The common chameleon Chamaeleo chamaeleon in southern Italy: evidence for allochthony of populations in Apulia and Calabria (Reptilia: Squamata: Chamaeleonidae)

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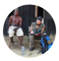

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The common chameleon *Chamaeleo chamaeleon* in southern Italy: evidence for allochthony of populations in Apulia and Calabria (Reptilia: Squamata: Chamaeleonidae)

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Abstract

The common chameleon *Chamaeleo chamaeleon* is present in many Mediterranean countries. Its occurrence in Italy is historically reported for Sicily, where it appears to be no longer present. While many contemporary findings across the Italian Penisula refer to single observations, likely due to introduced or released animals, the species turned out to be established in two southern regions (Apulia and Calabria) with acclimatised populations. To investigate their provenance, we analysed tissue samples of individuals from these localities. A fragment of the mitochondrial 16S rRNA gene was amplified and compared with sequences available in Genbank. Our results showed that individuals from Calabria share haplotypes with those from Tunisia (N. Africa), while those from Apulia are coincident to samples from Israel. This suggests that individuals were most likely introduced in Italy.

Keywords: *Allochthonous species,* Chamaeleo chamaeleon*, Chamaeleonidae, Italy*

Introduction

The common chameleon *Chamaeleo chamaeleon* (Linnaeus, 1758) is a saurian widely distributed in the Mediterranean Basin. According to Necas (1999), Glaw (2015) and Uetz (2016) it is present in or has been reported for Algeria, Cyprus, Egypt, Greece, Iran, Iraq, Israel, Italy, Jordan, Lebanon, Libya, Malta, Morocco, Palestine, Saudi Arabia, South Portugal, Spain, Turkey, Syria, Tunisia and Yemen. It is noteworthy that some of these findings refer to escaped/ sporadic individuals and to acclimatised populations derived from the importation of individuals from other localities. This is due to the fact that chameleons are peculiar and attractive reptiles, which have been always the objects of particular attention by local people, who traded them as pets. As a consequence, *C. chamaeleon* has been repeatedly released in private gardens and other sites, and sometimes succeeded in establishing reproductive populations. A similar situation was also observed for another allochthonous species, *C. africanus*, which occurs in mainland Greece, but which was introduced in historical times (Böhme 1989; Kosuch et al. 1999; Dimaki et al. 2008).

The genetic variation of *C. chamaeleon* across its entire native distribution has not been adequately investigated, and because of this the origin of several European localities is still not clear. Many papers are available on the topic, and populations of *C. chamaeleon* from Spain, Portugal, Malta and Italy appear to be the result of repeated introductions and acclimatisations (Arnold & Ovenden 2002; Razzetti & Sindaco 2006; Sindaco & Jeremenko 2008; Tilbury & Tolley 2009; Tilbury 2010; Glaw 2015). The species can be locally abundant in some European localities, namely in Andalucia (Spain) and Algarve (Portugal), where populations turned out to be the result of at least two introductions, one of which

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The presence of common chameleons was repeatedly reported for Italy (e.g. Razzetti & Sindaco 2006; Sindaco & Jeremenko 2008; Corti et al. 2011; Di Cerbo & Di Tizio 2011), and the species was usually listed as present (at least in the past) in Sicily (Bruno & Maugeri 1976; Gasc et al. 1997; Arnold & Ovenden 2002), although its acclimatisation was never confirmed (Razzetti & Sindaco 2006; Sindaco & Jeremenko 2008). More recently, apparently acclimatised populations were reported in two other regions, Apulia and Calabria (Basso & Calasso 1991; Fattizzo 1996; Fattizzo & Marzano 2002; Sperone et al. 2010). In this contribution we aim to (1) provide an overview of findings in Italian territory, (2) confirm the specific attribution of Apulian and Calabrian populations, and (3) test their origin using molecular methods.

Material and methods

Literature and museological research

We searched for information about chameleons in Italy by looking for published papers, within natural history museum collections, and on the Internet. We also consulted observation data available in the archives of Museo di Storia Naturale del Salento. These data were also supported by presence of preserved individuals (currently housed within the herpetological collection of Museo di Storia Naturale, Venice; see below).

Morphological comparison

Morphological comparisons were carried out with some selected specimens from the collection of Zoological Museum of Turin University, now managed by Museo Regionale di Scienze Naturali, Turin (Andreone & Gavetti 2010), such as: MZUT R1348.1–27, Libya, Tarabulus, Tripoli; MZUT R1344.1–4, Tunisia; MZUT R1333.1–6, Libya, Tarabulus, Gharyan.

Molecular analysis

We analysed tissue samples (tail tips) from eight individuals found in 2015: three from Nardò (Lecce Province, Apulia, Italy), and five from Palmi (Reggio Calabria Province, Calabria, Italy). We also performed DNA extractions from the preserved specimens housed in the Museo di Storia Naturale (Venice), and from a specimen held in the collection of Dipartimento di Biologia, Ecologia e Scienze della Terra (Calabria University). Two samples of *C. chamaeleon* from Cadiz (Spain) were used for comparison.

Total genomic DNA was extracted using proteinase K digestion (10 mg/mL concentration) followed by a standard salt extraction protocol (Bruford et al. 1992). We sequenced a fragment of ca. 550 bp of the 3′ terminus of the mitochondrial rrnL (large ribosomal RNA, or 16S rRNA gene). For primers and cycling protocols, see Crottini et al. (2009). Standard polymerase chain reactions (PCR) were performed in a final volume of 11 μL and using 0.3 μL each of 10 pmol primer, 0.25 μL of total dNTP 10 mM (Promega), 0.08 μL of 5 U/mL GoTaq, and 2.5 μL 5X Green GoTaq Reaction Buffer (Promega). Successfully amplified PCR products were treated to inactivate remaining primers and dNTPs. Purified PCR templates were sequenced using dye-labelled dideoxy terminator cycle sequencing on an ABI 3130 automated DNA sequencer or on an ABI 3730xl at Macrogen Inc.

Our sequences were compared with GenBank sequences, and chromatographs were visually checked and edited, when necessary, using Bioedit version 7.0.9 (Hall 1999). This alignment required the inclusion of gaps to account for indels in only a few cases. For Genbank accession numbers of the sequences used, see Table I and Figure 1.

Molecular analyses included sequences of *C. chamaeleon* from Apulia and Calabria (Italy) and Cadiz (Spain), and all homospecific sequences with information on locality of origin available in Genbank (see Table I). Homologous 16S rRNA gene sequences of three individuals of *C. africanus* from Chad, Niger and Greece, and one sequence of an individual of *C. calcaricarens* from Somalia, were added to the rrnL gene fragment alignment for outgroup rooting in the phylogenetic analyses. The purpose of the presented phylogenetic analyses is just to show the closest relationship of the Italian populations to the populations of *C. chamaeleon* originating from Tunisia and Israel, rather than to provide a strong phylogenetic hypothesis of the relationships among the *C. chamaeleon* samples analysed in this study. Analysed samples were grouped following their geographic origin, with the exception of the populations from Spain, Portugal and Malta, whose introduction has already been proven in previous studies (Paulo et al. 2002; Dimaki et al. 2008). Italian populations were grouped into two distinct groups. Full details on the grouping strategy used are provided in Table I and Figure 1. Uncorrected pairwise distances (p-distance transformed into percentage using the pairwise distance option) within individuals of the same group and between individuals of different groups analysed in this

Table I. List of samples included in the present study for molecular analyses, with: species identification, localities, grouping strategy used for the computation of genetic distances, and GenBank accession numbers. Sequences newly determined for this study are in bold.

Species	Subspecies	Country	Locality	Grouping	16S
C. chamaeleon	_	Italy	Lecce, Nardò, Pagani	Apulia	**KX118428**
C. chamaeleon	_	Italy	Lecce, Nardò	Apulia	**KX118429**
C. chamaeleon	_	Italy	Lecce, Nardò	Apulia	**KX118430**
C. chamaeleon	_	Italy	Calabria	Calabria	**KX118431**
C. chamaeleon	_	Italy	Calabria	Calabria	**KX118432**
C. chamaeleon	_	Italy	Reggio Calabria, Palmi	Calabria	**KX118433**
C. chamaeleon	_	Italy	Reggio Calabria, Palmi	Calabria	**KX118434**
C. chamaeleon	_	Italy	Reggio Calabria, Palmi	Calabria	**KX118435**
C. chamaeleon	*recticrista*	Israel	Magen Shaul	Israel North 1	JF317645
C. chamaeleon	*recticrista*	Israel	Baram	Israel North 1	JF317644
C. chamaeleon	*recticrista*	Israel	Shamir	Israel North 1	JF317642
C. chamaeleon	*recticrista*	Israel	Haon	Israel North 2	JF317643
C. chamaeleon	*recticrista*	Israel	Oosha	Israel South 1	JF317641
C. chamaeleon	*recticrista*	Israel	Habonim	Israel South 1	JF317639
C. chamaeleon	*recticrista*	Israel	Jerusalem	Israel South 2	JF317640
C. chamaeleon	*musae*	Israel	Revivim	Israel Malta musae South 3	JF317638
C. chamaeleon	*musae*	Israel	Kmehin	Israel Malta musae South 3	JF317637
C. chamaeleon	*musae*	Israel	Ramatbeka	Israel Malta musae South 3	JF317636
C. chamaeleon	_	Malta	Ghadira Bay	Israel Malta musae South 3	FM162017
C. chamaeleon	*musae*	Israel	Avshalom	Israel Yemen musae South 4	JF317635
C. chamaeleon	_	Yemen	Bani Hushaysh	Israel Yemen musae South 4	EF222199
C. chamaeleon	_	Cyprus	Alaykoy	Turkey Cyprus Greece	EF222200
C. chamaeleon	_	Greece	Samos	Turkey Cyprus Greece	FM162018
C. chamaeleon	_	Turkey	Hatay Province	Turkey Cyprus Greece	EF222202
C. chamaeleon	_	Turkey	Anamur Icel Province	Turkey Cyprus Greece	EF222201
C. chamaeleon	_	Tunisia	Tunis	Tunisia	FM162019
C. chamaeleon	_	Marocco	El Jadida	Portugal Morocco Spain	AF372127
C. chamaeleon	_	Portugal	Cabanas	Portugal Morocco Spain	EF222198
C. chamaeleon	_	Spain, Portugal, Marocco	Algarve, Huelva, Essauira, El Jadida	Portugal Morocco Spain	AF372128
C. chamaeleon	_	Spain	Cadiz	Portugal Morocco Spain	**KX118436**
C. chamaeleon	_	Spain	Cadiz	Portugal Morocco Spain	**KX118437**
C. chamaeleon	_	Malta	Ghadira Bay	Malta Morocco Malaga	FM162016
C. chamaeleon	_	Morocco	Erfoud	Malta Morocco Malaga	AF372129
C. chamaeleon	_	Morocco	Erfoud	Malta Morocco Malaga	AF372131
C. chamaeleon	_	Morocco	Al Hoceima	Malta Morocco Malaga	AF372133
C. chamaeleon	_	Morocco	Erfoud	Malta Morocco Malaga	AF372130
C. chamaeleon	_	Spain, Morocco	Malaga, Al Hoceima	Malta Morocco Malaga	AF372132
C. calcaricarens	_	Somalia	_	calcaricarens	EF222195
C. africanus	_	Niger	_	africanus	EF222197
C. africanus	_	Greece	_	africanus	AF121960
C. africanus	_	Chad	_	africanus	AF121955

study were computed using MEGA, version 6.06 (Tamura et al. 2013).

Bayesian inference searches of the mitochondrial 16S rRNA gene fragment were conducted in MrBayes 3.2.1 (Ronquist et al. 2012). The simple Jukes and Cantor model of substitution was used to avoid overparameterisation in the analyses of this short gene segment. We performed two runs of 10 million generations (started on random trees) and four incrementally heated Markov chains (using default heating values), sampling the Markov chains at intervals of 1000 generations. Stabilisation and convergence of likelihood values were checked by visualising the log likelihoods associated with the posterior distribution of trees in the software Tracer (Rambaut & Drummond 2007), and occurred after about 2.5–3 million generations. The first 3 million generations were therefore discarded, and 7 million trees were retained post burn-in and summarised to generate a majority rule consensus tree (Figure 1).

Results

An overview of common chameleons in Italy

In Italy, several historical records referring to single (likely escaped or deliberately released) chameleons

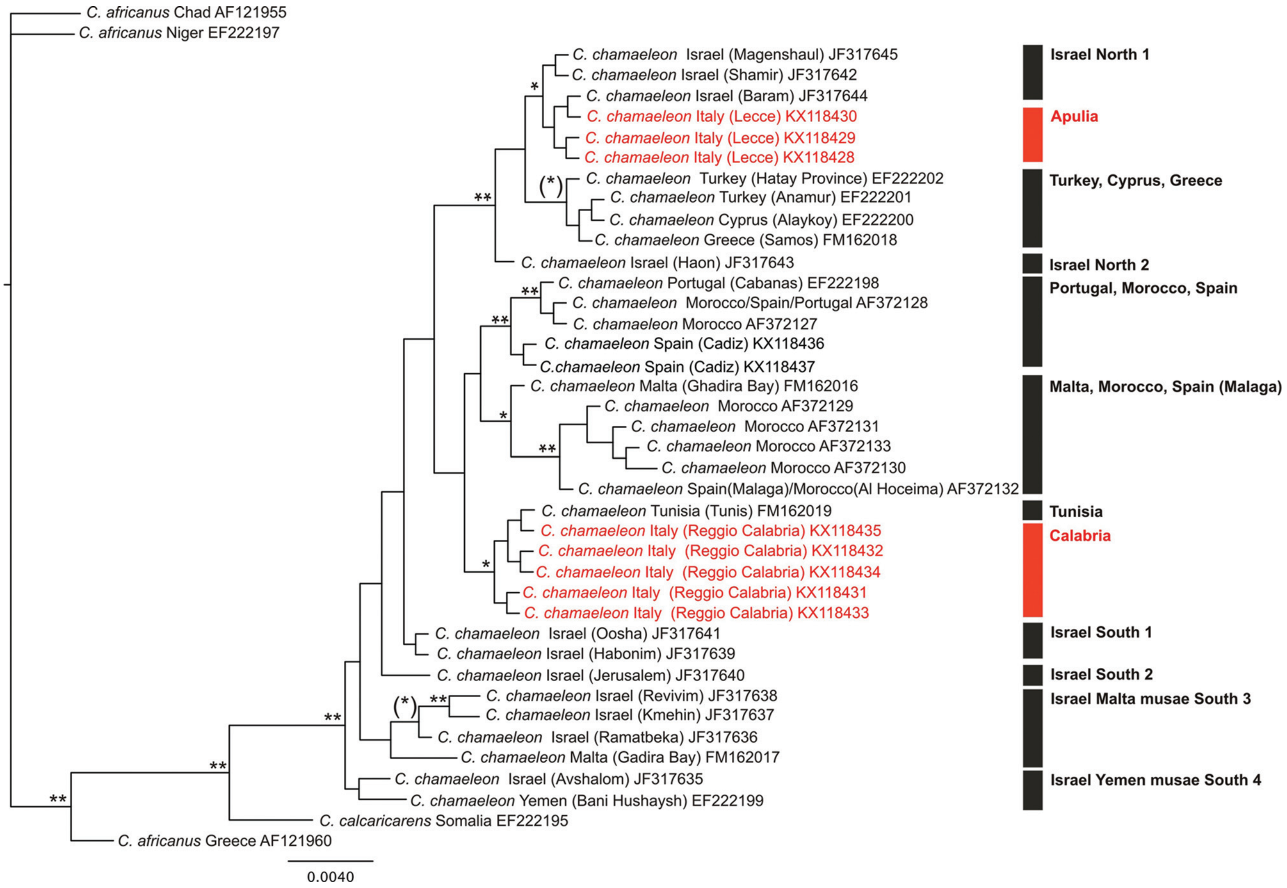

Figure 1. Bayesian inference tree of *Chamaeleo chamaeleon* and the two outgroup species based on 522 bp of the mitochondrial 16S rRNA gene fragment. Asterisks indicate Bayesian posterior probabilities values: (*): 97–98%; *: 99%; **: 100%.

are available. These include bibliographically quoted observations for Emilia Romagna (Di Cerbo & Di Tizio 2011), Friuli – Venezia Giulia (Lazzarini 1897), and Latium (Bologna et al. 2000). Further Internet quotes (e.g. Caroppo 2014) also report unverified findings in Liguria, Sardinia and the Po Delta area.

As already stated, the common chameleon has been repeatedly reported in Sicily (e.g. Bruno & Maugeri 1976; Gasc et al. 1997; Arnold & Ovenden 2002). All of this information is mostly referable to the findings of Monte Pellegrino (Palermo) which is reported back to the 19th century by Grohmann (1832). Other scattered data for Sicily included Catania (Biondi Giunta 1863; Doderlein 1871, 1881; De Betta 1874), Siracusa province and some further imprecise localities (Bruno & Maugeri 1976). However, neither the Italian herpetological atlas (Sindaco et al. 2006) nor the monographic reptile contribution within the "Fauna d'Italia" (Corti et al. 2011) confirmed the species exists in Sicily. Moreover, our search in major natural history museums did not provide any record of specimens collected in Sicily, and there is no evidence of recent observations either (Razzetti & Sindaco 2006; Sindaco & Jeremenko 2008).

According to Di Cerbo and Di Tizio (2011), preserved specimens of *C. chamaeleon* with verified Italian provenance are currently known from Emilia Romagna, Latium, Apulia and Calabria.

The quote for Emilia Romagna refers to a single individual found in Carpi (Modena), likely escaped from captivity or accidentally imported. This specimen is currently housed in the Museo Civico di Ecologia e Storia Naturale di Marano sul Panaro under the collection number 470/SL/31-9-2000.

The finding from Latium is relative to a female collected in November 1990 in Maccarese (Rome) and currently housed in the collection of Museo Civico di Zoologia di Roma (MCZRV R/01501). This finding is likely coincident with the one reported by Bologna et al. (2000) for Fiumicino (Rome), since the two localities are quite close. In the same contribution, another observation refers to Latium, notably to Tor San Lorenzo (Rome), but is not supported by any preserved specimen.

Repeated chameleon observations come in the last few decades from Apulia and Calabria, as reported by Basso and Calasso (1991), Fattizzo (1996), Fattizzo and Marzano (2002), Marzano and Scarafino (2010) and Sperone et al. (2010).

Findings of adult individuals have been reported in Apulia since the 1980s, mostly for Nardò (Lecce Province) surroundings (Figures 2–3). These were also confirmed by museum specimens, photographs/videos reported in books, local newspapers, Web news and direct observations. Older museum specimens also refer to Gallipoli (Lecce Province), but were not supported by recent findings. Preserved specimens are now housed in Museo di Storia Naturale, Venice, as follows: MSNVE-24030, one specimen, June 1951, Gallipoli (Lecce), found in a warehouse of a former pharmacy on 20 October 1988; MSNVE-24031, two specimens (likely male and female), Nardò (Lecce), July 1988, found dead in an olive grove, likely due to pesticide poisoning; MSNVE-24032, one specimen (pregnant female), Gallipoli (Lecce), 12 August 1989; MSNVE-24033, eggs laid in the Museum of Natural History, Calimera (Lecce); 13 August 1989; MSNVE-24034, one specimen without precise locality (likely from Salento area). Collectors and donors for these specimens were not available.

Observations in Calabria were first documented by Sperone et al. (2010) for Palmi (Reggio Calabria) surroundings and were also subsequently reported in the "Fauna d'Italia" by Di Cerbo and Di Tizio (2011). Acclimatisation was supported by regular observation of adults and juveniles in the subsequent years by one of us (ST) and by local naturalists. One individual is currently housed in the herpetological collection of Dipartimento di Biologia, Ecologia e Scienze della Terra, Arcavacata di Rende, as follows: CHCH001, one specimen from Palmi (Reggio Calabria), leg. P. Paolillo, 1994.

Figure 2. Indicative localisations of sampling sites of *Chamaeleo chamaeleon* in Apulia and Calabria (Italy), where the acclimatised populations were reported.

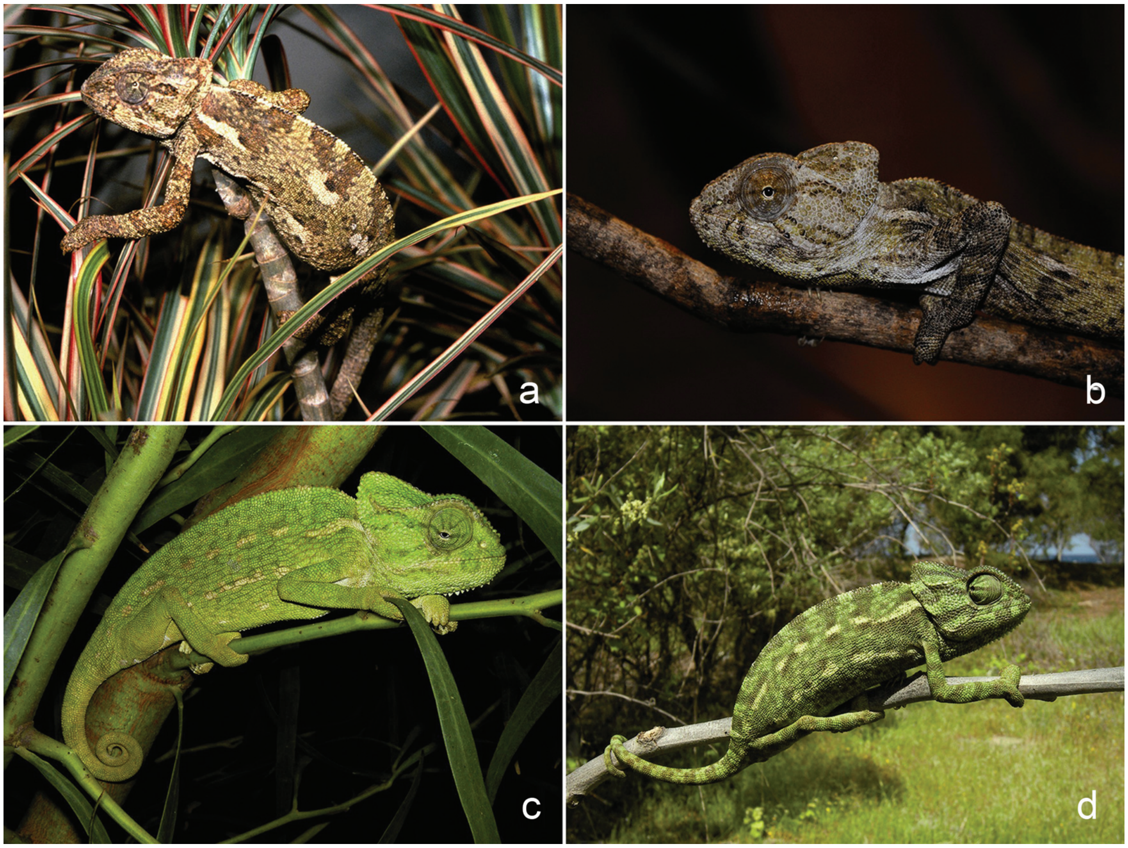

Figure 3. Live individuals of *Chamaleo chamaeleon* from acclimatised Italian populations. **a**, One of the first findings of common chameleons in Italy: A female from Nardò surroundings (Lecce Province, Apulia; photographed in Turin on 21 December 1987); **b**, a female from Nardò; **c**, a male from Palmi (Reggio Calabria Province, Calabria) surroundings (photographed on 29 April 2014); **d**, a female from Palmi surroundings. Photos by F. Andreone (A), P. Carlino (B), B. Bok (C, D).

Taxonomic attribution and haplotype sharing

The DNA extraction from specimens housed in collections and museums did not yield any positive result, likely due to bad sample preservation and use of inappropriate fixative liquids. On the other hand, all recent samples collected from live individuals were successfully amplified and sequenced, confirming the attribution of the chameleon populations from Apulia and Calabria to *C. chamaeleon*. Samples from Calabria share the same 16S rRNA sequence among them and also with an individual originating from Tunisia (Tunis, Genbank accession number FM162019). Similarly, the three analysed samples from Nardò (Apulia) are genetically uniform and share the same 16S rRNA haplotype with three samples of *C. chamaeleon* from northern Israel: populations of Shamir, Baram and Magen Shaul (Genbank accession numbers JF317642, JF317644, JF317645, respectively) (Figure 1; Table II). Interestingly, samples of Apulia and Calabria are also different from each other, showing an uncorrected p-distance of 0.8%, and, due to the low genetic variability observed for this gene fragment in this species (the maximum genetic distance observed between the analysed samples of *C. chamaeleon* is 1.5%), we deduce that these two populations have an independent origin. More details on genetic distances within the analysed populations of *C. chamaeleon*, and between them and the two other species used for outgroup rooting (*C. africanus* and *C. calcaricares*), are provided in Table II.

Discussion

Our study demonstrated that among the chameleon observations in Italy, only those from Apulia and Calabria refer to reproductively active *C. chamaeleon* populations. To our knowledge, all the other findings are referable to released/escaped individuals. We also excluded from contemporary observations the data for Sicily, although we cannot exclude that the species was present in the past, as reported by a well-

Table II. Within- (bold) and among-group genetic divergence values of the analysed 16S rRNA mitochondrial gene fragment, based on estimated uncorrected pairwise distance. The genetic distances of the Apulia and Calabria populations against all other defined groups are highlighted in black and light grey, respectively. The identity of the Apulia and Calabria populations with the Israel North 1 and the Tunisia groups is highlighted in dark grey.

	Chamaeleo chamaeleon													
	Italy Apulia	Italy Calabria	Israel North 1	Israel North 2	Israel South 1	Israel South 2	Israel Malta musae South 3	Israel Yemen musae South 4	Turkey Cyprus Greece	Tunisia	Portugal Morocco Spain	Malta Morocco Malaga	*Chamaeleo calcaricarens*	*Chamaeleo africanus*
Italy Apulia	**0%**													
Italy Calabria	0.80%	**0%**												
Israel North 1	0%	0.80%	**0%**											
Israel North 2	0.20%	0.60%	0.20%	_										
Israel South 1	0.80%	0.40%	0.80%	0.60%	**0%**									
Israel South 2	1.20%	0.80%	1.20%	1.00%	0.40%	_								
Israel Malta musae South 3	1.50%	1.10%	1.50%	1.30%	0.70%	0.90%	**0.60%**							
Israel Yemen musae South 4	0.90%	0.90%	0.90%	0.90%	0.50%	0.70%	0.90%	**0.60%**						
Turkey Cyprus Greece	0.40%	0.80%	0.40%	0.60%	0.80%	1.20%	1.50%	0.90%	**0%**					
Tunisia	1.00%	0%	1.00%	0.70%	0.50%	1.00%	1.20%	1.10%	1.00%	_				
Portugal Morocco Spain	1.40%	0.60%	1.40%	1.20%	0.50%	1.00%	1.20%	1.10%	1.40%	0.60%	**0.10%**			
Malta Morocco Malaga	1.30%	0.80%	1.30%	1.00%	0.80%	1.30%	1.50%	1.10%	0.90%	0.90%	0.80%	**0.30%**		
C. calcaricarens	2.90%	2.50%	2.80%	2.60%	2.00%	2.20%	2.40%	2.10%	2.80%	2.70%	2.30%	2.80%	_	
C. africanus	3.90%	3.90%	3.80%	3.60%	3.40%	3.80%	4.00%	3.60%	3.70%	4.50%	3.80%	3.70%	3.00%	1.30%

documented reference (Grohmann 1832), but we do not have any evidence whether the species was acclimatised.

Our analysis of the 16S rRNA mitochondrial gene fragment revealed some patterns which help in unveiling the origins of the Apulia and Calabria populations. In fact, the individuals from Apulia shared the haplotype with populations from Levant, and particularly with those from N. Israel. Individuals from this area were originally described as *C. c. recticrista* Boettger, 1880, based upon the holotype coming from Jerusalem (Yaacov et al. 2012; Glaw 2015). According to Tilbury and Tolley (2009) this subspecies is present in northern Israel and the northern part of the Levant (e.g. Turkey). Although *C. c. recticrista* is apparently distinguishable from *C. c. chameleon* for some morphological characters (e.g. straighter and less convex parietal crest, more prominent occipital lobes, larger body size and tarsal spurs present in some males), in the absence of a thorough comparative analysis it is difficult to ascertain whether *C. c. recticrista* is still a valid taxon, and for this reason we refrain from attributing the Apulian chameleons to this taxon.

Taken into account that the historical trade with southern Italy mostly involved North Africa, it was also difficult to believe that the Apulian population is the result of a palaeointroduction (*sensu* Amori & Lapini 1997) from Levant. We therefore searched for alternative evidence for the sources of provenance of these animals. Interviewing local people, we got confirmation that an Italian soldier was in service in Lebanon with the Italian Army in 1982 and kept in captivity a small group of chameleons in his barracks. When he went back to Italy (Nardò) he took with him some of these animals, which were kept as pets. Following this, the chameleons (which included some pregnant females) escaped and/or were released. According to original declarations, after some months he found chameleon newborns in the surroundings of his house, where presumably the adults settled. The first documented observations of a wild *C. chamaeleon* in Apulia date back to 1987. At that time an adult female was imported from Nardò to Turin (Piedmont, NW Italy) in November 1987 and subsequently photographed (but not conserved) by the first author (Figure 3A). This most likely refers to one of the first chameleons found in nature in this locality. Two adults from Nardò collected in July 1988 are currently housed in Venice and confirm that their acclimatatisation likely occurred in the late 1980s. Taking into account the genetic analysis and the historical reconstruction, we conclude that the population of *C. chamaeleon* in Apulia originated from at least one introduction event with individuals from Lebanon. The acclimatisation is also proved by the long extension of observations (Figure 4), which surpass the mean life span of the species (Marzano & Scarafino 2010).

The haplotype of the Calabrian individuals is coincident with the one of a chameleon from Tunisia, thus suggesting that the species' presence in Calabria is due to importation from N. Africa. Obviously, more analyses are needed to understand whether this population is the result of a recent introduction or if it is ancient and can be considered a palaeointroduction. This hypothesis finds further support in the fact that several elements of the Italian herpetofauna are likely the result of ancient introductions. This is the case, for example, for many tortoises (*Testudo* spp.) in Sardinia and several other sites on the Italian mainland (Fritz et al. 2009), for the gecko *Cyrtopodion kotschi* in Apulia (Picariello & Scillitani 1988) and for the treefrog *Hyla meridionalis* in NW Italy (Stöck et al. 2008). The recently found sand boa *Eryx jaculus* is also considered a possible palaeointroduced element for Sicily (Insacco et al.

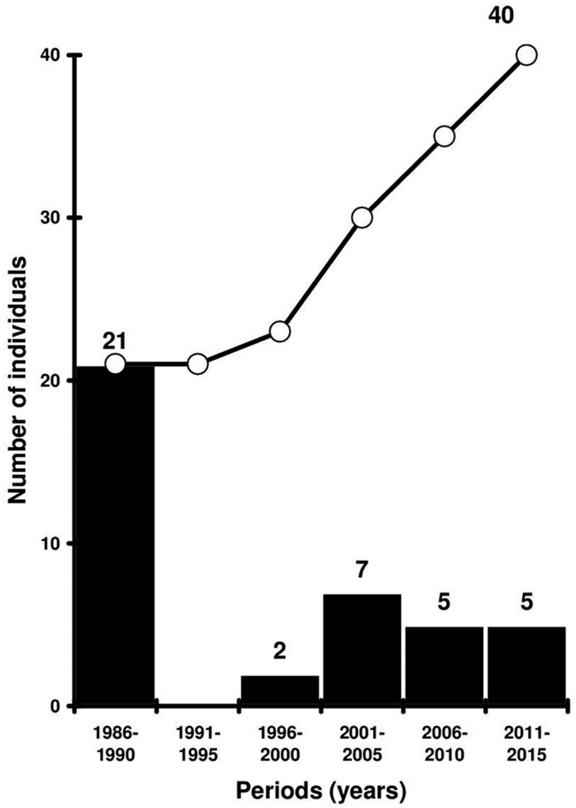

Figure 4. Number of findings of individuals of *Chamaeleo chamaeleon* for Nardò surroundings (Apulia), as obtained after consultation of data available in Museo di Storia Naturale del Salento and published information in Marzano and Scarafino (2010). Data are reported by year (histograms) and cumulative numbers (line).

2015). The evidence that chameleons in Italy derive from recent introductions is supported by the absence of fossil records from Italian sites despite a former broad distribution that included even Germany (Georgalis et al. 2016). Remarkably, all the acrodont lizards found so far in Italian sites are clearly referable to agamids and not to chamaeleonids (Delfino et al. 2008). This supports the allochthony of Italian populations, similar to what is observed for Portugal, Spain and Malta (Sindaco & Jeremenko 2008; Glaw 2015).

Finally, special consideration must be given for the management of Calabrian and Apulian populations of chameleons, similar to what was expressed for the African chameleon *C. africanus* in Greece (Böhme et al. 1998). Repeated observations of chameleons in Apulia indicate that the animals are currently rather common and abundant. Data obtained from published information (Marzano & Scarafino 2010) and from the database of Museo di Storia Naturale del Salento also show a good number of collected individuals from the 1980s (40 documented observations). The same is also true for Calabria where the individuals are easily found and the observation record is conspicuous. For this reason, it is now necessary to investigate more accurately the current species boundaries and distribution, as unpublished observations suggest that the areas could be wider than currently known. Finally, the impact on local fauna must be carefully ascertained, now taking into account the species' allochthony and its potential invasivity (Sciberras 2007).

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