.00	-8.03
9774		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	El Rhimiya	18.35	-9.14
9775		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	El Rhimiya	18.35	-9.14
9910		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Akouejât el Hemâr	19.60	-15.98
9911		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Akouejât el Hemâr	19.60	-15.98
13713		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Iboubaken	24.78	-11.34
13724		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Te-n-Ebdar	24.81	-10.54
13736		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Rhallamane	24.33	-10.40
A191		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07
A192		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07
A193		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07
A194	BEV 10587	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07
A195	BEV 10588	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07

A196	BEV 10589	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07
A197	BEV 10590	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07
A198	BEV 10591	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Niger	Ténéré: Tazolé well	17.23	9.07
A212	BEV 10598	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	S.Louis, 200km of	16.51	-14.73
A215		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	S.Louis peninsula	15.97	-16.51
A219	BEV 10600	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Senegal	PN Langue Barbarie: piste S.Louis-Louga	15.81	-16.51
A226	BEV 10604	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 80km S of	17.39	-16.06
A238	BEV 10576	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 30km S of	17.79	-16.04
A242	BEV 10631	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 30km S of	17.79	-16.04
A243	BEV 10632	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 30km S of	17.79	-16.04
A245	BEV 10536	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 10km N of	18.15	-16.03
A248	BEV 10633	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 10km N of	18.15	-16.03
A252	BEV 10634	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 12km N of	18.17	-16.03
A253	BEV 10542	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 12km N of	18.17	-16.03
A254	BEV 10635	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 12km N of	18.17	-16.03
A262	BEV 10616	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 15km N of	18.22	-16.03
A264	BEV 10581	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 15km N of	18.22	-16.03
A266	BEV 10582	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 15km N of	18.22	-16.03
A267	BEV 10583	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 15km N of	18.22	-16.03
A268	BEV 10584	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 15km N of	18.22	-16.03
A269		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 10km N of	18.15	-16.03
A270		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 10km N of	18.15	-16.03
A275	BEV 10619	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 70km NE of	18.70	-15.61
A276	BEV 10668	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouakchott, 70km NE of	18.70	-15.61
A287	BEV 10623	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Atar, 110km SW of	20.06	-13.81
A288	BEV 10624	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Atar, 90km SW of	20.16	-13.65
A290	BEV 10626	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Choûm, 40km W of	21.25	-13.28
A293	BEV 10636	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Choûm, 40km W of	21.25	-13.28
A328		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 200km E of	21.28	-15.47
A333	BEV 10551	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 90km E of	21.30	-16.37
A335	BEV 10552	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 90km E of	21.30	-16.37
A336	BEV 10553	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 90km E of	21.30	-16.37
A337	BEV 10554	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 160km S of	21.01	-16.29
A338	BEV 10555	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 160km S of	21.01	-16.29
A339	BEV 10556	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 160km S of	21.01	-16.29
A340	BEV 10557	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 160km S of	21.01	-16.29
A341	BEV 10558	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 160km S of	21.01	-16.29
A342	BEV 10559	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 160km S of	21.01	-16.29
A343		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 160km S of	21.01	-16.29
A348	BEV 10637	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bir el Gareb, 15km S of	20.51	-16.24
A349	BEV 10638	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bir el Gareb, 15km S of	20.51	-16.24
A350		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A351		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A352	BEV 10639	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A353	BEV 10640	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A354	BEV 10641	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A355	BEV 10642	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A356	BEV 10643	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A357	BEV 10644	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 110km S of	20.91	-16.40
A456	BEV 10560	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	40km E of Foum Zguid	29.85	-6.62
A468	BEV 10566	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics	Morocco	112km E of Foum Zguid	29.87	-6.01

A469	BEV 10567	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Morocco	60km E of Tagounite	30.18	-5.15
A517		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Morocco	12km N of Erfoud	31.54	-4.19
A773	ZFMK 79267	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mauritania	Tiguent, S of	17.10	-16.07
A776	ZFMK 20152	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Senegal	Niakoul Rap	14.78	-17.27
A778	ZFMK 20157	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Senegal	Cambèrene	14.77	-17.42
A800		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mauritania	Nouâmgghâr, 3km S of	19.33	-16.50
A825		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mauritania	Nouakchott, N of	18.83	-16.17
A826		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mauritania	Rkiz lake, E of	16.89	-14.98
A827		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mauritania	Kankossa, N of	16.11	-11.51
15778	BEV 3067	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mali	Tombouctou, near	16.67	-2.97
15756	BEV T3051	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mauritania	Tamaguott	19.53	-14.68
15745	BEV T3059	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Senegal	Saint Louis beach, Hotel Diamarek	15.98	-16.51
15783	BEV T3061	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Senegal	North	15.90	-16.50
15784	BEV T3062	<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Senegal	North	15.90	-16.50
15928		<i>Acanthodactylus dumerilii/senegalensis</i>	CIBIO - genetics		Mauritania	Ain eç Çefra, SW of	19.46	-12.12
KT3	IRD4025	<i>Acanthodactylus dumerilii/senegalensis</i>	Paper - genetics	Tamar et al., 2016	Algeria	Near Taghit	30.93	-2.04
KT248	NMP6V74299-1	<i>Acanthodactylus dumerilii/senegalensis</i>	Paper - genetics	Tamar et al., 2016	Morocco	Mhamid	29.83	-5.71
KT249	NMP6V74299-2	<i>Acanthodactylus dumerilii/senegalensis</i>	Paper - genetics	Tamar et al., 2016	Morocco	Mhamid	29.83	-5.71
KT46	IBES1342	<i>Acanthodactylus dumerilii/senegalensis</i>	Paper - genetics	Tamar et al., 2016	Morocco	15 km N. of Merzouga	31.21	-4.03
KT140		<i>Acanthodactylus dumerilii/senegalensis</i>	Paper - genetics	Tamar et al., 2016	Morocco	Tifariti	26.16	-10.56
KT186		<i>Acanthodactylus dumerilii/senegalensis</i>	Paper - genetics	Tamar et al., 2016	Mauritania	Walatah	17.29	-7.02
KT187		<i>Acanthodactylus dumerilii/senegalensis</i>	Paper - genetics	Tamar et al., 2016	Mauritania	Walatah	17.29	-7.02
ZFMK_017468	ZFMK_017468	<i>Acanthodactylus dumerilii/senegalensis</i>	ZFMK - observ		Senegal	20 km sud of Richard Toll	16.32	-15.72
ZFMK_017494	ZFMK_017494	<i>Acanthodactylus dumerilii/senegalensis</i>	ZFMK - observ		Senegal	10 km west of Linguère	15.39	-15.24
ZFMK_017512	ZFMK_017512	<i>Acanthodactylus dumerilii/senegalensis</i>	ZFMK - observ		Senegal	Nianing	14.34	-16.93
ZFMK_020158	ZFMK_020158	<i>Acanthodactylus dumerilii/senegalensis</i>	ZFMK - observ		Senegal	Between Kayar and Bayakh	14.88	-17.13
ZFMK_073892	ZFMK_073892	<i>Acanthodactylus dumerilii/senegalensis</i>	ZFMK - observ		Senegal	Mbour (Plage)	14.38	-16.95
MCZ28672	MCZ:Herp:R-28672	<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania	Trarza	17.93	-14.83
CAS134627	CAS:HERP:134627	<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania	5 km N of Nouakchott	18.11	-15.95
CAS134620	CAS:HERP:134620	<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania	15 km N of Nouakchott Airport	18.23	-15.95
GBIF_440154656		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania		18.61	-16.11
GBIF_440154647		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania		18.52	-16.07
GBIF_440041679		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania		18.58	-16.09
GBIF_440154654		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania		19.13	-16.28
GBIF_440154651		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania		19.11	-16.20
GBIF_440023547		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania		19.03	-16.21
GBIF_440117938		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania		18.97	-16.20
GBIF_2833599415		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Morocco	C.R. Aousserd	23.10	-14.94
GBIF_2294408810		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Morocco	Oued el Dahab	23.19	-15.17
GBIF_2826318755		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Morocco	Oued el Dahab	22.96	-14.78
GBIF_2836793004		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Morocco	C.R. Aousserd	22.86	-14.69
GBIF_2843064356		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Morocco	C.R. Aousserd	22.81	-14.59
GBIF_2832810229		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Morocco	C.R. Aousserd	22.75	-14.61
GBIF_440057744		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mali	Goundam	16.39	-3.67
GBIF_1019675016		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Niger	Termit, Oued	15.79	11.42
GBIF_1019675031		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Niger	Termit	15.89	11.46
GBIF_1019675012		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Niger	Termit	16.38	11.45
GBIF_440068019		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Senegal	Linguere	15.40	-15.13
GBIF_440111662		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Senegal	Lompoul	15.43	-16.68
GBIF_165333296		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Mauritania	Bougari	16.54	-10.80
GBIF_1317928467		<i>Acanthodactylus dumerilii/senegalensis</i>	GBIF - observ		Senegal	Louga, 7 km E of	15.62	-16.16

1795		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Grâret Timit	19.91	-12.90
1940		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Léhélim dunes	19.31	-11.93
2734		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bguent	19.63	-16.24
2736		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bguent	19.63	-16.23
2739		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Mdeinet Taouadouaddît	19.77	-16.19
2740		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Mdeinet Taouadouaddît	19.77	-16.19
2742		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	El Mounâne, SE of	20.05	-16.18
2745		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, 5km E of El Mounâne	20.07	-16.09
2746		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Oued Nouafferd	20.13	-16.09
2831		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Azeffâl dunes, S of Chami	19.85	-15.94
2841	BEV 10645	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Akchâr dunes, N of Akjoujt	20.26	-14.31
2866		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Ech Chig	20.73	-13.37
2894	BEV 10646	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	El Beyyed	21.49	-11.34
2955		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Tâmkarkart, extreme SE of	18.92	-12.98
2980		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Tamassoumit, oued 20km E of	18.55	-12.45
3497		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	El Mabrouk well, 3km NE of	17.90	-14.48
3503		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Mednet el Fras	18.49	-14.62
3521	BEV 10818	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Bir Boû Khbeira wells, 8km SW of	18.03	-15.23
3526		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Anagoum puit, 2km W of	19.46	-16.09
3535		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Tâfrajoût	19.45	-16.22
3542		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Oûdei el Ghassâl	19.56	-16.12
3557		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Tifegtene, 2km SW of	19.40	-16.40
3561		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Nouâmghâr, 15km E of	19.35	-16.39
3562		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Nouâmghâr, 15km E of	19.35	-16.39
3563		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Nouâmghâr, 15km E of	19.35	-16.39
3572		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aleib et Talah, 7km W of	19.66	-16.19
3607		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, louïk, 16km SE of	19.82	-16.21
5019		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Bennichâb, 15km NW of	19.48	-15.24
5025		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Agoueilil el Hâmi	19.32	-15.57
5037		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Sebkhet Te-n-Dghâmcha	19.08	-15.95
5040		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Goûd Anagoum, 2km NW of	19.38	-16.12
5041		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Goûd Anagoum, 5km NW of	19.41	-16.13
5045		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Goûd Anagoum, 6km NW of	19.43	-16.11
5047		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Afreighilât 2	19.53	-16.10
5049		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Oûdei el Ghassâl, 1km S of	19.56	-16.07
5054		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aleib et Talah 1	19.63	-16.09
5062		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Mednet ed Dâya 1	19.69	-16.06
5069		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Mednet ed Dâya 3	19.71	-16.06
5070		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Mednet ed Dâya 3	19.71	-16.06
5073		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl 1	19.75	-16.05
5075		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl 2	19.78	-16.04
5076		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl 2	19.78	-16.04
5080		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl 3	19.80	-16.04
5087		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl, Elb en Nouçç 1	19.85	-16.04
5093		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl, Elb en Nouçç, 1km N of	19.89	-16.01
5094		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl, Elb en Nouçç, 1km N of	19.89	-16.01
5098		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl, Elb en Nouçç, 2km N of	19.91	-16.01
5099		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Azeffâl, Elb en Nouçç, 3km N of	19.92	-16.03
5106		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Taguilâlet Jreik 1	19.97	-16.07
5110		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Gherd Ayyer	20.00	-16.01
5119		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Aguilâl, 1km W of	20.15	-16.17

5137	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Oued Nouafferd 1	20.15	-16.12
5163	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, E side 1	20.75	-16.58
5164	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, E side 1	20.75	-16.58
5167	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, E side 2	20.73	-16.59
5168	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, central 1	20.73	-16.60
5177	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Kerekchet et Teintâne, W side 3	20.76	-16.62
5192	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Goût	20.00	-15.51
5258	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Çtel Ogmâne	21.05	-15.30
5274	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Ntalfa, 6km SE of	20.67	-15.53
5805	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Tâjâlet el Gara	22.07	-12.70
5846	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Guelb el Hâlma	21.83	-12.81
5883	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Aderg	21.37	-11.91
5996	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Nouâmghâr, 2km E of	19.37	-16.49
6076	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Nega pass	17.62	-11.35
6298	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Chrîfiya	19.51	-16.27
6301	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Sebkhet Râs el Mâ	19.58	-16.28
6302	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Toueigueret, 1km SW of	19.59	-16.33
6306	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Toueigueret, 2km SW of	19.58	-16.35
6308	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Tîla	19.51	-16.41
6317	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Kôra	19.65	-16.28
6318	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Kôra	19.65	-16.28
6319	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Ackenjeîl	19.66	-16.26
6320	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Ackenjeîl	19.66	-16.26
6322	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Ackenjeîl, 2km NE of	19.68	-16.23
6339	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Elb en Nouçç, extreme S	19.81	-16.15
6340	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Elb en Nouçç, extreme S	19.81	-16.15
6348	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Grâret Agoueifa	19.78	-16.19
6349	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Grâret Agoueifa	19.78	-16.19
6352	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Taguîlâlet Jreik	19.79	-16.21
6356	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Taguîlâlet Jreik, 1km W of	19.85	-16.20
6369	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Adeim el Marrâr, 4km W of	20.06	-16.10
6374	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Oued Nouafferd, 2km S of	20.08	-16.13
6383	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Aguilâl	20.10	-16.17
6386	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Aguilâl	20.10	-16.17
6414	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Îmgoûtene, 5km NE of	20.50	-16.34
6436	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Sebkhet Dbâdeb et Teintâne, W margin	20.79	-16.55
6438	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, extreme S	20.68	-16.59
6451	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.82	-16.59
6452	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PNBA: Kerekchet et Teintâne, central	20.82	-16.59
6663	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ngourti, 30km S of	15.07	13.22
6680	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ti-N-Toumma	16.70	13.13
6702	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ti-N-Toumma	15.88	11.66
9711	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Tinigart	18.15	-8.11
9790	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Tîchît, 5km NW of	18.47	-9.52
9807	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Foum Ajâr	18.53	-10.26
9912	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chami, NW of	20.09	-15.80
9913	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chami, NW of	20.09	-15.80
9914	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chami, NW of	20.09	-15.80
9915	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chami, NW of	20.09	-15.80
9917	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chami, NW of	20.09	-15.80
12952	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Chad	Ounianga Serir, easternmost lake	18.92	20.91

12965		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Chad	Ounianga Serir, easternmost lake	18.92	20.91
13668		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Sfariat, N of	23.97	-11.25
13754		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Zednes, 5km NE of	23.83	-10.59
15707		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Algeria	Tadrart	24.12	10.93
A004	BEV 10649	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Guelb Nouatil	18.37	-9.06
A094		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Tunisia	Douz, 11km NW of	33.49	8.91
A116	BEV 10580	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Tunisia	Ksar Ghilane at the Roman fort	33.07	9.62
A147		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Libya	Ghadames, 7km NW of	30.18	9.44
A170	BEV 10655	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Libya	Crossroad to Al Katrun; 100km E of Murzuq	26.12	14.90
A180	BEV 10657	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ténéré: Madama	21.95	13.66
A182	BEV 10659	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ténéré: Dirkou, 40km N of	19.37	12.86
A184	BEV 10661	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ténéré: Bilma, 15km N of	18.79	12.89
A187		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ténéré: Fachi	18.16	11.61
A271	BEV 10664	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Akchâr dunes; 115km N of Nouakchott	19.10	-16.26
A273	BEV 10666	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Nouakchott, 20km NE of	18.32	-15.80
A281	BEV 10669	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Akjoujt, 100km SW of	19.04	-15.12
A296	BEV 10675	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Choûm, 50km W of	21.26	-13.39
A311	BEV 10687	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Choûm, 100km W of	21.19	-14.14
A318	BEV 10694	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Choum, 140km W of	21.26	-14.62
A332	BEV 10700	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 200km E of	21.28	-15.47
A334	BEV 10701	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Nouâdhibou, 90km E of	21.30	-16.37
A344	BEV 10702	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bir el Gareb, 15km S of	20.51	-16.24
A345	BEV 10703	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bir el Gareb, 15km S of	20.51	-16.24
A346	BEV 10704	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bir el Gareb, 15km S of	20.51	-16.24
A347	BEV 10705	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	PN Banc d'Arguin, Bir el Gareb, 15km S of	20.51	-16.24
A462	BEV 10706	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Morocco	Erg Mhazil - 80km E of Foum Zguid	29.85	-6.23
A526		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Morocco	Erg Chebbi	31.07	-3.97
A784	ZFMK 32467	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Sudan	Darfur: Merga (Nukheila)	19.05	26.32
A796		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Herrour ridge	20.75	-11.92
A797		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Agouadir, 5km SW of	20.98	-11.48
A798		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Idîni, 75km NE of	18.33	-14.90
15772	BEV 12667	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Algeria	Aïn Sefra dunes, Hotel Mekter, 230m from	32.74	-0.58
15774	BEV T3102	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Egypt	Farafra	27.34	28.14
15757	BEV T4245	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Algeria	Meniaa road, pk 747, MEN2	31.33	3.53
15838		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chinguetti, 32km NE of	20.65	-12.13
15839		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chinguetti, 32km NE of	20.65	-12.13
15841		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Chinguetti, 34km NE of	20.65	-12.11
15843		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Herrour	20.76	-11.92
15846		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Herrour	20.76	-11.92
15851		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Agouadir, 11km NE of	21.02	-11.34
15853		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Agouadir, 31km E of	21.00	-11.14
15862		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Ouarâne 3	21.18	-10.60
15864		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Ouarâne 4	21.07	-10.45
15866		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Ouarâne 6	20.96	-10.38
15879		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Mauritania	Ouarâne 13	20.82	-10.60
KT131		<i>Acanthodactylus longipes</i>	Paper - genetics	Algeria	Tinduf	27.68	-8.15
6667		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Niger	Ngourti, 80km N of	16.08	13.13
8990		<i>Acanthodactylus longipes</i>	CIBIO - genetics	Morocco	Chott Tigri, 12km W of	32.79	-1.88
A766	ZFMK 49633	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Algeria	Guerzim	29.65	-1.68
15771	BEV 10175	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Algeria	Erg d'Admer, Djanet, 65km WNW of	24.78	8.87
15773	BEV T3098	<i>Acanthodactylus longipes</i>	CIBIO - genetics	Egypt	Maghra, SE of	30.03	29.08

A160		<i>Acanthodactylus longipes</i>	CIBIO - observ		Libya	Idri, 17km E of, Ash Shati	27.49	13.23
A161		<i>Acanthodactylus longipes</i>	CIBIO - observ		Libya	Lake Gabrun, Awbari	26.80	13.54
DA9		<i>Acanthodactylus longipes</i>	CIBIO - observ		Mauritania	Guelb Azreg, Hodh Ech Chargui	17.78	-7.63
9725		<i>Acanthodactylus longipes</i>	CIBIO - observ		Mauritania	Aklé Aoukâr, Hodh Ech Chargui	18.35	-8.42
2966		<i>Acanthodactylus longipes</i>	CIBIO - observ		Mauritania	Aoukâr dunes, SE of Boû Nâga, Trarza	18.57	-12.92
DA1		<i>Acanthodactylus longipes</i>	CIBIO - observ		Mauritania	Zarga mountains, S face of, Adrar	20.35	-12.77
11387		<i>Acanthodactylus longipes</i>	CIBIO - observ		Mauritania	Areirid Fai, Trarza	18.66	-14.25
13763		<i>Acanthodactylus longipes</i>	CIBIO - observ		Mauritania	Zednes, 10km W of, Tiris Zemmour	23.76	-10.91
12940		<i>Acanthodactylus longipes</i>	CIBIO - observ		Chad	Erg Djourab, Borkou-Ennedi-Tibesti	16.42	18.58
SMB8562	SMB8562	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Karawin, Farafra Oasis	27.06	27.98
SMB11130	SMB11130	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Karawin, Farafra Oasis	27.06	27.98
SMB11131	SMB11131	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Karawin, Farafra Oasis	27.06	27.98
SMB11082	SMB11082	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Karawin, Farafra Oasis	27.06	27.98
SMB11088	SMB11088	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Karawin, Farafra Oasis	27.06	27.98
SMB11081	SMB11081	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	White Desert, Farafra Oasis	27.06	27.98
SMB11087	SMB11087	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	White Desert, Farafra Oasis	27.06	27.98
SMB11132	SMB11132	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Qattanya Dune	29.77	30.33
SMB11133	SMB11133	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Qattanya Dune	29.77	30.33
SMB11134	SMB11134	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis	30.25	28.94
SMB11332	SMB11332	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis	30.25	28.94
SMB11333	SMB11333	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	El Maghra Oasis	30.25	28.94
SMB11323	SMB11323	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Fasulat El Rammak	29.90	29.13
SMB11334	SMB11334	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Fasulat El Rammak	29.90	29.13
SMB11256	SMB11256	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Rammak Dune	29.20	29.47
BMNH1938.4.4.33	BMNH1938.4.4.33	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB57	SMB57	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB58	SMB58	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB179	SMB179	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB10576	SMB10576	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB10592	SMB10592	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB10593	SMB10593	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB10594	SMB10594	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB11174	SMB11174	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB11175	SMB11175	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB11176	SMB11176	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB11260	SMB11260	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
SMB11263	SMB11263	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Siwa Oasis	29.18	25.52
FMNH66104	FMNH66104	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Ain Shefa, Siwa Oasis	29.18	25.52
SMB8380	SMB8380	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Shayata Oasis, W. of Siwa	29.32	25.17
FMNH171902	FMNH171902	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Egypt	Bir Kurayim	22.27	29.73
BMNH1971.724	BMNH1971.724	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Kerzaz	29.46	-1.44
BMNH1971.725	BMNH1971.725	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Kerzaz	29.46	-1.44
BMNH1971.726	BMNH1971.726	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Kerzaz	29.46	-1.44
BMNH1946.9.3.74	BMNH1946.9.3.74	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	El Wadi E. of Tuggurt	33.09	6.11
BMNH1946.8.4.30	BMNH1946.8.4.30	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Wargala	31.95	5.26
BMNH1946.8.4.31	BMNH1946.8.4.31	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Wargala	31.95	5.26
BMNH1946.8.4.32	BMNH1946.8.4.32	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Wargala	31.95	5.26
BMNH1946.9.3.75	BMNH1946.9.3.75	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Wadi El Nça to El Alia	33.14	5.79
BMNH1988.648	BMNH1988.648	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	65 km W. of Illizi	26.52	7.85
BMNH1988.649	BMNH1988.649	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Algeria	Hassi Bel Guebbour	28.50	6.68
BMNH1982.388	BMNH1982.388	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Chad		19.07	20.60

BMNH1982.389	BMNH1982.389	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Chad		19.07	20.60
BMNH1982.390	BMNH1982.390	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Chad		19.07	20.60
BMNH1982.391	BMNH1982.391	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Libya	8 km. S. Murzuk, Fezzan	25.86	13.91
BMNH1954.1.6.42	BMNH1954.1.6.42	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Libya	Sebga, Fezzan	27.00	14.53
BMNH1975.1399	BMNH1975.1399	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Mali		20.17	-4.15
BMNH1975.1402	BMNH1975.1402	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Mali		20.15	-4.82
BMNH1975.1398	BMNH1975.1398	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Mauritania		20.45	-8.80
BMNH1975.1400	BMNH1975.1400	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Mauritania		20.00	-6.83
BMNH1975-1401	BMNH1975-1401	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Mauritania		20.74	-10.50
BMNH1982.140	BMNH1982.140	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Mauritania		20.74	-10.50
BMNH1962.523	BMNH1962.523	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Morocco	Erg Chebbi	31.07	-3.97
BMNH1977.743	BMNH1977.743	<i>Acanthodactylus longipes</i>	Paper - observ	Baha El Din, 2007	Niger		19.62	9.18
ZFMK_026201	ZFMK_026201	<i>Acanthodactylus longipes</i>	ZFMK - observ		Morocco	Between Erfoud and Merzouga	31.29	-4.01
ZFMK_026205	ZFMK_026205	<i>Acanthodactylus longipes</i>	ZFMK - observ		Morocco	Merzouga / Tafilalt, Er Chebbi	31.14	-3.97
ZFMK_049663	ZFMK_049663	<i>Acanthodactylus longipes</i>	ZFMK - observ		Algeria	Guerzim	29.65	-1.68
GBIF_1056624270		<i>Acanthodactylus longipes</i>	GBIF - observ		Chad	Ennedi West	19.07	20.60
GBIF_1019675014		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	around Termit Kaoboul	15.65	11.58
GBIF_1056726500		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Agadez	19.62	9.18
GBIF_2421794589		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Ngourti, 80km N of	16.08	13.13
GBIF_2421794587		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Ti-N-Toumma	16.70	13.13
GBIF_2421794582		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Ti-N-Toumma	16.42	12.62
GBIF_2421794579		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Ti-N-Toumma	15.88	11.66
GBIF_2421794577		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Ti-N-Toumma	16.70	13.13
GBIF_2421794575		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Ti-N-Toumma	16.02	11.86
GBIF_2421794574		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Ti-N-Toumma	16.56	12.93
GBIF_2421794572		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger	Koussa Arma well	16.15	13.22
GBIF_1056419895		<i>Acanthodactylus longipes</i>	GBIF - observ		Mali	Timbuktu	20.17	-4.15
GBIF_1056163112		<i>Acanthodactylus longipes</i>	GBIF - observ		Mauritania	Adrar	20.46	-8.80
GBIF_1055612925		<i>Acanthodactylus longipes</i>	GBIF - observ		Mauritania	Hodh ech Chargui	20.00	-6.08
GBIF_1056539592		<i>Acanthodactylus longipes</i>	GBIF - observ		Mali	Timbuktu	20.15	-4.82
GBIF_1019675021		<i>Acanthodactylus longipes</i>	GBIF - observ		Niger		15.80	11.68
GBIF_1056610409		<i>Acanthodactylus longipes</i>	GBIF - observ		Algeria	30km from Hassi Bel Guebbour	28.68	6.48
GBIF_212096633		<i>Acanthodactylus longipes</i>	GBIF - observ		Algeria	3 km NW Beni Abbes	30.15	-2.19
GBIF_1019669072		<i>Acanthodactylus longipes</i>	GBIF - observ		Algeria	Erg d'Admer	24.22	9.24
GBIF_440155910		<i>Acanthodactylus longipes</i>	GBIF - observ		Mali	Adrar des Iforas	19.12	1.75
15662		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Djanet, about 40km W of	24.64	9.16
15663		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Tikoubaouine	24.79	9.10
A086		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Tunisia	Tozeur, 7km W of	33.90	8.05
A092		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Tunisia	Douz, 11km NW of	33.49	8.91
A103		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Tunisia	Pipeline track, 40km N of Ksar Ghilane	33.34	9.73
A110		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Tunisia	Pipeline track, 22km NE of Ksar Ghilane	33.11	9.77
A120	BEV 10525	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Tunisia	Pipeline track, 20km SE of Ksar Ghilane	32.91	9.76
A122		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Tunisia	Tataouine, 17km NE of	33.00	10.61
A133		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Jadi Resort; 7km E of Zuara	32.90	12.15
A134	BEV 10586	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Jadi Resort; 7km E of Zuara	32.90	12.15
A136		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Nalut, 10km S of	31.79	10.96
A137		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Nalut, 10km S of	31.79	10.96
A140	BEV 10530	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Nalut, 72km S of	31.30	10.62
A154		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Idri, 105km N of	28.38	12.83
A155		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Idri, 95km N of	28.28	12.88
A162		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Libya	Messak Mallet; 95km W of Tesawa	25.99	12.69



A768	ZFMK 49648	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Bou Trekfine	33.58	2.95
A787	ZFMK 32448	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	Gilf Kebir	22.77	25.60
A792	ZFMK 77549	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	Bahariya oasis	28.25	28.95
A793	ZFMK 18046	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	El Oued	33.33	6.87
A817		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	23km W Foughala	34.75	5.13
15782	BEV 11047	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	El Bayadh, Kaloua et sidi Ech chikh; falaise de Krekda	33.56	1.18
15777	BEV 11344	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	Lake Nasser margin, N of Abu Simbel	22.43	31.65
15761	BEV 13316	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Laghouat, 9km after heading to Aflou	33.87	2.83
15762	BEV 13319	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Ourir, 3.5km W of (El Meghaïer)	34.01	5.91
15763	BEV 13342	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Arbaouat, next to Sidi Mammam Ben Alia mausoleum	33.11	0.59
15758	BEV 13593	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Bouchagroun, N of (near Tolga)	34.74	5.45
15760	BEV 15138	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Abiodh Sidi Cheikh, 9km S of (crossroad to Brezina and Benoud)	32.81	0.58
15749	BEV 9008	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	Lac Nasser, W marginn, NE of Abu Simbel	22.36	31.63
15750	BEV 7014	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Mauritania	Ouâdane	20.93	-11.62
15751	BEV 7015	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Mauritania	Ouâdane	20.93	-11.62
15775	BEV 8974	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	El Arish, 4km W of	31.10	33.67
15747	BEV 8993	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	Wadi Arabah, 44km after Zafarana heading to Koraimat	29.01	32.23
15748	BEV 8995	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	Wadi Arabah, 59km after Zafarana heading to Koraimat	28.96	32.10
15780	BEV 9208	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Taadmit (= Tadmit), 7km before road coming from Djelfa	34.30	3.14
15781	BEV 9209	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Laghouat, 25km before coming from Djelfa	34.03	2.93
15779	BEV 9385	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Djelfa, ca.30km E of and Muchbara, ca.10km E of	34.34	3.49
15770	BEV T4244	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	El Ateuf dam, Garghaia	32.44	3.78
EGY 02/2012 - 20					Algeria	El Khattara, W bank, Aswan	24.18	32.86
HUJ - 23473	HUJ - R.23473	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Israel	Nizzanim sands	31.72	34.60
IBES3533	IBES3533	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	11172 - Sitra Oasis	28.43	26.52
15791	NHMC_80.3.110.9	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	Ras el Sudr, 10km S of	29.52	32.73
TAU - R.16389	TAU - R.16389	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Israel	Bir Mashash sands	31.10	34.81
TAU - R.16410	TAU - R.16410	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Israel	Holon sands	32.00	34.80
15884		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Mauritania	Guelb er Richât, SE of	21.02	-11.36
KT29		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Egypt	Dakhla Oasis	25.54	29.14
KT100	MCCI-R1466	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Libya	Between Erg Ouan Kasa and Erg Murzuq	25.48	11.77
KT101	MCCI-R1465	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Libya	15 km N. of Dirj	30.30	10.45
KT102	MCCI-R1467	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Libya	Between Erg Ouan Kasa and Erg Murzuq	25.90	12.24
KT92	MCCI-R1463	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Libya	Akacus, Adadh area	25.57	10.40
KT99	MCCI-R1464	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Libya	Akacus, Awiss area	24.81	10.38
KT304	MCCI-R1468(1)	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Libya	50 km N. of Dirj	30.58	10.33
KT222		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Mauritania	60 km S. of Zouerat (Tiris Zemmour)	22.35	-12.66
KT223		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Mauritania	60 km S. of Zouerat (Tiris Zemmour)	22.35	-12.66
KT14	HUJ - R.23946	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Israel	Nativ Ha-Asara sands	31.58	34.52
KT44	TAU - R.16402	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Israel	Holon sands	32.00	34.78
KT215		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Egypt	25 km NE. of Ismalia, E. bank of Nile	30.56	32.01
KT219		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Egypt	Sinai, 55 km W. of Zaranîq	31.00	32.85
KT20	TAU - R.16397	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Israel	Bir Mashash sands	31.07	34.85
KT226		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Egypt	El Omayed protected area	30.82	29.20
KT24	IBES3537	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Egypt	Al-Natroun Road	30.48	30.20
KT103	MCCI-R1345	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Tunisia	2 km SW. of Béni Kheddache	33.24	10.18
KT210		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Algeria	El Aricha	34.48	-1.27
KT94	MCCI-R1347	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Tunisia	33 km S. of Tataouine	32.65	10.32
KT93	MCCI-R1341	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Tunisia	29 km E. of Douz	33.48	9.36
KT96	MCCI-R1344(1)	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Tunisia	2 km W. of Béni Keddache	33.26	10.19
KT95	MCCI-R1334(1)	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Tunisia	Between Hazoua and Matrouha	33.54	7.67

KT97	MCCI-R1332(1)	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Tamar et al., 2016	Tunisia	Between Nefta and Hazoua	33.86	7.75
8992		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Morocco	Oued Es Safsaf, dunes above dam	32.37	-1.32
A769	ZFMK 49673	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Near the exit for Abfahrt Ain Ourka	32.90	-0.28
15754	BEV 5649	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Niger	Ajir, 110km NE of Arlit	19.61	7.89
15765	BEV 14834	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Tiout. 15km SE of, High Plateaux W of Aïn Ourka	32.65	-0.33
A101		<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Tunisia	Douz, 18km N of	33.62	9.01
A785	ZFMK 32469	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Sudan	Darfur: Rahib wells	17.55	27.07
A786	ZFMK 22800	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Algeria	Ideles, 50km N of; Irr-err-err	24.07	6.25
15776	BEV 9028	<i>Acanthodactylus scutellatus</i>	CIBIO - genetics		Egypt	El Alamein new road, 63 km SSW Alexandria	30.66	29.62
NHMC 80.3.110.10	NHMC 80.3.110.10	<i>Acanthodactylus scutellatus</i>	Paper - genetics	Psonis et al., 2016	Libya	Farwa, on the island	33.11	11.72
Siwa population		<i>Acanthodactylus scutellatus</i>	Paper - genetics	Khannoon et al., 2013	Egypt	Siwa Oasis	29.18	25.52
15753	BEV_5648	<i>Acanthodactylus scutellatus</i>	CIBIO - observ		Niger	In-Bkikas, Tamesna	18.00	7.00
GBIF_1055351876		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Mali	Ahanko, Kidal	20.00	1.00
GBIF_1056127687		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Niger	Adrar Bouss, Agadez	20.00	8.67
GBIF_1055394968		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Niger	Arilit, 400m, Agadez	18.72	7.38
GBIF_1057212966		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Al Kufrah	24.20	23.30
CAS127484	CAS:HERP:127484	<i>Acanthodactylus scutellatus</i>	GBIF - observ		Tunisia	5 km SW of Gafsa	34.40	8.72
CAS138964	CAS:HERP:138964	<i>Acanthodactylus scutellatus</i>	GBIF - observ		Tunisia	23 km E Tozeur on rd to Gafsa	34.09	8.25
GBIF_1055833929		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Egypt	Al Jizah, Siwa	29.07	29.50
GBIF_1056303766		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Algeria	In Salah	27.25	2.51
GBIF_1056573216		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Egypt	Wed Hebron, Mt Sinai	28.57	33.98
GBIF_1057154518		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Sudan	Dongola, Nubia	19.17	30.48
GBIF_1055326368		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Sudan	Wadi Halfa, Nubia	21.80	31.36
GBIF_1055304511		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Chad	Zouar, SW Tibesti	20.45	16.52
GBIF_1057380930		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Sidi Benour, 40km E, of Tripoli, Tripolitania	32.72	13.75
GBIF_1057288896		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Kufra	24.22	23.27
GBIF_1057341388		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Homs	32.64	14.25
GBIF_1057241250		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Cyrenaica, Bescer	30.32	19.44
GBIF_1057110773		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Gargaresc, Tripolitania	32.87	13.11
GBIF_1056807274		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Brega	30.40	19.57
GBIF_1056675220		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	50km N. of Hon, Tripolitania	29.53	16.07
GBIF_1056075411		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Benghazi	32.07	20.05
GBIF_1055386203		<i>Acanthodactylus scutellatus</i>	GBIF - observ		Libya	Gialo, Cyrenaica, N. Africa	29.03	21.54
ZFMK_018049	ZFMK_018049	<i>Acanthodactylus scutellatus</i>	ZFMK - observ		Tunisia	10km W of Tozeur	33.90	8.02
ZFMK_022789	ZFMK_022789	<i>Acanthodactylus scutellatus</i>	ZFMK - observ		Algeria	90 km südlich Ouargla	31.30	5.38
ZFMK_022800	ZFMK_022800	<i>Acanthodactylus scutellatus</i>	ZFMK - observ		Algeria	Hoggar: 50 km nördlich Ideles, Irr-err-err	24.21	5.90
ZFMK_022799	ZFMK_022799	<i>Acanthodactylus scutellatus</i>	ZFMK - observ		Algeria	Hoggar: Oued Tegert	21.31	6.53
ZFMK_022798	ZFMK_022798	<i>Acanthodactylus scutellatus</i>	ZFMK - observ		Algeria	Hoggar: Amgid	26.42	5.36
ZFMK_022794	ZFMK_022794	<i>Acanthodactylus scutellatus</i>	ZFMK - observ		Algeria	Hoggar: 30 km nördlich Amgid	26.66	5.35
5821		<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Mauritania	Zouérat, 17km NE of	22.84	-12.33
5823		<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Mauritania	Zouérat, 11km NE of	22.80	-12.38
13679		<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Mauritania	Tourassin, S of	24.57	-11.39
13705		<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Mauritania	Guemgoum	25.04	-11.50
13732		<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Mauritania	Te-n-Ebdar, 10km S of	24.70	-10.49
15463	BEV T9556	<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Algeria	El-Abiod Sidi Cheikh, 54km after (Road N59); heading Benoud	32.47	0.34
15464	BEV T9557	<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Algeria	Benoud, 5.8km W-NW of	32.34	0.19
15786	BEV 14828	<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Mauritania	Fdérik, 123km NE of	23.54	-11.95
15787	BEV 14829	<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Mauritania	Bir Moghreïn, 110km SSW of	24.37	-11.87
E7021323		<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Algeria	El-Abiodh Sidi Cheikh, 3 km au sud de la décharge	32.86	0.52
E7021324		<i>Acanthodactylus taghitensis</i>	CIBIO - genetics		Algeria	El-Abiodh Sidi Cheikh, 3 km au sud de la décharge	32.86	0.52
MNHN-RA-1995.1201	MNHN-RA-1995.1201	<i>Acanthodactylus taghitensis</i>	GBIF - observ		Algeria	Taghit, région de Beni	30.87	-2.02

13656		<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Mauritania	El Ouissat, Tiris Zemmour	23.44	-11.90
13766		<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Mauritania	El Ouissat, Tiris Zemmour	23.60	-11.50
15460	BEV 5992	<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Algeria	El Gor, Béchar	27.46	-7.93
15461	BEV 7785	<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Mauritania	Ouan n'Namour, reg du Nord-Tagenzé, Adrar	21.38	-11.41
15462	BEV 11658	<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Algeria	El-Abiodh Sidi Cheikh, 3 km au sud de la décharge, Saida	32.82	0.56
BEVO_251	BEV_OBS_903	<i>Acanthodactylus taghitensis</i>	BEV - observ	Mauritania	Bir Moghreïn, 132km SSSE of, Tiris Zemmour	24.07	-11.28
BEVO_252	BEV_OBS_913	<i>Acanthodactylus taghitensis</i>	BEV - observ	Mauritania	Bir Moghreïn, 117km SSSE of, Tiris Zemmour	24.20	-11.33
13656	CIBIO_13656	<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Mauritania	El Ouissat, Tiris Zemmour	23.44	-11.90
13766	CIBIO_13766	<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Mauritania	El Ouissat, Tiris Zemmour	23.60	-11.50
15461	CIBIO_15461	<i>Acanthodactylus taghitensis</i>	CIBIO - observ	Mauritania	Ouan n'Namour, reg du Nord-Tagenzé, Adrar	21.38	-11.41
London_226	NHM 1982.292	<i>Acanthodactylus taghitensis</i>	BEV - observ	Mauritania	Fdérik, Tiris Zemmour	22.69	-12.72
London_227	NHM 1982.293	<i>Acanthodactylus taghitensis</i>	BEV - observ	Mauritania	Fdérik, Tiris Zemmour	22.69	-12.72
OO_042	PGOO_436	<i>Acanthodactylus taghitensis</i>	BEV - observ	Mauritania	Caabiat, Tiris Zemmour	26.55	-8.57
OO_052	PGOO_445	<i>Acanthodactylus taghitensis</i>	BEV - observ	Mauritania	El Meskur, Tiris Zemmour	22.28	-12.42

Article reference – “Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards”

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**Supporting Information**

**APPENDIX S1 – Supplementary figures (captions)**

**Figure S1.1** Study area and samples used in this work. The range of *Acanthodactylus scutellatus* group was modified from Roll et al. (2017). Circles represent sampling sites used in the phylogenetic analysis. Main mountains and hydrological features are indicated in bold and italics, respectively. Projection: WGS84.

**Figure S1.2** Bayesian mt-nuDNA phylogeny of *Acanthodactylus scutellatus* group including all haplotypes of the concatenated dataset (12S, Cytb, and C-mos; 1213 bp). Black dots represent supported nodes, with posterior probabilities (pp) >0.95; lower values are shown for species and lineage splits.

**Figure S1.3** Maximum Likelihood mt-nuDNA phylogeny of *Acanthodactylus scutellatus* group including all haplotypes of the concatenated dataset (12S, Cytb, and C-mos; 1213 bp). Black dots represent supported nodes, with bootstrap values > 85; lower values are shown for species and lineage splits.

**Figure S1.4** Time-calibrated Bayesian mt-nuDNA phylogeny of *Acanthodactylus scutellatus* group (12S, Cytb, and C-mos; 1213 bp). Split times (Mya) are given next to the nodes. Horizontal bars represent the 95% HPD. The vertical blue line corresponds to the temporal threshold used to delimit intra-specific lineages (earliest lineage split within *A. aureus*, 1.84 Mya); a more conservative threshold (oldest split, 3.09 Mya) is depicted by a purple line.

**Figure S1.5** Inter-specific nuDNA (C-mos) haplotype network of *Acanthodactylus scutellatus* group. White dots represent mutation steps. Dashed squares depict alleles from the three northern lineages of *A. dumerilii/senegalensis* (Merzouga, NW Sahara, and Zagora). Numbers correspond to samples in Table S2.1.

**Figure S1.6** Intra-specific mtDNA (12S) and nuclear (C-mos) haplotype networks of *Acanthodactylus scutellatus* group. White dots represent mutation steps. Numbers correspond to samples listed in Table S2.1.

**Figure S1.7** Small-ranged lineage hotspots highlighted in Figure 3. Top: (A) *Acanthodactylus longipes* in north-western Sahara; (B) *A. dumerilii/senegalensis* and *A. scutellatus* in north-western Sahara; and (C) *A. scutellatus* in the Afro-Arabian suture zone. Maps show the distribution of nuDNA (C-mos) haplotypes for intra-specific lineages. White dots in the haplotype networks represent mutation steps. Allele numbers correspond to samples in Table S2.1. The time-calibrated phylogenetic trees (mt-nuDNA; 1213 bp) depict each lineage's positions within the main group clades (in dashed squares). Bottom: (D) Transition between the Saharan Atlas and the Great Western Erg; (E) Transition between Chott paleolakes and the Great Eastern Erg; and (F) Afro-Arabian suture zone. Black asterisks depict individual lineages. Projection: WGS84.

**Figure S1.8** Ecological niche models for species of *Acanthodactylus scutellatus* group, clipped to the species' ranges (modified from Roll et al., 2017). Projection: WGS84.

**Figure S1.9** Binary maps of habitat suitability for species of *Acanthodactylus scutellatus* group, derived from the ensemble models and TSS cut-off thresholds. Projection: WGS84.

**Figure S1.10** Clamping mask implementation on the ecological niche models for species of *Acanthodactylus scutellatus* group. Species' observations and model calibration areas are represented. Projection: WGS84.

**Figure S1.11** STRUCTURE HARVESTER graphic outputs of Delta (K) and Mean L(K), based on microsatellite analyses of *Acanthodactylus scutellatus* group in the sympatry zone Parc National du Banc d'Arguin.

**Figure S1.12** The two first axes of the Factorial Correspondence Analyses (FCoA) run on individual genotypes of *Acanthodactylus scutellatus* group from the Parc National du Banc d'Arguin sympatry zone. The lack of overlap among clusters with homogeneous species identity indicates lack of gene-flow.

Figure S1.1

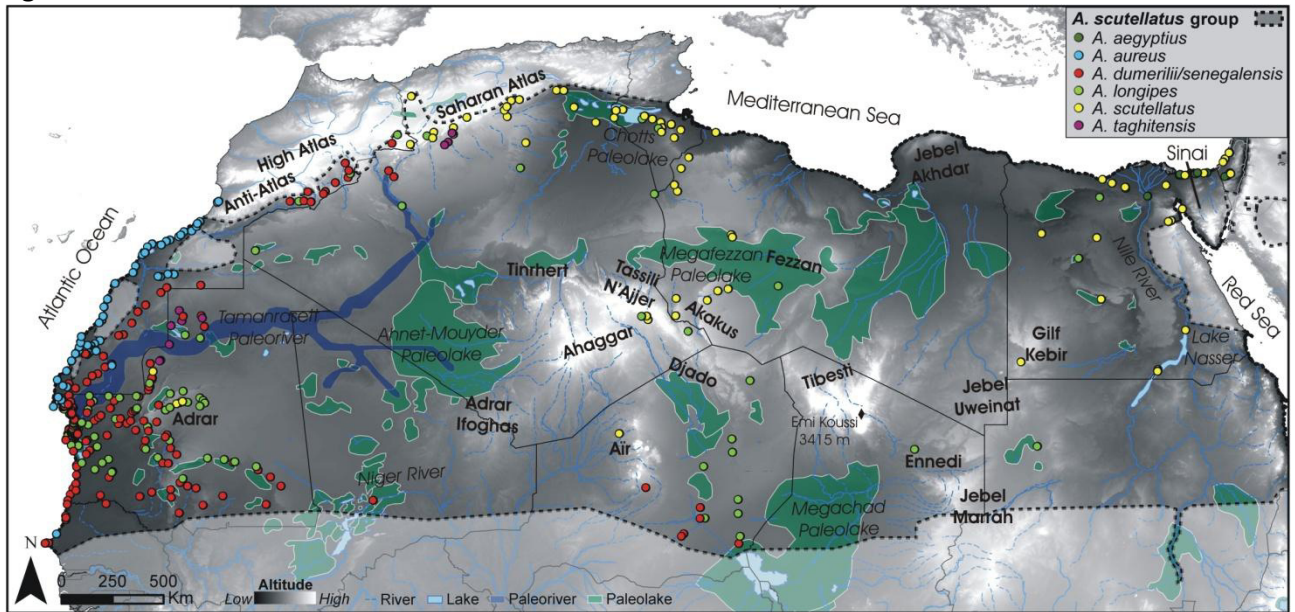


Figure S1.2

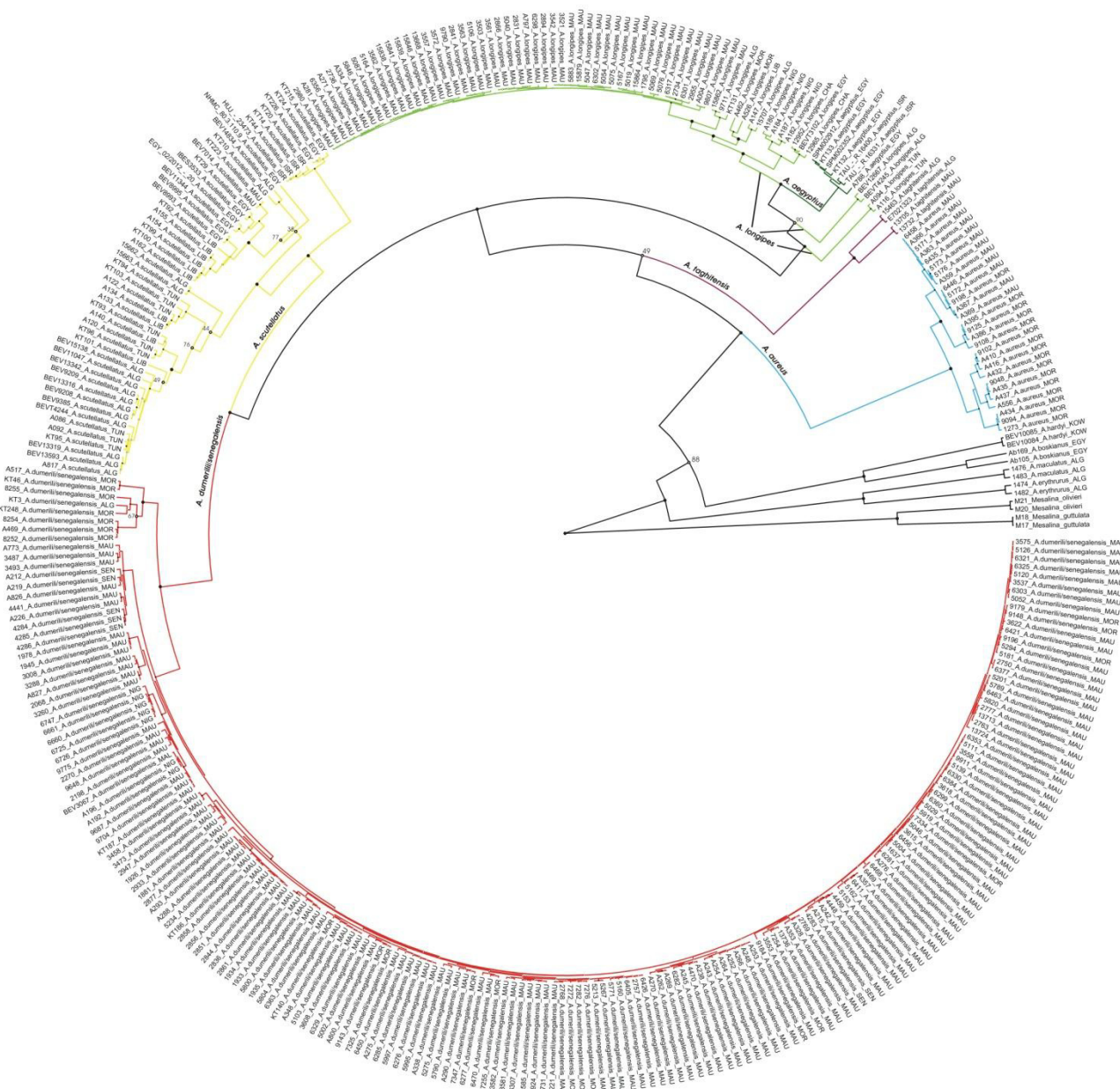


Figure S1.3

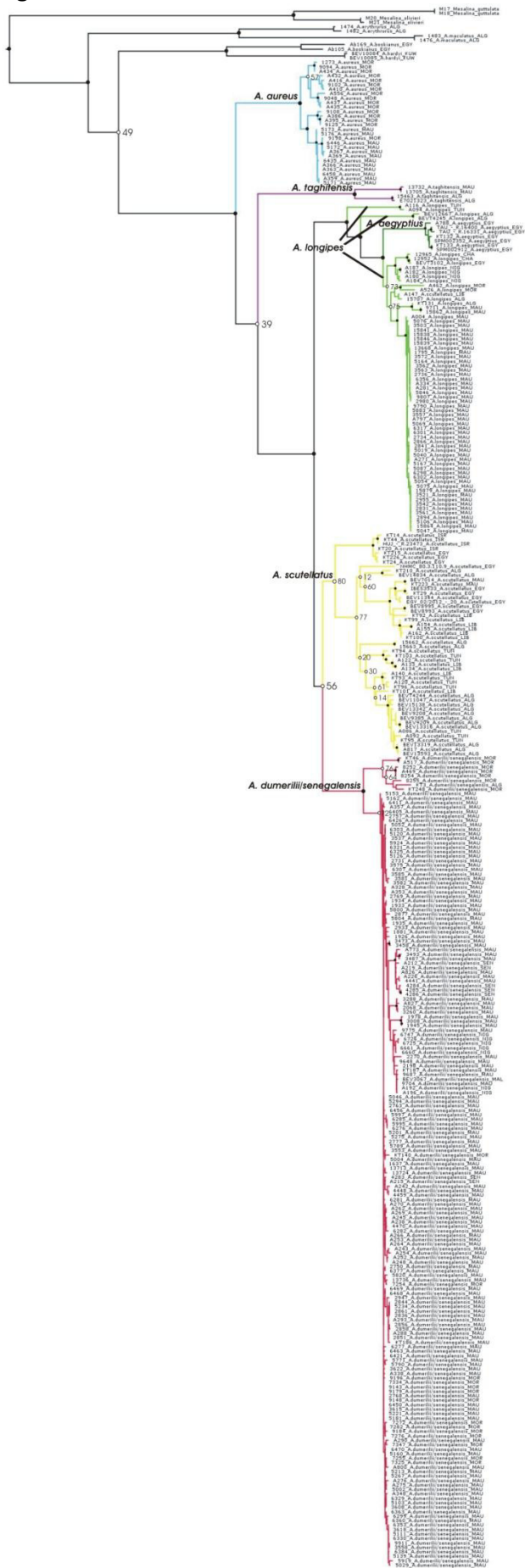




Figure S1.4



Figure S1.5

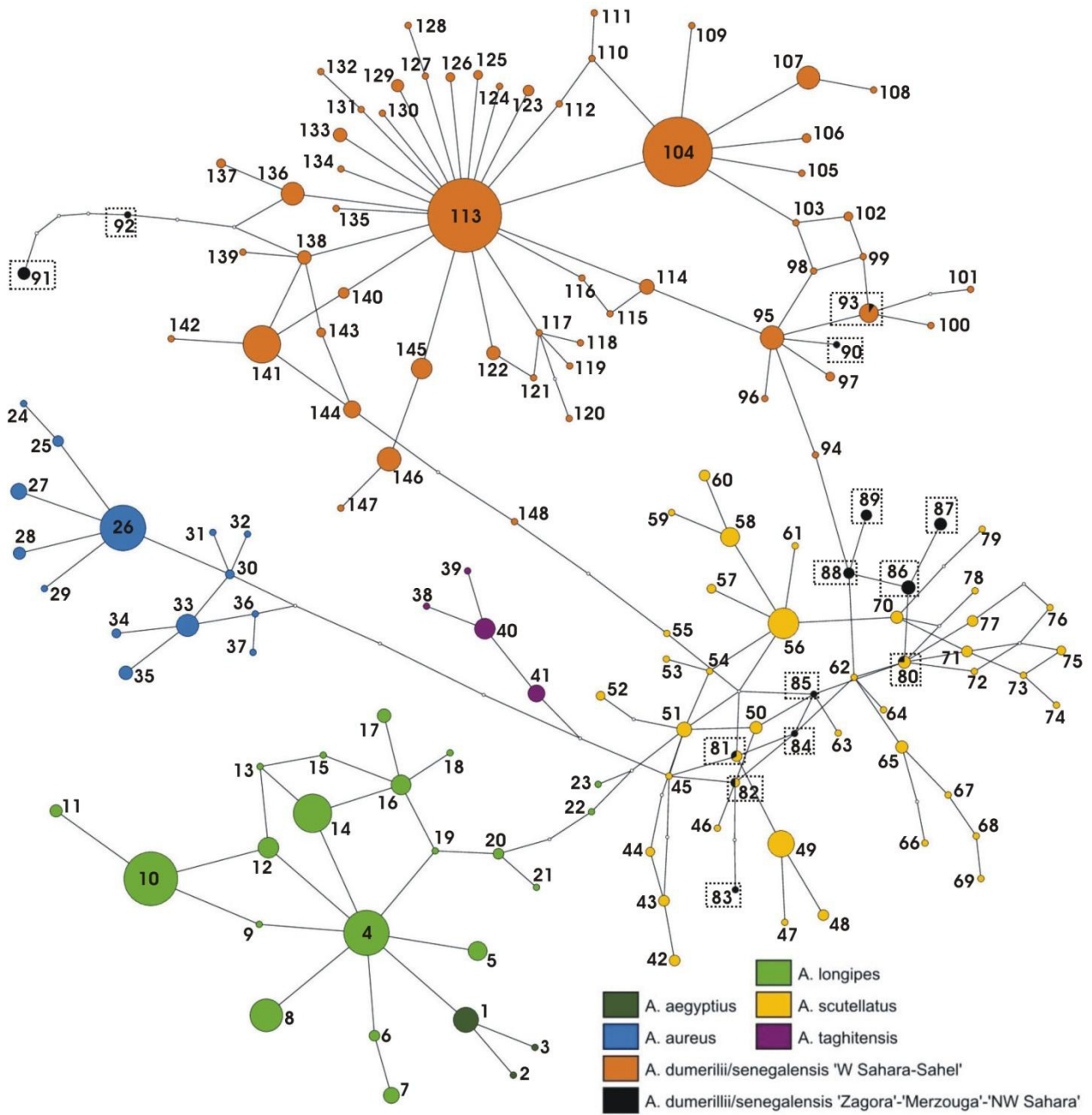


Figure S1.6

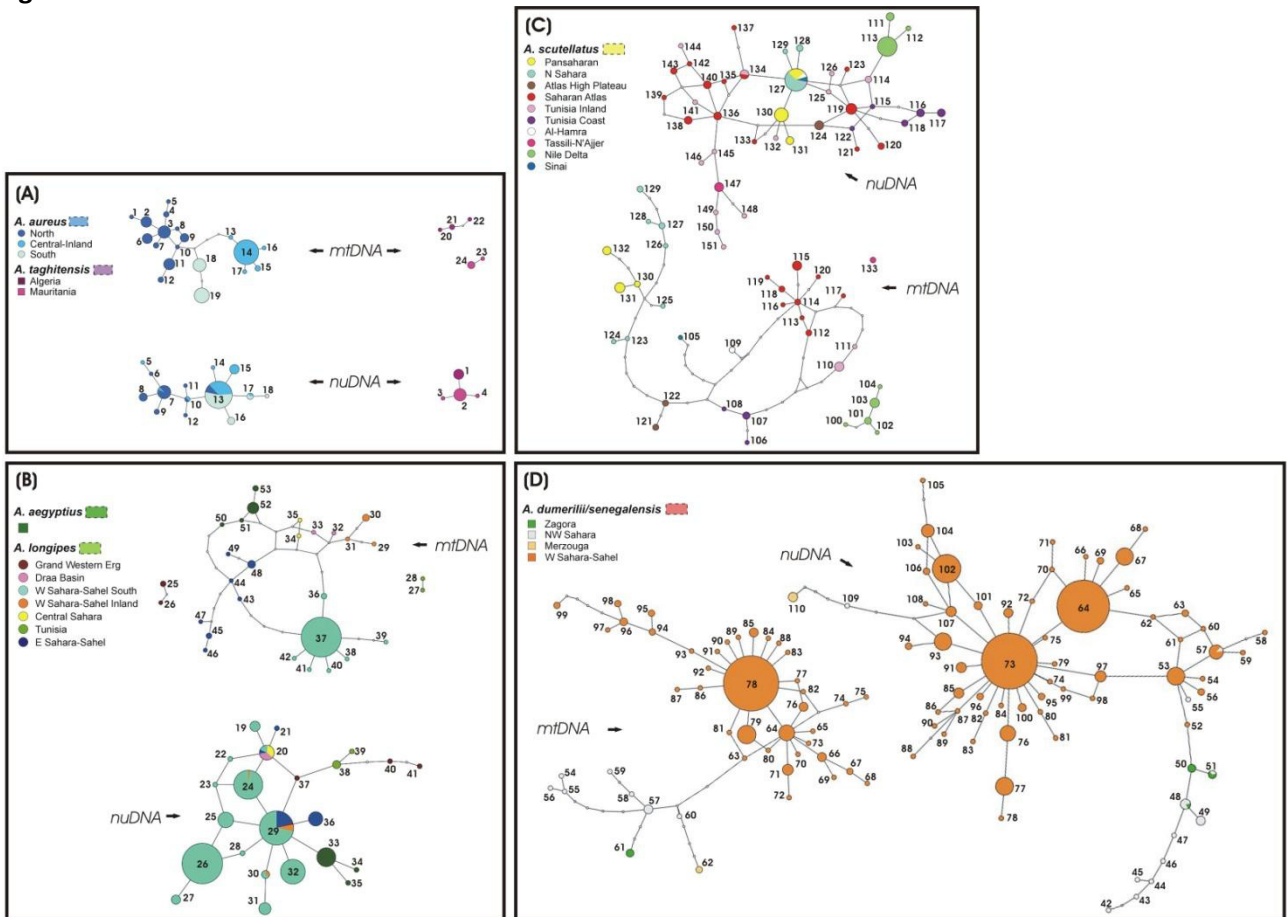


Figure S1.7

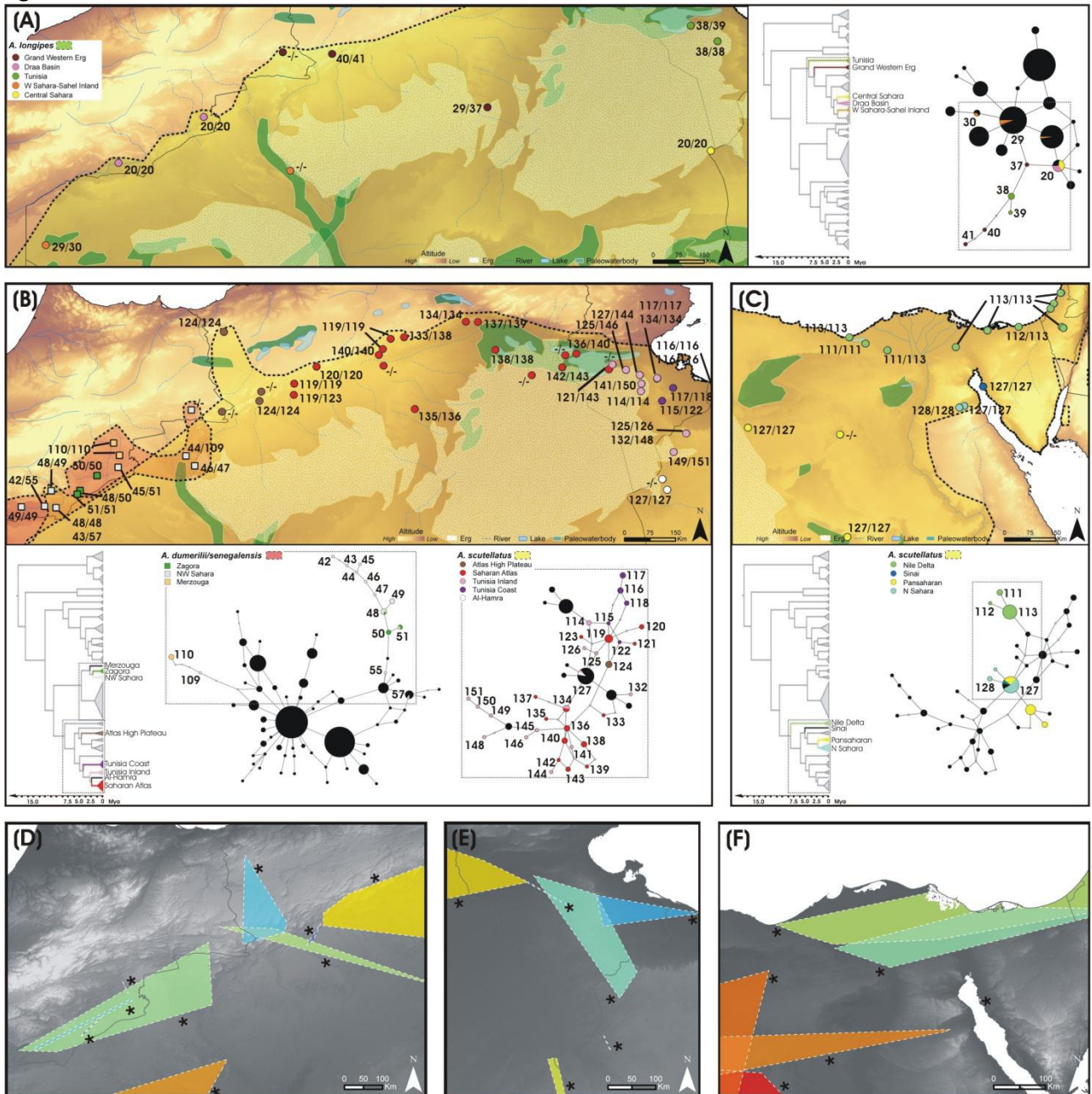


Figure S1.8

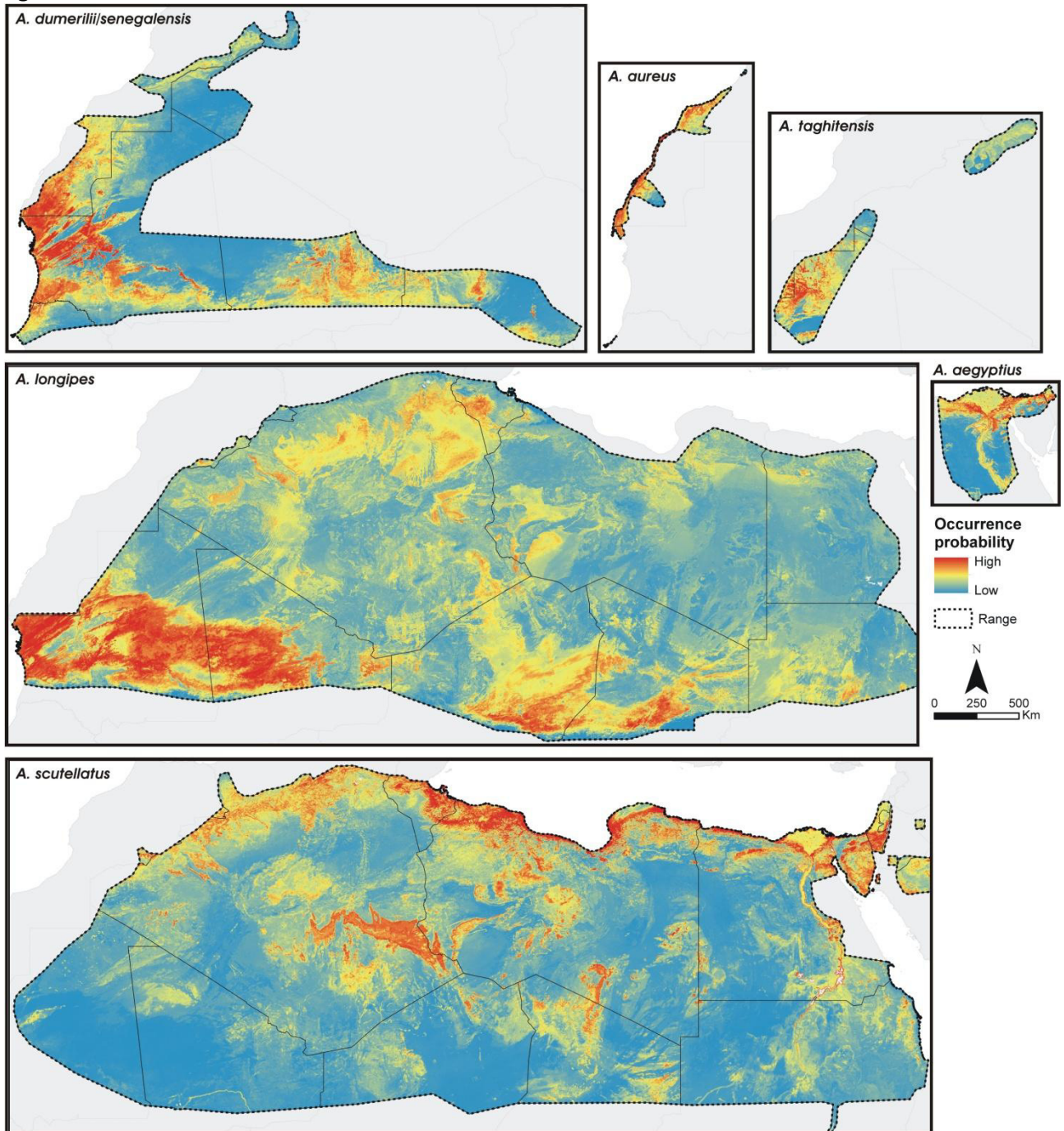


Figure S1.9

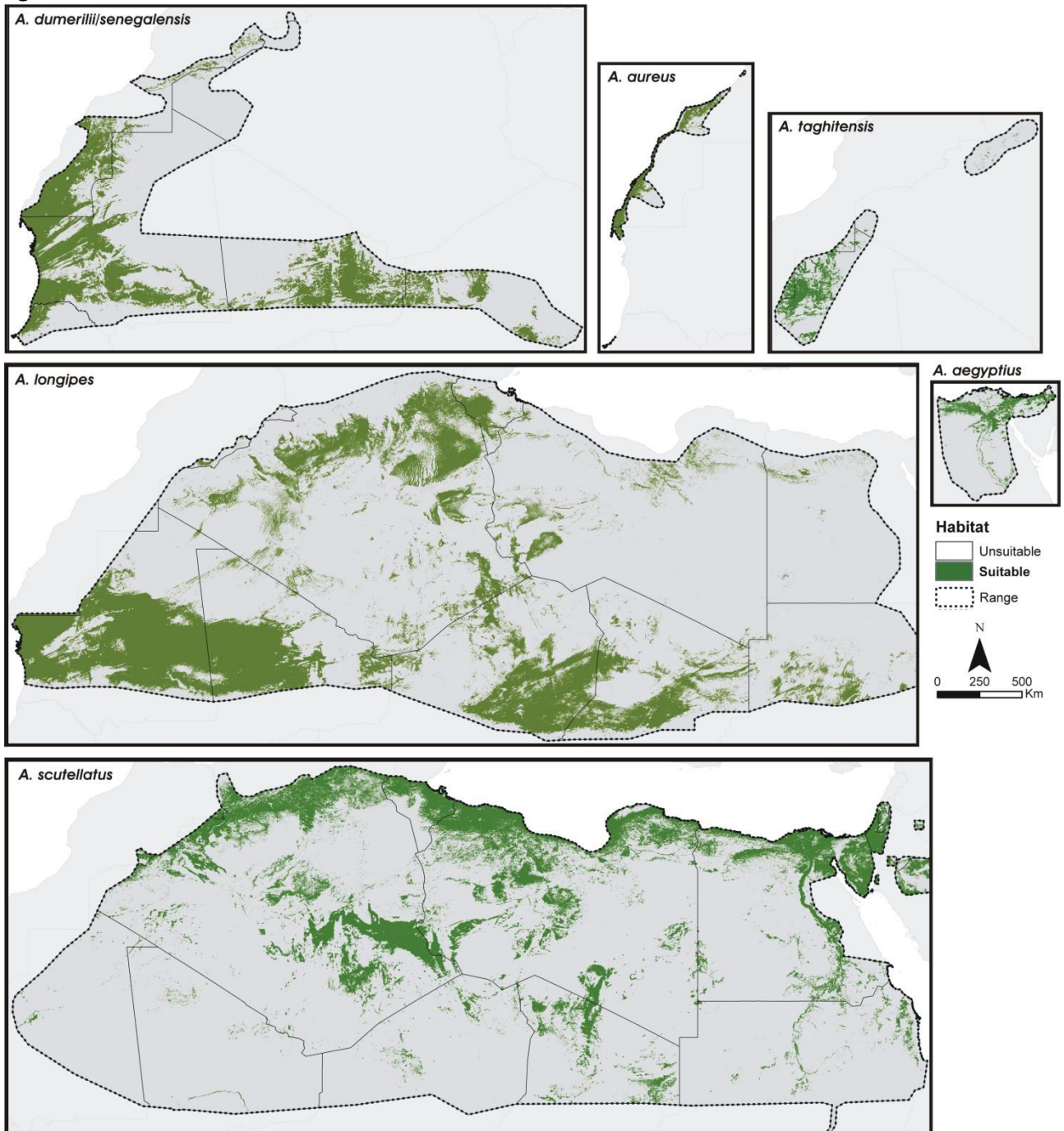


Figure S1.10

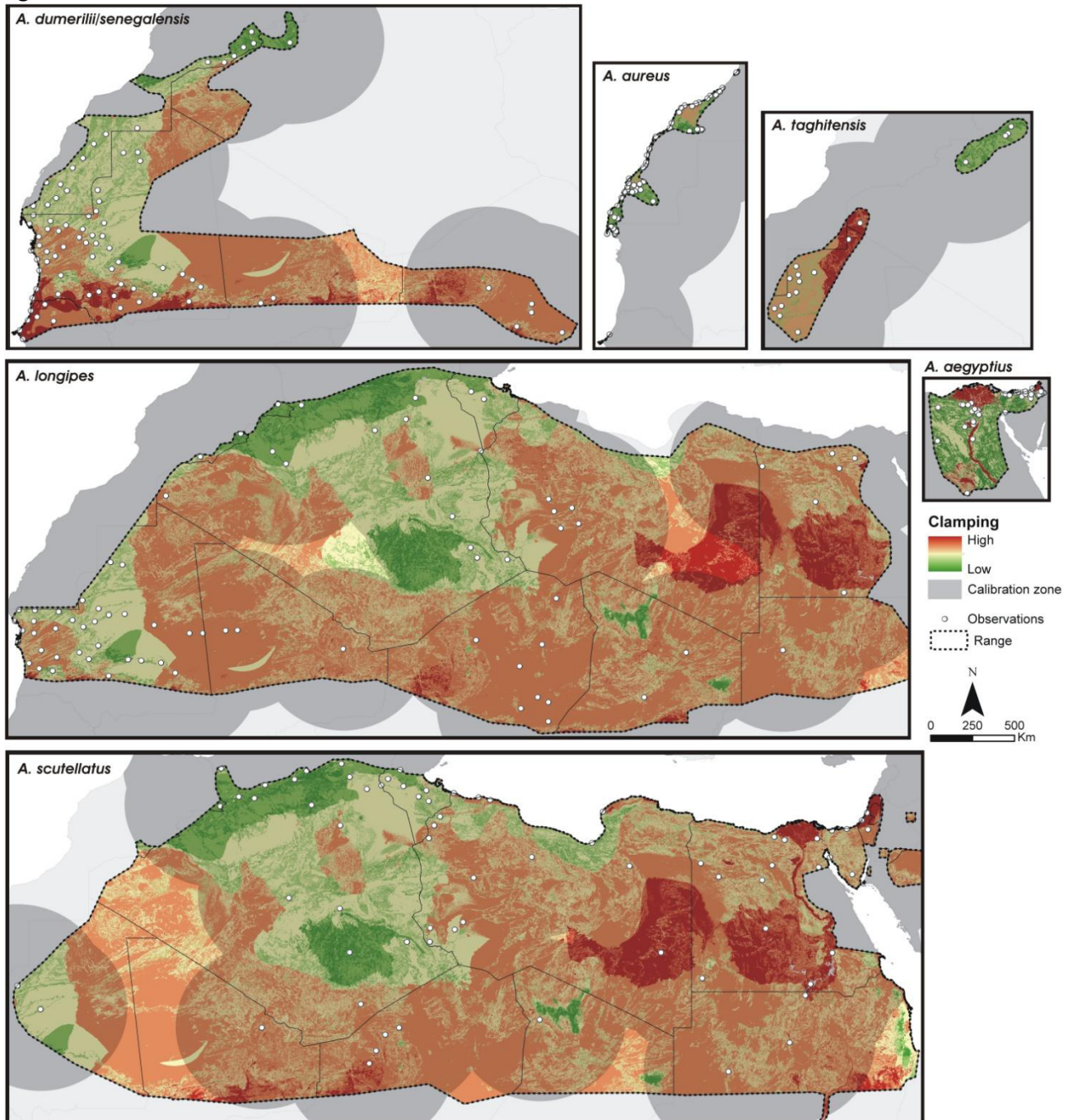


Figure S1.11

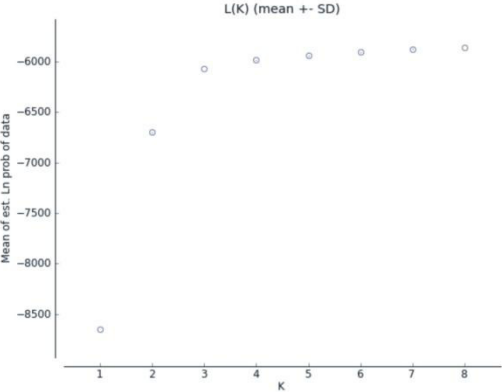
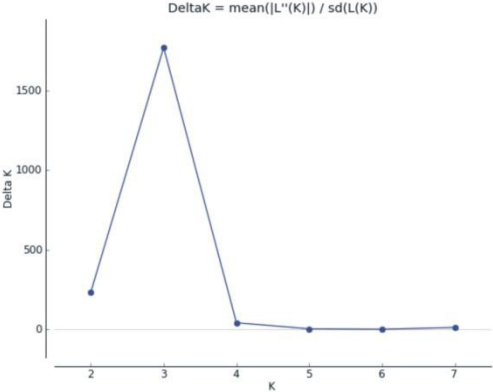
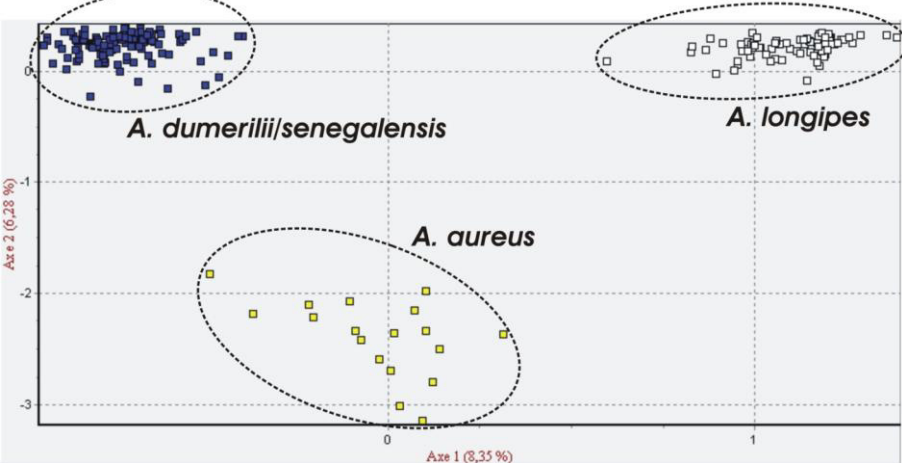




Figure S1.12



**Article reference – “Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards”**

André Vicente Liz<sup>1,2,3,4</sup>, Dennis Rödder<sup>4</sup>, Duarte Vasconcelos Gonçalves<sup>2,3,5</sup>, Guillermo Velo-Antón<sup>1,3,6</sup>, Pedro Tarroso<sup>1,3,7</sup>, Philippe Geniez<sup>8</sup>, Pierre-André Crochet<sup>9</sup>, Silvia B. Carvalho<sup>1,2,3</sup>, José Carlos Brito<sup>1,2,3</sup>

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**Supporting Information**

**APPENDIX S2 – Supplementary tables (captions)**

**Table S2.1** Samples of *Acanthodactylus scutellatus* group used in this study. The first and second sheets list the specimens and observations included in the genetic and ecological modelling analyses, respectively. Newly produced sequences are highlighted in bold.

**Table S2.2** Environmental variables included in the ecological niche models.

**Table S2.3** Primers for the sequenced gene fragments of mtDNA and nuDNA.

**Table S2.4** PCR conditions for the sequenced gene fragments of mtDNA and nuDNA, and genotyped microsatellite markers.

**Table S2.5** Characteristics of the 11 microsatellite loci used in the final dataset.

**Table S2.6** Outgroups and taxa used in the time-calibration of the phylogenetic tree. Newly produced sequences are highlighted in bold.

**Table S2.7** Details of the phylogenetic analyses. The number of samples included in each dataset is shown between brackets (ingroups only). UclD refers to relaxed uncorrelated lognormal clock. Priors not mentioned in the table were left as default.

**Table S2.8** Biogeographic events used to time-calibrate the phylogenetic inference.

**Table S2.9** Mean 12S pairwise genetic distances (p-distances) among species and intra-specific lineages.

**Table S2.10** Generalized Linear Models exploring correlations between different sets of topographic and land-cover predictors and (A) mtDNA haplotype distinctiveness (n = 421) or (B) lineages' range sizes (n = 20). For each group of predictors, the best-fitting model is highlighted in bold.

**Table S2.11** Metrics measuring the performance of the ensemble models and threshold values used to generate the binary maps.

**Table S2.12** Importance of environmental predictors (mean ± SD) in the ecological niche models. Full variable names are given in Table S2.2. The three most important variables in each case are highlighted in bold. The number replicates passing the threshold of TSS > 0.7 is shown between brackets.

**Table S2.13** Observations of heterozygote deficiency (Hdef) and null alleles (Nall) in *Acanthodactylus aureus*, *A. dumerilii/senegalensis*, and *A. longipes* from the Parc National du Banc d'Arguin sympatry zone. Significant values after Bonferroni correction are marked with an asterisk (\*). Two asterisks indicate observations of stuttering (\*\*).

**Table S2.14** Pairwise  $F_{ST}$  values based on microsatellites for the three identified genetic clusters from the Parc National du Banc d'Arguin sympatry zone. (+) indicate significance ( $\alpha=0.05$ ).

**Table S2.1**

*--- Uploaded as a separate .xlsx file ---*

**Table S2.2** Environmental variables included in the ecological niche models.

Code	Source	Meaning of derive variable
ED1503_bio7	MODIS V4 Band 03 Synoptic Months: Middle Infra-Red	Annual Range of Middle Infra-Red
ED1503_bio10	MODIS V4 Band 03 Synoptic Months: Middle Infra-Red	Mean Middle Infra-Red of Highest Quarter
ED1503_bio11	MODIS V4 Band 03 Synoptic Months: Middle Infra-Red	Mean Middle Infra-Red of Lowest Quarter
ED1514_bio1	MODIS V4 Band 14 Synoptic Months: Normalised Difference Vegetation Index	Annual Mean of Normalized Difference Vegetation Index (NDVI)
ED1514_bio7	MODIS V4 Band 14 Synoptic Months: Normalised Difference Vegetation Index	Annual Range of Normalized Difference Vegetation Index (NDVI)
ED1515_bio7	MODIS V4 Band 15 Synoptic Months: Enhanced Vegetation Index	Annual Range of Enhanced Vegetation Index (EVI)
ED150708_bio1	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Annual Mean Temperature
ED150708_bio2	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Mean Diurnal Range (Mean of monthly (max temp - min temp))
ED150708_bio3	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Isothermality (BIO2/BIO7) (* 100)
ED150708_bio4	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Temperature Seasonality (standard deviation *100)
ED150708_bio5	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Maximum Temperature of Highest Month
ED150708_bio6	MODIS V4 Band 07+08 Synoptic Months: Day-+Night-time Land Surface Temperature	Minimum Temperature of Lowest Month
bio12	Worldclim	Annual Precipitation
bio14	Worldclim	Precipitation of Driest Month
bio17	Worldclim	Precipitation of Driest Quarter
200	Globcover	Bare Areas
201	Globcover	Consolidated Bare Areas (hardpans, gravels, bare rock, stones, boulders)
202	Globcover	Non-consolidated Bare Areas (sandy desert)

References: MODIS V4 dataset from the EDENext project ([www.edenextdata.com](http://www.edenextdata.com)); Worldclim dataset from Fick and Hijmans, 2017 (<https://www.worldclim.org/data/worldclim21.html>); Globcover dataset from Bicheron et al., 2009 ([http://due.esrin.esa.int/page\\_globcover.php](http://due.esrin.esa.int/page_globcover.php)).

**Table S2.3** Primers for the sequenced gene fragments of mtDNA and nuDNA.

Gene	Primers	DNA strand	Sequence 5'- 3'
12S	12Sa	Forward	AAACTGGGATTAGATACCCCACTAT
	12Sb	Reverse	GAGGGTGACGGGCGGTGTGT
Cytb	Gludg	Forward	TGACTGAARAACCAAYCGTTG
	Cytb2	Reverse	CCCTCAGAATGATATTGTCCTCA
C-mos	Lsc1-F	Forward	CTCTGGKGGCTTTGGKKCTGTSTACAAGG
	Lsc2-R	Reverse	GGTGATGGCAAANGAGTAGATGTCTGC

**Table S2.4** PCR conditions for the sequenced gene fragments of mtDNA and nuDNA, and genotyped microsatellite markers.

Gene	Amplification step	Temperature	Duration	Nº of cycles
12S	Initial denaturation	94 °C	5 minutes	1
	Denaturation	94 °C	30 seconds	35
	Annealing	56 °C	40 seconds	
	Extension	72 °C	60 seconds	
	Final extension	72 °C	5 minutes	1
Cytb	Initial denaturation	94 °C	5 minutes	1
	Denaturation	94 °C	30 seconds	35
	Annealing	49 °C	45 seconds	
	Extension	72 °C	90 seconds	
	Final extension	72 °C	5 minutes	1
C-mos	Initial denaturation	94 °C	5 minutes	1
	Denaturation	94 °C	30 seconds	35
	Annealing	57 °C	45 seconds	
	Extension	72 °C	70 seconds	
	Final extension	72 °C	5 minutes	1
MP1	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	59-55 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	54 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	
MP2	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	57-53 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	53 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	
MP3	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	58-54 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	54 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	
MP4	Initial denaturation	95 °C	15 minutes	1
	Denaturation	95 °C	30 seconds	9
	Annealing	55-51 °C (Touchdown -0.5 °C)	90 seconds	
	Extension	72 °C	30 seconds	
	Denaturation	95 °C	30 seconds	31
	Annealing	51 °C	60 seconds	
	Extension	72 °C	30 seconds	
Final extension	60 °C	30 minutes	1	

**Table S2.5** Characteristics of the 11 microsatellite loci used in the final dataset.

Locus	Repeat	Primer sequence (5'- 3')	Multiplex	Ta	Dye
Ac1	(ATAC) <sub>8</sub>	F: CTGTGGTATATCCCCTGCCA R: GGTGGCTTCTCCACAGCTATT	1	58/54 °C	FAM
Ac5	(AAC) <sub>15</sub>	F: GTTGCTCAACTGCTCCTCC R: AGTGTCTGTGCACAACCAG	1	58/54 °C	VIC
Ac8	(TTG) <sub>11</sub>	F: GACATCTGAAGGCAGCCCTA R: GGTGTAGCCTGGAGCAGAA	1	58/54 °C	NED
Ac13	(AAC) <sub>14</sub>	F: TCCATGGGGTCACAAAGAGT R: TCTCCAGCACTTATCTGATGC	2	58/54 °C	FAM
Ac14	(CAA) <sub>10</sub>	F: TTAAGTGGCAATGTGTTGCAT R: TCCCACATGGTGGGTTACTT	2	58/54 °C	VIC
Ac19	(AAC) <sub>14</sub>	F: TCATTTCACTTCAAACCTGTGG R: ACTGATGTTGGGTTTGGAGC	2	58/54 °C	PET
Ac20	(GTT) <sub>11</sub>	F: ATGCATAAGTACGAAAAGGGGA R: TCTACAGAGAAAGAGAAATAACAACAA	2	58/54 °C	PET
Ac32	(TTC) <sub>15</sub>	F: TAGTCCGTAACCTTGTGGGTCA R: TTCTCAGACAACAGACACCCA	3	58/54 °C	FAM
Ac36	(TGT) <sub>9</sub>	F: GTCACGTTGATTGCATTGCT R: GCCAACTGGGAAACCTAGC	3	58/54 °C	VIC
Ac43	(CAA) <sub>13</sub>	F: AGCTTTGTACGTTTCTTTGC R: CCAGAGAAAACACATATGCAAGC	4	55/51 °C	FAM
Ac45	(CAA) <sub>10</sub>	F: AGGCAATGGAAGACAGGGA R: GCCTACAGTTTGTGCATAGGG	4	55/51 °C	VIC



**Table S2.6** Outgroups and taxa used in the time-calibration of the phylogenetic tree. Newly produced sequences are highlighted in bold.

ID	Taxon	Source	Country	Local	12S GB	Cytb GB	C-mos GB	mt-nuDNA tree	mt-nuDNA dating
10084	<i>Acanthodactylus hardyi</i>	<b>This study</b>	Kuwait	Sabah Al-Ahmed Natural Reserve	<b>OP218993</b>	<b>OP220505</b>	<b>OP220960</b>	X	X
10085	<i>Acanthodactylus hardyi</i>	<b>This study</b>	Kuwait	Al-Abraq to Al-Khabari road	<b>OP218994</b>	<b>OP220506</b>	<b>OP220961</b>	X	X
1474	<i>Acanthodactylus erythrurus</i>	<b>This study</b>	Algeria	PN Theniet el Had: Kaf Sahchine	<b>OP219005</b>	<b>OP220047</b>	<b>OP220548</b>	X	X
1476	<i>Acanthodactylus erythrurus</i>	<b>This study</b>	Algeria	Dar Chioukh - 40 km Nord Est Djelfa	<b>OP219006</b>	<b>OP220048</b>	<b>OP220549</b>	X	X
1482	<i>Acanthodactylus erythrurus</i>	<b>This study</b>	Algeria	Medrissa - 60 km Sud Tiaret	<b>OP219007</b>	<b>OP220049</b>	<b>OP220550</b>	X	X
1483	<i>Acanthodactylus maculatus</i>	<b>This study</b>	Algeria	Medrissa - 60 km Sud Tiaret	<b>OP219008</b>	<b>OP220050</b>	<b>OP220551</b>	X	X
Ab105	<i>Acanthodactylus boskianus</i>	Tamar et al., 2014	Egypt	Serabit el Khadim - Gebel Raqaba	KJ567672	KJ567768	KJ547966	X	X
Ab169	<i>Acanthodactylus boskianus</i>	Tamar et al., 2014	Egypt	Sidi Brani	KJ567729	KJ567813	KJ548015	X	X
M17	<i>Mesalina guttulata</i>	Tamar et al., 2016	Israel	4 km W. to Arad	KX296984	KX297187	KX297735	X	X
M18	<i>Mesalina guttulata</i>	Tamar et al., 2016	Israel	Hirbet Nizana	KX296985	KX297188	KX297736	X	X
M20	<i>Mesalina olivieri</i>	Tamar et al., 2016	Israel	Hirbet Mamshit	KX296987	KX297191	KX297738	X	X
M21	<i>Mesalina olivieri</i>	Tamar et al., 2016	Israel	Ramat Hovav	KX296988	KX297190	KX297739	X	X
Gat1	<i>Gallotia atlantica atlantica</i>	Arribas et al., 2006	Spain	Lanzarote	AY151915	AY151836	AY151999	X	X
Gatma1	<i>Gallotia atlantica mahoratae</i>	Arribas et al., 2006	Spain	Fuerteventura	AY151916	AY151837	AY152000	X	X
Gcaca1	<i>Gallotia caesaris caesaris</i>	Arribas et al., 2006	Spain	El Hierro	AY151922	AY151843	AY152006	X	X
Gcago1	<i>Gallotia caesaris gomerae</i>	Arribas et al., 2006	Spain	La Gomera	AY151921	AY151842	AY152005	X	X
Ggo1	<i>Gallotia bravoana</i>	Hernández et al., 2001	Spain	La Gomera	AJ272395	AJ272396		X	X
Ggae1	<i>Gallotia galloti eisentrauti</i>	Arribas et al., 2006	Spain	Tenerife	AY151918	AY151839	AY152002	X	X
Ggaga1	<i>Gallotia galloti galloti</i>	Arribas et al., 2006	Spain	Tenerife	AY151919	AY151840	AY152003	X	X
Ggapa1	<i>Gallotia galloti palmae</i>	Arribas et al., 2006	Spain	La Palma	AY151920	AY151841	AY152004	X	X
Gin1	<i>Gallotia intermedia</i>	Arribas et al., 2006	Spain	Tenerife	AY151923	AY151844	AY152007	X	X
Gsima1	<i>Gallotia simonyi machadoi</i>	Arribas et al., 2006; Carranza et al., 1999	Spain	El Hierro	AY151924	AF101219	AY152008	X	X
Gst1	<i>Gallotia stehlini</i>	Arribas et al., 2006	Spain	Gran Canaria	AY151917	AY151838	AY152001	X	X
Pcr1	<i>Podarcis cretensis</i>	Kapli et al., 2013; Poulakakis et al., 2003	Greece	Crete		AF486216	KF003242	X	X
Pcr2	<i>Podarcis cretensis</i>	Kapli et al., 2013; Poulakakis et al., 2003	Greece	Crete		AF486218	KF003244	X	X
Pli1	<i>Podarcis lilfordi</i>	Brown et al., 2008	Spain	Menorca	EF694766	EF694810	EF679323	X	X
Pli2	<i>Podarcis lilfordi</i>	Brown et al., 2008	Spain	Cabrera	EF694764	EF694805	EF679302	X	X
Ppe1	<i>Podarcis peloponnesiacus</i>	Kapli et al., 2013; Poulakakis et al., 2005	Greece	Peloponnese		AY896121	KF003245	X	X
Ppe2	<i>Podarcis peloponnesiacus</i>	Kapli et al., 2013; Poulakakis et al., 2005	Greece	Peloponnese		AY896124	KF003246	X	X
Ppi1	<i>Podarcis pityusensis</i>	Brown et al., 2008	Spain	Ibiza	EF694768	EF694814	EF679324	X	X
Ppi2	<i>Podarcis pityusensis</i>	Brown et al., 2008	Spain	Espardell	EF694769	EF694815	EF679325	X	X
Pal1	<i>Psammadromus algirus</i>	Arribas et al., 2006	-	-	AY151914	AY151835	AY151998	X	X
Pal2	<i>Psammadromus algirus</i>	Harris et al., 1998	Morocco	S. of Tizi Chika, High Atlas	AF080308	AF080309		X	X

**Table S2.7** Details of the phylogenetic analyses. The number of samples included in each dataset is shown between brackets (ingroups only). Priors not mentioned in the table were left as default.

Phylogenetic analysis	Dataset ( <i>N</i> tips)	Partition	Length	Nucleotide substitution model	Clock model	Tree model	Run Specifications
<b>Bayesian Inference</b>	mt-nuDNA haplotypes (338)	<i>12S</i>	368	GTR+I+G; estimated bf	Ucld	Coalescent: Constant Size. Random starting tree	2 runs; 10 <sup>8</sup> generations; 10 <sup>4</sup> sampling frequency; 10% burn-in
		<i>cytb</i>	377	GTR+I+G; estimated bf	Ucld		
		<i>C-mos</i>	468	HKY+I+G; equal bf	Strict		
<b>Maximum Likelihood</b>	mt-nuDNA haplotypes (338)	<i>12S</i>	368	GTR+I+G; estimated bf			
		<i>cytb</i>	377				
		<i>C-mos</i>	468				
<b>Bayesian Inference (splits dating)</b>	mt-nuDNA (74 + 21 samples used for time-calibrating)	<i>12S</i>	371	GTR+I+G; estimated bf	Ucld	Speciation: Yule Process Random starting tree	2 runs; 10 <sup>8</sup> generations; 10 <sup>4</sup> sampling frequency; 10% burn-in
		<i>cytb</i>	377	GTR+I+G; estimated bf	Ucld		
		<i>C-mos</i>	468	HKY+I+G; equal bf	Strict		

Abbreviations: Ucld refers to relaxed uncorrelated lognormal clock; bf refers to base frequencies.

**Table S2.8** Biogeographic events used to time-calibrate the phylogenetic inference.

Event	Period	Value	Taxa
Fragmentation of Balearic Islands	End of the Messinian Salinity Crisis	5.32 ± 0.05	<i>Podarcis pityusensis</i> – <i>Podarcis lilfordi</i>
Isolation of Greece from Peloponnesus	End of the Messinian Salinity Crisis	5.32 ± 0.05	<i>Podarcis cretensis</i> – <i>Podarcis peloponnesiacus</i>
Origin of Fuerteventura and Lanzarote	Age of the Canary Islands	18 ± 2	<i>Gallotia</i> spp. – <i>Psammodromus algirus</i>
Origin of La Gomera	Age of the Canary Islands	6 ± 3	<i>Gallotia galloti</i> – <i>Gallotia caesaris</i>
Origin of La Palma	Age of the Canary Islands	1 ± 0.5	<i>Gallotia galloti palmae</i> – ancestor of <i>Gallotia galloti galloti</i> & <i>Gallotia galloti eisentrauti</i>
Origin of El Hierro	Age of the Canary Islands	0.8 ± 0.2	<i>Gallotia bravoana</i> – <i>Gallotia simonyi machadoi</i>
Origin of El Hierro	Age of the Canary Islands	0.8 ± 0.2	<i>Gallotia caesaris caesaris</i> – <i>Gallotia caesaris gomerae</i>

**Table S2.9** Mean 12S pairwise genetic distances (p-distances) among species and intra-specific lineages.

SPECIES									
	<i>A. aegyptius</i>	<i>A. aureus</i>	<i>A. dumerilii/senegalensis</i>	<i>A. longipes</i>	<i>A. scutellatus</i>	<i>A. taghitensis</i>			
<i>A. aegyptius</i>									
<i>A. aureus</i>	0.077								
<i>A. dumerilii/senegalensis</i>	0.040	0.076							
<i>A. longipes</i>	0.016	0.087	0.048						
<i>A. scutellatus</i>	0.040	0.079	0.052	0.049					
<i>A. taghitensis</i>	0.091	0.080	0.094	0.101	0.095				
LINEAGES									
<i>A. taghitensis</i>	Mauritania								
Mauritania									
Algeria	0.040								
<i>A. aureus</i>	North Central-Inland								
North									
Central-Inland	0.015								
South	0.010	0.015							
<i>A. dumerilii/senegalensis</i>	Zagora	NW Sahara	Merzouga						
Zagora									
NW Sahara	0.018								
Merzouga	0.019	0.024							
W Sahara-Sahel	0.018	0.022	0.022						
<i>A. longipes</i>	Tunisia	Great Western Erg	Aegyptius	E Sahara-Sahel	Central Sahara	Draa Basin	W Sahara-Sahel Inland		
Tunisia									
Great Western Erg	0.040								
Aegyptius	0.034	0.026							
E Sahara-Sahel	0.044	0.032	0.013						
Central Sahara	0.040	0.021	0.011	0.016					
Draa Basin	0.037	0.027	0.008	0.016	0.006				
W Sahara-Sahel Inland	0.039	0.028	0.015	0.020	0.011	0.011			
W Sahara-Sahel South	0.042	0.028	0.015	0.016	0.011	0.014	0.019		
<i>A. scutellatus</i>	Nile Delta	Sinai	Atlas High Plateau	Pansaharan	N Sahara	Tassili-N'Ajjer	Tunisia Coast	Tunisia Inland	Saharan Atlas
Nile Delta									
Sinai	0.045								
Atlas High Plateau	0.031	0.023							
Pansaharan	0.042	0.042	0.029						
N Sahara	0.042	0.044	0.028	0.016					
Tassili-N'Ajjer	0.040	0.040	0.031	0.048	0.049				
Tunisia Coast	0.037	0.020	0.010	0.029	0.028	0.032			
Tunisia Inland	0.048	0.025	0.020	0.033	0.033	0.031	0.013		
Saharan Atlas	0.046	0.028	0.024	0.036	0.037	0.036	0.019	0.019	
Al-Hamra	0.040	0.023	0.020	0.031	0.033	0.028	0.014	0.017	0.018

**Table S2.10** Generalized Linear Models exploring correlations between different sets of topographic and land-cover predictors and (A) mtDNA haplotype distinctiveness (n = 421) or (B) lineages' range sizes (n = 20). For each group of predictors, the best-fitting model is highlighted in bold.

(A) diversification model	Model	Comparison	Predictors	df	AIC
	<i>Mod1</i>	Topography	Hapl. disct. ~ x(Altitude) + x(TRI) + nearest + sp	10	-2464.4
<i>Mod2</i>	Topography	Hapl. disct. ~ x(Altitude) + nearest + sp	9	-2458.6	
<b><i>Mod3</i></b>	<b>Topography</b>	<b>Hapl. disct. ~ x(TRI) + nearest + sp</b>	<b>9</b>	<b>-2445.5</b>	
<i>Mod1</i>	Land-cover 1	Hapl. disct. ~ x(Erg) + x(Reg) + x(BA) + nearest + sp	11	-2424.1	
<b><i>Mod2</i></b>	<b>Land-cover 1</b>	<b>Hapl. disct. ~ x(Erg) + x(Reg) + nearest + sp</b>	<b>10</b>	<b>-2424.7</b>	
<i>Mod3</i>	Land-cover 1	Hapl. disct. ~ x(Erg) + x(BA) + nearest + sp	10	-2425.5	
<i>Mod4</i>	Land-cover 1	Hapl. disct. ~ x(Reg) + x(BA) + nearest + sp	10	-2425.8	
<b><i>Mod1</i></b>	<b>Land-cover 2</b>	<b>Hapl. disct. ~ x(Erg) + nearest + sp</b>	<b>9</b>	<b>-2419.4</b>	
<i>Mod2</i>	Land-cover 2	Hapl. disct. ~ x(Reg) + nearest + sp	9	-2426.4	
<i>Mod3</i>	Land-cover 2	Hapl. disct. ~ x(BA) + nearest + sp	9	-2425.1	
<b>FINAL</b>		<b>Hapl. disct. ~ x(TRI) + x(Erg) + nearest + sp</b>	<b>10</b>	<b>2443.5</b>	

(B) connectivity model	Model	Comparison	Predictors	df	AIC
	<i>Mod1</i>	Topography	Diameter ~ x(Altitude) + x(TRI) + n + sp	10	349.6
<i>Mod2</i>	Topography	Diameter ~ x(Altitude) + n + sp	9	348.4	
<b><i>Mod3</i></b>	<b>Topography</b>	<b>Diameter ~ x(TRI) + n + sp</b>	<b>9</b>	<b>347.8</b>	
<i>Mod1</i>	Land-cover 1	Diameter ~ x(Erg) + x(Reg) + x(BA) + n + sp	11	335.7	
<i>Mod2</i>	Land-cover 1	Diameter ~ x(Erg) + x(Reg) + n + sp	10	334.7	
<b><i>Mod3</i></b>	<b>Land-cover 1</b>	<b>Diameter ~ x(Erg) + x(BA) + n + sp</b>	<b>10</b>	<b>333.9</b>	
<i>Mod4</i>	Land-cover 1	Diameter ~ x(Reg) + x(BA) + n + sp	10	346.2	
<b><i>Mod2</i></b>	<b>Land-cover 2</b>	<b>Diameter ~ x(Erg) + n + sp</b>	<b>9</b>	<b>334.8</b>	
<i>Mod3</i>	Land-cover 2	Diameter ~ x(BA) + n + sp	9	345.3	
<b>FINAL</b>		<b>Diameter ~ x(TRI) + x(Erg) + n + sp</b>	<b>10</b>	<b>336.8</b>	

**Table S2.11** Metrics measuring the performance of the ensemble models and threshold values used to generate the binary maps.

Species	TSS				AUC		
	TSS	Sensitivity	Specificity	Threshold	AUC	Sensitivity	Specificity
<i>A. aegyptius</i>	0.926	97.143	95.416	0.584	0.986	97.143	95.486
<i>A. aureus</i>	0.967	100.000	96.625	0.575	0.992	100.000	96.695
<i>A. dumerilii/senegalensis</i>	0.850	97.436	87.504	0.457	0.963	97.436	87.744
<i>A. longipes</i>	0.813	98.701	82.570	0.472	0.952	98.701	82.940
<i>A. scutellatus</i>	0.795	95.714	83.759	0.466	0.941	95.714	84.209
<i>A. taghitensis</i>	0.967	100.000	96.689	0.568	0.991	100.000	96.729



		GAM	GBM	GLM	ANN	CTA	Maxent	Ensemble
		(9)	(10)	(10)	(10)	(10)	(10)	(59)
<i>A. scutellatus</i>	ED1503_bio7	0.42 ± 0.17	0.05 ± 0.03	0.00 ± 0.00	0.31 ± 0.17	<b>0.10 ± 0.21</b>	0.08 ± 0.10	0.20 ± 0.26
	ED1503_bio10	<b>0.66 ± 0.10</b>	0.02 ± 0.01	0.03 ± 0.07	0.42 ± 0.32	0.04 ± 0.09	0.02 ± 0.05	0.19 ± 0.29
	ED1503_bio11	0.53 ± 0.11	<b>0.15 ± 0.10</b>	<b>0.20 ± 0.40</b>	<b>0.56 ± 0.32</b>	<b>0.80 ± 0.29</b>	0.08 ± 0.10	<b>0.38 ± 0.36</b>
	ED1514_bio1	0.14 ± 0.06	0.03 ± 0.01	0.01 ± 0.02	0.05 ± 0.05	0.02 ± 0.05	0.14 ± 0.10	0.06 ± 0.08
	ED1514_bio7	0.27 ± 0.06	0.01 ± 0.00	0.05 ± 0.08	0.09 ± 0.08	0.01 ± 0.04	0.03 ± 0.04	0.08 ± 0.10
	ED1515_bio7	0.34 ± 0.04	0.05 ± 0.04	0.06 ± 0.12	0.08 ± 0.08	0.02 ± 0.06	0.18 ± 0.15	0.12 ± 0.14
	ED150708_bio1	<b>0.74 ± 0.10</b>	0.01 ± 0.01	0.01 ± 0.03	0.48 ± 0.36	0.01 ± 0.03	0.05 ± 0.10	0.21 ± 0.32
	ED150708_bio2	0.61 ± 0.26	0.03 ± 0.01	0.00 ± 0.00	0.34 ± 0.26	0.02 ± 0.05	0.10 ± 0.21	0.18 ± 0.28
	ED150708_bio3	0.55 ± 0.19	0.03 ± 0.02	0.05 ± 0.14	0.11 ± 0.15	0.00 ± 0.01	0.10 ± 0.16	0.13 ± 0.22
	ED150708_bio4	0.55 ± 0.13	<b>0.12 ± 0.04</b>	<b>0.42 ± 0.48</b>	<b>0.70 ± 0.24</b>	0.02 ± 0.04	<b>0.46 ± 0.25</b>	<b>0.37 ± 0.34</b>
	ED150708_bio5	0.62 ± 0.20	0.01 ± 0.01	0.00 ± 0.00	0.30 ± 0.23	0.03 ± 0.09	0.02 ± 0.05	0.16 ± 0.26
	ED150708_bio6	<b>0.62 ± 0.13</b>	0.05 ± 0.02	<b>0.07 ± 0.12</b>	<b>0.54 ± 0.31</b>	0.04 ± 0.13	0.07 ± 0.08	<b>0.23 ± 0.29</b>
	bio12	0.20 ± 0.05	<b>0.10 ± 0.05</b>	0.02 ± 0.07	0.15 ± 0.13	0.06 ± 0.13	<b>0.24 ± 0.14</b>	0.13 ± 0.13
	bio14	0.13 ± 0.05	0.00 ± 0.00	0.00 ± 0.00	0.03 ± 0.04	0.00 ± 0.00	0.21 ± 0.28	0.06 ± 0.14
	bio17	0.20 ± 0.05	0.01 ± 0.01	0.00 ± 0.00	0.06 ± 0.06	<b>0.11 ± 0.14</b>	0.18 ± 0.27	0.09 ± 0.15
	200	0.35 ± 0.06	0.02 ± 0.02	0.02 ± 0.03	0.01 ± 0.02	0.02 ± 0.06	0.12 ± 0.09	0.08 ± 0.13
	201	0.37 ± 0.09	0.00 ± 0.00	0.00 ± 0.00	0.02 ± 0.03	0.02 ± 0.06	0.04 ± 0.04	0.07 ± 0.14
202	0.45 ± 0.16	0.06 ± 0.02	0.05 ± 0.14	0.01 ± 0.02	0.01 ± 0.04	<b>0.38 ± 0.21</b>	0.15 ± 0.22	
<i>A. taghitensis</i>		GAM	GBM	GLM	ANN	CTA	Maxent	Ensemble
		(9)	(10)	(8)	(10)	(6)	(10)	(53)
	ED1503_bio7	0.81 ± 0.20	0.04 ± 0.02	0.00 ± 0.00	<b>0.79 ± 0.13</b>	0.00 ± 0.00	0.09 ± 0.14	0.25 ± 0.36
	ED1503_bio10	0.72 ± 0.23	0.15 ± 0.07	0.07 ± 0.17	0.61 ± 0.23	0.13 ± 0.22	0.01 ± 0.02	0.26 ± 0.32
	ED1503_bio11	0.68 ± 0.27	0.04 ± 0.02	0.00 ± 0.00	<b>0.82 ± 0.14</b>	0.01 ± 0.04	0.00 ± 0.00	0.22 ± 0.35
	ED1514_bio1	0.58 ± 0.25	<b>0.17 ± 0.08</b>	<b>0.22 ± 0.33</b>	0.23 ± 0.14	<b>0.45 ± 0.42</b>	<b>0.27 ± 0.05</b>	<b>0.33 ± 0.29</b>
	ED1514_bio7	0.62 ± 0.30	0.01 ± 0.01	0.02 ± 0.06	0.27 ± 0.09	0.03 ± 0.09	0.02 ± 0.05	0.15 ± 0.26
	ED1515_bio7	0.45 ± 0.27	0.01 ± 0.01	0.00 ± 0.00	0.25 ± 0.05	0.02 ± 0.06	0.00 ± 0.00	0.11 ± 0.21
	ED150708_bio1	0.81 ± 0.23	0.00 ± 0.00	0.00 ± 0.00	0.79 ± 0.10	0.04 ± 0.08	0.00 ± 0.00	0.24 ± 0.37
	ED150708_bio2	<b>0.92 ± 0.17</b>	0.13 ± 0.04	<b>0.38 ± 0.43</b>	0.59 ± 0.24	0.06 ± 0.14	0.00 ± 0.00	<b>0.32 ± 0.39</b>
	ED150708_bio3	<b>0.90 ± 0.19</b>	<b>0.22 ± 0.06</b>	0.00 ± 0.00	0.51 ± 0.25	0.10 ± 0.16	0.12 ± 0.03	0.29 ± 0.34
	ED150708_bio4	0.83 ± 0.25	0.03 ± 0.02	0.02 ± 0.04	0.76 ± 0.19	0.04 ± 0.13	0.00 ± 0.00	0.24 ± 0.38
	ED150708_bio5	0.86 ± 0.15	0.16 ± 0.06	0.03 ± 0.08	0.75 ± 0.26	<b>0.28 ± 0.28</b>	<b>0.25 ± 0.07</b>	<b>0.36 ± 0.34</b>
	ED150708_bio6	0.90 ± 0.15	0.01 ± 0.01	0.00 ± 0.00	<b>0.78 ± 0.16</b>	0.00 ± 0.00	0.01 ± 0.01	0.24 ± 0.39
	bio12	0.59 ± 0.26	0.16 ± 0.04	0.08 ± 0.15	0.42 ± 0.26	0.08 ± 0.13	0.11 ± 0.04	0.23 ± 0.25
	bio14	0.39 ± 0.26	0.00 ± 0.00	0.01 ± 0.04	0.20 ± 0.20	0.00 ± 0.00	0.08 ± 0.06	0.11 ± 0.19
	bio17	0.70 ± 0.24	0.05 ± 0.03	0.17 ± 0.32	0.37 ± 0.17	0.03 ± 0.08	0.13 ± 0.03	0.23 ± 0.29
200	0.88 ± 0.12	0.00 ± 0.00	0.01 ± 0.03	0.02 ± 0.03	0.07 ± 0.14	0.01 ± 0.03	0.17 ± 0.33	
201	<b>0.96 ± 0.06</b>	0.05 ± 0.04	<b>0.37 ± 0.26</b>	0.09 ± 0.11	<b>0.19 ± 0.29</b>	0.07 ± 0.06	0.29 ± 0.36	
202	0.84 ± 0.11	<b>0.21 ± 0.08</b>	0.09 ± 0.21	0.04 ± 0.04	0.13 ± 0.20	<b>0.36 ± 0.09</b>	0.29 ± 0.30	



**Table S2.13** Observations of heterozygote deficiency (Hdef) and null alleles (Nall) in *Acanthodactylus aureus*, *A. dumerilii/senegalensis*, and *A. longipes* from the Parc National du Banc d'Arguin sympatry zone. Significant values after Bonferroni correction are marked with an asterisk (\*). Two asterisks indicate observations of stuttering (\*\*).

Locus	<i>A. aureus</i>		<i>A. dumerilii/senegalensis</i>		<i>A. longipes</i>	
	Hdef	Nall	Hdef	Nall	Hdef	Nall
Ac1						
Ac5				*		
Ac8			*			
Ac13			*	**		
Ac14						
Ac19					*	**
Ac20						
Ac32			*	**		
Ac36						
Ac43			*	**		
Ac45						

**Table S2.14** Pairwise  $F_{ST}$  values based on microsatellites for the three identified genetic clusters from the Parc National du Banc d'Arguin sympatry zone. (+) indicate significance ( $\alpha=0.05$ ).

	<i>A. aureus</i>	<i>A. dumerilii/senegalensis</i>	<i>A. longipes</i>
<i>A. aureus</i>		+	+
<i>A. dumerilii/senegalensis</i>	0.267		+
<i>A. longipes</i>	0.371	0.277	

**Article reference – “Overlooked species diversity in the hyper-arid Sahara Desert unveiled by dryland-adapted lizards”**

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**Supporting Information**

**APPENDIX S3 – Supplementary texts**

**Text S3.1 Ecological variables (extended details).**

The heterogeneity of desert landscapes is poorly represented in land-cover maps (Campos and Brito, 2018). To minimize this issue, for ecological models we used primarily multi-temporal remote sensing variables, derived from pre-processed monthly variables from MODIS sensors of two NASA satellites (EDENext project; data set MODIS v4). These sources provide non-interpolated continuous measurements for the target temporal resolution, and covered the following bands and derived products: middle infra-red [MIR; indicating the water content of the surface (Jensen, 2007)]; day and night time land surface temperatures; normalized difference vegetation index [NDVI (Tucker, 1979)]; and enhanced vegetation index [EVI (Huete et al., 1997)]. Annual and seasonal variations were computed with the ‘dismo’ (Hijmans and Etten, 2012) and ‘raster’ (Hijmans et al., 2012) R packages, using temporal snapshots analogue to bioclimatic predictors [for details, see Ahmadzadeh et al. (2016)]. Additionally, we included the eight precipitation-related bioclimatic variables (bio12–bio19) for current climatic conditions from WorldClim 2.0 (Fick and Hijmans, 2017) and three desert-specific land-cover variables derived from the Globcover dataset (Bicheron et al., 2009): bare areas, consolidated bare areas (*regs*), and non-consolidated bare areas (*ergs*). The land-cover predictors were produced by upscaling the original variable (~300×300 m) to 30 arc-sec resolution (~1×1 km) and calculating the pixel percentage of the target land-cover type at the new scale. All remaining variables were downloaded at 30 arc-sec resolution and cropped to the study area. The complete set of variables describes seasonal changes in environmental conditions in terms of temperature, precipitation, humidity, and vegetation structure, while controlling for the substrate type. Pairwise correlations were assessed based on Spearman’s  $R_2 < 0.7$ , selecting a final subset of 18 low-correlated variables (Table S2.2). The absence of spatial artefacts in the final variables was verified.

**Text S3.2 DNA extraction, amplification, sequencing, and genotyping (extended details).**

Genomic DNA extractions were performed from ethanol-preserved tissues using QIAGEN’s EasySpin Kit and stored at -20°C prior to amplification. The success of DNA extractions was evaluated by electrophoresis on 0.8% agarose gels stained with Gel Red, in TBE 0.5x buffer.

All samples were amplified and sequenced for two mitochondrial fragments, the 12S ribosomal RNA (12S; 368 base pairs) and the cytochrome-b (Cytb; 377 bp), and the nuclear fragment oocyte maturation factor MOS (C-mos; 468 bp). Polymerase chain reactions (PCRs) were performed in 10 µl reaction volumes comprising 5 µl of MyTaq (MyTaq™ Mix; Bioline), 3 µl of ultrapure water, 0.5 µl of forward and reverse primers, and 1 µl of template DNA. Primers and PCR conditions are given in Tables S2.3 and S2.4, respectively. PCR products were cleaned with ExoSAP, and the purification and sequencing for the forward strand was outsourced to MacroGen Inc., NL (<https://www.macrogen-europe.com/>). Chromatograms were verified in GENEIOUS PRO v.4.8.5 (Drummond et al., 2010) and sequences were aligned using MAFFT v.7 (Kato and Standley, 2013). Gene alignments were proofread and the absence of stop codons in coding regions was verified. Topological incongruences between markers were checked by inferring Neighbour-Joining trees for each marker in MEGA v.7 (Tamura et al., 2013).

A set of 22 microsatellites previously developed for the *Scutellatus* group (Lopes et al., 2015) was used to genotype the samples from the sympatry zone. Of those, 14 amplified consistently, were polymorphic, and showed less than 40% of missing data for the target taxa (see Table S2.5 for the final set of markers). PCRs were performed in 10 µl reaction volumes comprising 5 µl of Master Mix, 3 µl of ultrapure water, 1 µl of primer mix, and 1 µl of template DNA. Loci were combined into four multiplexes using varying amounts of primer concentrations (Table S2.4). Microsatellites PCR products were later separated by capillary electrophoresis on an automatic sequencer ABI3130xl Genetic Analyzer (AB Applied Biosystems), using 1 µl of amplification product and 10 µl of formamide + 75-400 (-250) LIZ NEW size standard. Allele calling was performed in GENEMAPPER v4.0 (Applied Biosystems, 2005) and manually checked twice.

### **Text S3.3 Phylogenetic inference (extended details).**

The best-fit models of molecular evolution were inferred in the mt-nuDNA dataset using PARTITIONFINDER v1.1.1 (Lanfear et al., 2012), implementing partitions schemes by gene and the parameters linked branch lengths, mrbayes models, BIC model selection criterion, and greedy search scheme. Bayesian Inference (BI) analyses were performed in BEAST v.1.10.4 (Suchard et al., 2018), after collapsing haplotypes with FABOX (Villesen, 2007). BEAST was run on the CIPRES gateway (Miller et al., 2010) in two independent runs of  $10^8$  generations, sampling at every  $10^4$ , with unlinked substitution and clock models (Drummond et al., 2006), a constant population size coalescent tree prior (Kingman, 1982), and considering ambiguities in the nuclear partition (manually editing the .xml file to Ambiguities = true). Detailed settings are given in Table S2.7. The convergence of chains and Effective Sample Sizes higher than 200 for all parameters was verified using TRACER v.1.7.1 (Rambaut et al., 2018). Log and tree files of the independent runs were combined using LOGCOMBINER and the subsequent maximum clade credibility summary tree with posterior probabilities for each node, using mean values, was obtained using TREEANNOTATOR (both from the BEAST package). The resulting trees were visualised and edited with FIGTREE v.1.4.3 (Rambaut, 2016). To complement the BI assessment, Maximum Likelihood (ML) analyses were performed in the mt-nuDNA dataset using RAXMLGUI (Silvestro and Michalak, 2012). A bootstrapping tree was built based on 1,000 rapid bootstrap replications, GTR+G+I substitution model and rates, and a nearest-neighbour interchange heuristic method. BI and ML nodes were considered supported if they received a posterior probability > 0.95 or bootstrap support > 85 respectively.

### **Text S3.4 Ecological niche modelling (extended details).**

Three regression-based (GAM, generalized additive models, GBM, generalized boosting models; and GLM, generalized linear models) and three machine learning-based (ANN, artificial neural networks; CTA, classification tree analysis; and MAXENT.Philipps, maximum entropy) algorithms were chosen to reduce the uncertainties associated with modelling techniques (Thuiller et al., 2019). All models were run using default parameters. Background areas for each species were limited by a radial buffer of 500 km from presence records, to avoid excessive biases towards regions with no occurrence when selecting pseudo-absences (Anderson and Raza, 2010). As pseudo-absences, 10,000 random points were sampled randomly from the buffer area, with a minimum distance of 10 km from presence records (Barbet-Massin et al., 2012).

Ten model replicates were run for each of the six algorithms for each species, and each of them was subsequently rescaled using a binomial GLM (an internal routine from the biomod2 package to make the

single models comparable). Presence data for each model replicate were selected randomly by cross-validation, using 80% of data for training. Individual model replicate performance was evaluated using true skill statistic (TSS) metric (Allouche et al., 2006) and the area under the receiver operating characteristic curve (AUC; Fielding & Bell, 1997). Across all potential models, only those with AUC scores > 0.7 were combined in a final ensemble model, weighted proportionally according to predictive performance (Marmion et al., 2009). The contributions of the environmental variables to the ensemble models by algorithm were evaluated by averaging the relative contribution to individual model replicates.

### **Text S3.5 Microsatellite analyses (extended details).**

Bayesian clustering analyses were conducted using STRUCTURE 2.3.4 (Pritchard et al., 2000). The admixture model was used, assuming correlated allele frequencies, and without incorporation of sampling localities. Ten runs were carried out for each K value, from 1 to 8 (exceeding the number of intra-specific lineages detected with the phylogenetic analyses), with an initial burn-in of 200,000 iterations and additional  $10^6$  iterations after the burn-in. STRUCTURE HARVESTER v.0.6.94 (Earl, 2012) was used to estimate the optimal number of clusters (K) through the examination of  $\ln p(X|K)$  as well as the  $\Delta K$  (Evanno et al., 2005; Pritchard et al., 2000). The results were averaged across runs using CLUMPP v.1.1.2 (Jakobsson and Rosenberg, 2007). Genetic differentiation ( $F_{ST}$ ) among the resultant clusters were computed in ARLEQUIN (Excoffier and Lischer, 2010) using the Weir and Cockerham's estimator  $\Theta$ , performing 10,000 permutations to test for significance. Factorial Correspondence Analyses (FCoA) on individual genotypes were run in GENETIX (Belkhir et al., 2004) using default options, to visualize the relationships among clusters.

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**Supporting Information**

**APPENDIX S4 – Supplementary files (captions)**

**File S4.1** Updated range for *Acanthodactylus dumerilii/senegalensis* in format .shp.

**File S4.1**

*--- Uploaded as a separate ZIP file ---*