

Resampling Bouché's historical localities reveals three new species and helps identifying a new genus of earthworms (Oligochaeta, Hormogastridae and Lumbricidae) in Southeastern France

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1	Resampling Bouché's historical localities reveals three new species and helps identifying
2	a new genus of earthworms (Oligochaeta, Hormogastridae and Lumbricidae) in
3	Southeastern France.

Le rééchantillonnage des localités historiques de Bouché permettent la découverte de trois
nouvelles espèces et d'un nouveau genre de vers de terre (Oligochaeta, Hormogastridae
et Lumbricidae) dans le Sud-Ouest de la France.

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16 The present paper has not been submitted to another journal, nor will it be in the 6 months after

17 initial submission to *Zoosystema*. All co-authors are aware of the present submission.

18

19 ABSTRACT

20 Southern France has been highlighted as an important hotspot of earthworm diversity mostly by the work of Marcel Bouché, who sampled more than 1300 localities in mainland 21 France including Corsica in the 1960s. We resampled some of the Bouché's localities and 22 23 conducted molecular phylogenetic analysis. It leads to the identification of a new Lumbricidae genus (Flabellodrilus n. gen.), for which Allolobophora bartolii should be the type species, 24 improving the clarity of the catch all genus Allolobophora. It also allowed us to discover two 25 new species of Lumbricidae (Flabellodrilus luberonensis n. sp. and Allolobophora delitescens 26 n. sp.), and one new species of Hormogastridae (Vignvsa callasensis n. sp.). These three new 27 species underline the great earthworm diversity of southeastern France. Their discovery in a 28 previously well-sampled area further suggests that these species have narrow geographic ranges 29 and small populations. They also seem to be specialized for open habitats that are declining in 30 31 the French Mediterranean landscape. These different characteristics suggest a relatively high risk of extinction for these three new species. 32

33 KEYWORDS

34 Earthworms, new species, *Flabellodrilus* n. gen., *Allolobophora*, *Vignysa*, France

35 RÉSUMÉ

36 Le sud de la France est considéré comme un point chaud de diversité pour les vers de terre, comme mis en évidence par le travail de Marcel Bouché, qui a échantillonné plus de 1300 37 localités en France métropolitaine incluant la Corse dans les années 1960. Nous avons ré-38 échantillonné certaines de ces localités et réalisé des analyses phylogénétiques moléculaires. 39 Ce travail nous a conduit à identifier un nouveau genre de Lumbricidae (*Flabellodrilus* n. gen.) 40 dont l'espèce type devrait être Allolobophora bartolii, ce qui apporte plus de clarté pour le genre 41 42 "fourre-tout" Allolobophora. Cela nous a également permis de découvrir deux nouvelles espèces de Lumbricidae (Flabellodrilus luberonensis n. sp. et Allolobophora delitescens n. sp.), 43

ainsi qu'une nouvelle espèce d'Hormogastridae (*Vignysa callasensis* n. sp.). Ces trois nouvelles
espèces soulignent l'importante diversité de vers de terre dans le sud-est de la France. Leur
découverte dans une région précédemment bien échantillonnée suggère une aire de répartition
géographique restreinte et de petites populations pour ces espèces. Elles semblent par ailleurs
spécialisées dans les habitats ouverts qui tendent à diminuer dans les paysages méditerranéens
français. Ces différentes caractéristiques suggèrent un risque d'extinction relativement élevé
pour ces trois nouvelles espèces.

51 MOTS CLES

52 Vers de terre, espèces nouvelles, *Flabellodrilus* n. gen., *Allolobophora*, *Vignysa*, France

53

54 INTRODUCTION

South West Europe is recognised as a diversity hotspot for earthworms, with France, 55 Spain and Italy being the most diverse countries at the continent scale in terms of number of 56 species (Brown et al. 2023; Misirlioğlu et al. 2023; DriloBASE taxo). South Western Europe 57 is also considered to be the origin and one of the centers of diversification of the family 58 Lumbricidae Rafinesque-Schmaltz, 1815 (Omodeo & Rota 2008), and the only area of 59 particular genera (e.g. Scherotheca Bouché, 1972, Gatesona Qiu & Bouché, 1998a, 60 61 Prosellodrilus Bouché, 1972) and of the whole family Hormogastridae Michaelsen, 1900 (Marchán et al. 2018). 62

At a smaller scale, Southern France has a regional diversity and a proportion of endemics 63 higher than anywhere else in the country (Bouché 1972; Rota 1994; Qiu & Bouché 1998b, 64 65 1998c, 1998d, 1998f; Marchán et al. 2020). This was in particular highlighted by the historical work of Bouché (1972) who sampled earthworms in 1363 localities in mainland France and 66 Corsica Island during the 1960s. This extensive sampling served as a basis for his monography 67 of French earthworms (i.e. "Lombriciens de France") in which he synthesized all the knowledge 68 of the time and described a number of species new to science. Since this major publication, it 69 was commonly admitted that France was one of the temperate countries with the best known 70 earthworm fauna. Fifty years later, the project #Vers2022 aimed at resampling Bouché's 71 localities to assess how earthworm distribution and community patterns have changed after 50 72 years of global change. The sampling effort carried out as part of this project also provided 73 fresh samples that are now used to build molecular phylogenies and to search for undescribed 74 species. This resulted in the discovery of several species new to science like for instance in the 75 genus Scherotheca (Marchán et al. 2022, 2023a, 2023b). 76

In this study, we describe one new genus (*Flabellodrilus* n. gen) and two new species of
Lumbricidae (*Flabellodrilus luberonensis* n. sp., *Allolobophora delitescens* n. sp.), and one new

species of Hormogastridae (*Vignysa callasensis* n. sp.) that were discovered during the resampling of Bouché's localities in southeastern France.

81 MATERIAL and METHODS

82 EARTHWORM SAMPLING

The specimens of the newly described species were sampled as part of the #Vers2022 project. The descriptions of the localities are given in Table 1, along with the other species found in those samples. The sampling method consisted of soil digging and hand-sorting. The specimens were then washed with water and fixed in 99% ethanol for long-time storing and molecular analyses.

TABLE 1. – List, geolocation and habitat cover of the type localities of three new earthworm
species in Southeastern France (Provence–Alpes–Côte d'Azur).

	Teer	Coordinates	Code in Bouché		Other species
Species	Location	(lat/long)	(1972)	Habitat	in the sample
					Aporrectodea
	Vaucluse				balisa
	1				Aporrectodea
Flabellodrilus	department,	43.963°N,		Mediterranean	rubra
luberonensis	Saint-	5 337°E	ECORDRE_0527	shrubland	Aporrectodea
n. sp.	Saturnin-	5.557 E		Sindonand	nporrecioucu
	les-Apt				trapezoides
	1				Octolasion
					cyaneum
Allolobophora	Var	42 572001			4
<i>delitesca</i> n.	department,	43.573°N,	ECORDRE_0496	Mediterranean	Aporrectodea
sp.	Callas	6.530°E		grassland in	caliginosa

				an old olive	Aporrectodea
				grove	rubra
					acidicola
					Flabellodrilus
					bartolii
					Octolasion
					cyaneum
					Scherotheca
					rhodana
					<u>Allolobophora</u>
					<u>chlorotica</u>
					<u>Aporrectodea</u>
					<u>caliginosa</u>
Vignysa	Var	12 597°N		Dinorion	<u>Aporrectodea</u>
<i>callasensis</i> n.	department,	43.387 N, 6.538°E	ECORDRE_0503	regeland	<u>rosea</u>
sp.	Callas			grassland	<u>Scherotheca</u>
					<u>porotheca</u>
					<u>Scherotheca</u>
					<u>rhodana</u>

91 MORPHOLOGICAL DESCRIPTIONS

Ethanol-fixed specimens were firstly studied following a classical morpho-anatomical
description workflow. The following characters were used to describe the external morphology:
body shape, body pigmentation, body length (after ethanol fixation), body mass, diameter

(preclitellar, clitellar and postclitellar regions), number of segments, type of prostomium, 95 arrangement of setae, position of clitellum, position of genital markings, position and shape of 96 tubercula pubertatis, position of male pores, position of ovipores, spermathecal pores and 97 nephridial pores. A few specimens of each species were dissected, and their internal anatomy 98 was described using the following characters: thickness of the septa, position of gizzard, 99 position of crop, position and shape of calciferous glands, position of esophagus-intestine 100 101 transition, position and shape of typhlosole, position of hearts, shape of nephridia, type of testis sacs, position and shape of seminal vesicles, position and shape of spermathecae. 102

We then compared the morpho-anatomical characters of studied specimens to those of already known species in the genera concerned. When a series of specimens differed from already known species by at least one morpho-anatomical character of specific diagnostic value, we considered it represented a species putatively new to science.

107 DNA AND PHYLOGENETIC ANALYSES

108 A few specimens of each possibly new species were used for DNA analyses. Total genomic DNA was extracted from ventral integument samples of approximately 5 x 5 mm by 109 using the SpeedTools Tissue DNA Extraction kit (Biotools). Regions of the nuclear gene 28S 110 rRNA and mitochondrial 16S rRNA, 12S rRNA, NADH dehydrogenase (ND1) and cytochrome 111 oxidase subunit 1 (COI) were amplified by polymerase chain reaction (PCR), using the primers 112 described in Pérez-Losada et al. (2009) and Folmer et al. (1994). PCR reactions were carried 113 out using a GeneAmp Multicycler Ep gradient (Eppendorf) with the following conditions: an 114 initial denaturation step (5 min at 94°C); 40 cycles (35 for ND1) consisting in denaturation at 115 95 °C for 30 s, annealing (ranging from 45 °C to 55 °C) for 45 s, and extension at 72 °C for 1 116 min; and a final extension step (5 min at 72 °C). The amplified PCR products were purified 117 using the Multiscreen PCRµ96 purification kit (Millipore) and sequenced in Macrogen (Spain). 118

Sequences were aligned with MAFFT v.7 (Katoh & Standley 2013) with default settings
and concatenated with BioEdit (Hall 1999), resulting in a matrix of 3,210 base pairs for each
species. Sequences reported by Domínguez *et al.* (2015), Pérez-Losada *et al.* (2009, 2011),
Paoletti *et al.* (2016), de Sosa *et al.* (2019) and Marchán *et al.* (2020), including representatives
of most of the Lumbricini (sensu Marchán *et al.* 2022) genera were downloaded from GenBank
and used as a reference dataset. The species included are listed in Suppl. Material 1.

125 All the DNA sequences obtained in this study are available in GenBank, under accession 126 numbers X (to be provided). COI sequences (new and datamined from GenBank), together with 127 metadata, are publicly available in the dataset DS-EWNSPSG (doi xxxxxxx) in the Barcode 128 of Life Datasystem (BOLD, Ratnasingham & Hebert 2007).

129 In order to perform phylogenetic analyses, the best fitting evolutionary model for each 130 partition was selected with jModelTest v. 2.1.3 (Darriba et al. 2012) by applying the Akaike information criterion (AIC; Akaike 1973) and the Bayesian information criterion (BIC; 131 Schwarz 1978). The best-fitting evolutionary models were GTR+I+G for COI, 28S, and ND1, 132 GTR+G for 12S and HKY+I+G were chosen for 16S. Parameters were set to 50 million 133 generations and sampled every 5,000th generation (10,000 trees). Two independent runs each 134 with four chains were performed and 20% of the trees were discarded as burn-in. The remaining 135 trees were combined and summarized on a 50% majority-rule consensus tree. Clade support 136 values over 70% and 90% (for Bootstrap and Posterior probability respectively) were 137 138 considered high. Uncorrected average pairwise distances between the studied species for the molecular markers COI were calculated in MEGA 11 (Tamura et al. 2021) in order to support 139 their status as separate species. 140

141 SPECIES DESCRIPTIONS

When a species considered as putatively new to science based on its morphology was 142 further confirmed as distinct from its nearest neighbors by the molecular phylogenetic analysis, 143 we proceeded to its formal description. We then compiled a table containing the collection data 144 of all the studied specimens for each species, and a second table describing the morpho-145 anatomical characters of each of them. We used the R Markdown (Allaire et al. 2022) scripts 146 proposed by Decaëns et al. (2023) to automatically (1) write the information about collection 147 data of holotypes and paratypes, and (2) generate a standardized description of each species 148 including external morphological characters and internal anatomy. 149

150 ABBREVIATIONS

151 MNHN: Museum national d'Histoire naturelle, Paris

152 Eco&Sols: Eco&Sols collection, Montpellier

153 **RESULTS**

The morpho-anatomical analysis of the samples revealed three sets of specimens 154 belonging to three different species putatively new to science that were initially assigned to the 155 genera Allolobophora Eisen, 1874 (Lumbricidae) for two of them, and Vignysa Bouché, 1970 156 (Hormogastridae) for the third one. We obtained a complete set of genes (i.e. COI, 16S, ND1, 157 12S, 28S) for one specimen in each Lumbricidae species, and COI DNA barcodes for four 158 specimens of Vignysa. These sequences and others datamined from GenBank and other projects 159 160 were used to produce 1) a phylogenetic tree of the Lumbricidae genera closely related to Allolobophora, based on the concatenated sequence of COI-16S-ND1-12S-28S molecular 161 markers (Fig. 1), and 2) a DNA barcode tree of the genus Vignysa (Fig. 2). Both of these trees 162 confirmed the separation of the three species from their nearest neighbors, and highlighted their 163 relationships with closely related species. 164

Some individuals collected in Callas and assigned to the genus *Allolobophora* based on their morphology, appeared clearly separated from other species in the genus as highlighted by the position of the specimen SG-0046 in Fig. 1. This species, which we describe under the name *Allolobophora delitescens* n. sp., is closely related to *Allolobophora icterica* Savigny, 1826 in the reconstructed phylogeny.

Another specimen from a second set of individuals initially assigned to Allolobophora 170 (i.e. DFM-1016) appeared closely related to Allolobophora bartolii Bouché, 1972, although 171 172 different enough to be considered as belonging to a separate species (Fig. 1). These two sister species form a clade which is separated enough from its nearest neighbors to be considered as 173 a distinct genus. We propose here to describe this new genus under the name Flabellodrilus n. 174 175 gen. with Flabellodrilus bartolii n. comb. as type species, and we describe the newly discovered 176 species under the name Flabellodrilus luberonensis n. sp.. The moderately low support for the nodes connecting Flabellodrilus n. gen., Perelia Easton, 1983 (represented by Perelia 177 178 kaznakovi (Michaelsen, 1910)) and Eophila Rosa, 1893 makes it complicated to know the exact relative position of these genera, but they appear to belong to a well-supported clade together 179 with Imetescolex Szederjesi, Marchán & Csuzdi, 2022, and clearly separated from 180 Allolobophora sensu stricto as defined by Bouché (1972). 181



FIG. 1. – Multilocus phylogenetic tree focused on *Allolobophora*-related Lumbricidae genera (the full
phylogenetic tree is shown in Suppl. Material 1). The tree was obtained from Bayesian inference based
on the concatenated sequences of the COI-16S-ND1-12S-28S molecular markers. Posterior probability
values are shown beside nodes. White boxes show target genera while grey boxes indicate closely related
genera (species labels shown in Suppl. Material 1).

Finally, the four specimens of the *Vignysa* species appeared clearly separated from the two previously known species within the genus (Fig. 2). We propose to describe these specimens under the name *Vigysa callasensis* n. sp.



FIG. 2. – DNA barcode tree of the genus *Vignysa*. The tree was obtained from Bayesian inference based
on the sequences of COI barcodes. Posterior probability values are shown above branches. Grey bars
delimit individuals belonging to each species.

Uncorrected average pairwise distances between the new species and their closest relatives are 12.4% for *F. luberonensis* n. sp. versus *F. bartolii* (Table 2), 18.5% for *V. callasensis* n. sp. versus *Vignysa teres* (Dugès, 1828) (Table 3), and 15% for *A. delitescens* n. sp. versus *Allolobophora dubiosa* (Örley, 1881) (Table 2). These distances are within the range of divergence usually found among well-established lumbricid species, thus supporting the delimitation of the three new species obtained from both morpho-anatomical characters and phylogenetic analyses.

TABLE 2. – Uncorrected average pairwise distances (in percentage) calculated for the COI barcodes
 between the newly described Lumbricidae species and their closest relatives.

	All. delitescens sp. nov.	All. chlorotica	All. dubiosa	All. molleri	All. monchicana	All. burgondiae	All. icterica	Fl. bartolii	Fl. luberonensis sp.nov.	Fla
<u></u>										
delitescens										
sp. nov.										
All.										
chlorotica	17.20									
All. dubiosa	15.01	18.21								
All. molleri	15.85	18.89	14.84							
All.										
monchicana	16.02	18.89	16.36	10.62						
All.										
burgondiae	18.21	18.55	18.21	17.88	16.53					
All. icterica	16.02	18.55	16.36	16.36	16.36	16.36				
Fl. bartolii	18.38	20.74	18.38	17.54	18.72	19.39	18.38			
Fl.										
luberonensis										
sp.nov.	19.39	19.90	17.54	20.40	20.24	18.89	18.38	12.14		
Flabellodrilus										
sp.	16.69	18.72	17.88	18.04	19.06	17.03	17.20	10.29	11.47	
Eo. gestroi	19.56	19.73	19.73	17.71	21.42	17.71	20.07	16.19	16.53	
Eo. tellini	19.39	18.89	19.90	20.91	20.74	20.07	19.73	17.37	17.71	
Pe. kaznakovi	20.24	18.21	20.40	21.59	20.57	19.56	19.73	16.69	18.04	

207 TABLE 3. – Uncorrected average pairwise distances (in percentage) calculated for the COI barcodes

208 between the newly described Hormogastridae species and their closest relatives.

	V. teres	V. callasensis sp. nov.	V. vedovinii
Vignysa teres	10.0		
Vignysa callasensis sp. nov.	18.5	0.0	
Vignysa vedovinii	19.6	20.0	0.0

212 TAXONOMY

213	Phylum ANNELIDA Lamark, 1802
214	Class CLITELLATA Michaelsen, 1919
215	Sub-class OLIGOCHAETA Grube, 1850
216	Order CRASSICLITELLATA Jamieson, 1988
217	Family LUMBRICIDAE Rafinesque, 1815

218

Genus Flabellodrilus Gérard, Decaëns & Marchán n. gen.

219 TYPE SPECIES. – *Allolobophora bartolii* Bouché, 1972: 454

ETYMOLOGY. – The genus name is derived from the fan-shaped clitellum of the two speciescurrently attributed to this genus (flabellum, a: fan).

222 DIAGNOSIS. - Medium-sized worms with faint brown pigmentation (sometimes absent) and mid-segmental dark dots in the cephalic region. Prostomium epilobous, no transversal furrows. 223 Setae closely paired. First dorsal pore in 5/6. Male pores in 1/2 15 with well-developed 224 porophores. Spermathecal pores in 9/10, 10/11, double (rarely in (8/9)9/10-12/13, simple or 225 double). Nephridial pores aligned. Clitellum moderately posterior between XXXII and XLIV. 226 Calciferous glands in X-XIV with diverticula in X. Typhlosole with four lamellae. 227 Spermathecae double in X and XI, globular and intracoelomic (rarely simple or double in 228 (IX)X-XIII. Two pairs of seminal vesicles in XI-XII. Nephridial bladders sigmoid with a sub-229 230 terminal constriction followed by a loop.

DIFFERENTIAL DIAGNOSIS. – *Flabellodrilus* can be differentiated from closely related genera by
 some morpho-anatomical characters. It differs from *Allolobophora* by the more anterior
 position of the clitellum, pigmentation (faint brown with pigmentary dots vs frequently green),

repetition of spermathecae (double vs simple), number of seminal vesicles (two pairs in XI and 234 XXII versus four pairs in IX to XII) and shape of nephridial bladders (sigmoid with subterminal 235 constriction versus U-shaped). It differs from Panoniona Mršić & Šapkarev, 1988 by the more 236 posterior position of the clitellum, pigmentation (faint brown vs absent), repetition of 237 spermathecae (double versus double-multiple) and shape of nephridial bladders (sigmoid with 238 subterminal constriction and loop versus sigmoid with subterminal constriction and bag-like 239 distension). Flabellodrilus differs from Eophila by its generally smaller size, its pigmentation 240 (faint brown with pigmentary dots versus purplish-brown in bands or light grey) and repetition 241 of spermathecae (double versus simple), and from Imetescolex, Helodrilus and Proctodrilus by 242 243 the presence of nephridial bladders in all segments. Finally, the loosely defined genus Perelia is similar to Flabellodrilus in the shape of their nephridial bladders, but they differ in their 244 pigmentation (pigmentary dots not documented in Perelia) and in the repetition of their 245 spermathecae (double versus simple). 246

247 INCLUDED SPECIES. –

248 Flabellodrilus bartolii n. comb. (Bouché, 1972: 454)

249 Flabellodrilus luberonensis n. sp.

DIVERSITY AND DISTRIBUTION. – The genus *Flabellodrilus* is composed of two species
distributed in the Provence sedimentary basin, at the east of the Rhône river, and in the external
Alps (Barronies and Nice Prealps).

REMARKS.- The subspecies *Allolobophora bartolii meougensis* (Bouché, 1970) is significantly
different from *Flabellodrilus bartolii* n. comb. In the position of the clitellum and position and
repetition of spermathecae (8/9–12/13 *versus* 9/10–10/11, simple *versus* double). It thus appears
likely that it constitutes a separate species from *F. bartolii*. In the absence of detailed morph-

anatomical analysis and molecular data, we conservatively maintain this subspecies as *Flabellodrilus bartolii meougensis* n. comb. (Bouché, 1970).

259

260

Flabellodrilus luberonensis Gérard, Decaëns & Marchán n. sp.

261

(Figs. 3, 4)

TYPE MATERIAL. – Holotype. France • One adult specimen; Provence–Alpes–Côte d'Azur,
Vaucluse, D943, 84490 Saint–Saturnin–les–Apt, in the soil; latitude/longitude:
43.963°N/5.337°E; elevation: 434 m asl; 25 November 2021; T. Decaëns, D. F. Marchán leg.;
deposited at MNHN (BOLD Sample ID: DFM-1016).

Paratypes. France • Four adult specimens; same data as Holotype; deposited as follow: two
specimens at Eco&Sols (BOLD Sample ID: DFM-1017, DFM-1020), two specimens at MNHN
(BOLD Sample ID: DFM-1018, DFM-1019).

Other material. France • Nine sub-adult specimens; same data as Holotype; deposited at
Eco&Sols.

271 ETYMOLOGY. – The species name is derived from the massif of Luberon where the type
272 specimens were found.

273 DESCRIPTION

274 *External morphology*. (Fig. 3A, B)

Body shape cylindrical. Body pigmentation absent, mid-segmental dark dots in the cephalic region. Average body length after ethanol fixation: 80 mm (range: 70 to 100 mm; n= 3 adult specimens). Average body mass: 1.163 g (range: 0.855 to 1.398 g; n= 3). Average diameter: 4.6 mm in the preclitellar region (range: 4.2 to 5.4 mm; n = 5), 5.8 mm in the clitellum (range: 5.2 to 6.8 mm; n = 5), 4.6 mm in the postclitellar region (range: 4.2 to 5.2 mm; n = 5). Average number of segments: 283 (range: 187 to353; n = 3). Prostomium of closed epilobic type. Setae
closely paired. Setal arrangement: aa:ab:bc:cd:dd = 14:2:8:1:32. Clitellum in XXXII–XLII
(XLIII). Genital markings in XI–XII, randomly unpaired in XVI–XXVIII, intraclitellar in
XXXIV, in ab. Tubercula pubertatis: protruding band in XXXV–XL. Male pores: one pair in
XV. Ovipores: one pair in 1/2 XIV, at 1 x ab dorsally from b. Spermathecal pores not visible.
Nephridial pores not visible.

286 Internal anatomy. (Fig. 3C, 4)

Septa: thickened from 5/6 to 9/10, otherwise membranous. Crop in XV-XVI. Muscular gizzard 287 288 in XVII–XVIII followed by a membranous pouch in XIX, with an average size (width x length) of 3.55 x 2.10 mm. Calciferous glands: in X-XIV, forming a pair of spherical lobes in X. 289 Esophagus-intestine transition in XV. Typhlosole starts in XX, forming four folded lamellae. 290 291 Hearts: in VI-XI. Excretory apparatus: one pair of holonephridia per segment, nephridial vesicles sigmoid with a sub-terminal constriction followed by a loop (Fig. 4). Seminal vesicles: 292 two pairs in XI-XII, large and lobulated. Spermathecae: two pairs in X-XI, intracoelomic, 293 294 sessile and double (Fig. 3C).

ECOLOGY. - F. luberonensis n. sp. was found in a Mediterranean shrubland (garrigue) soil at
low elevation (434 m asl).

DISTRIBUTION. – F. luberonensis n. sp. is only known from the type locality, near the city of
Saint-Saturnin-les-Apt, between the massif of Luberon and the Vaucluse mountains in the
Vaucluse department (Provence-Alpes-Côte d'Azur, France) (Fig. 5). It is located in the
Luberon Regional Natural Park (Parc Naturel Régional du Luberon).

REMARKS. – This species can be distinguished from its closest relative *F. bartolii* n. comb. by the position of its clitellum and tubercula pubertatis (Table 4) and by their remarkably high genetic distance (12.14% uncorrected pairwise COI distance).



FIG. 3. – *Flabellodrilus luberonensis* n. sp.: A) External view of the anterior body; B) Lateral
view of the anterior body; C) Dissection of the anterior body. All images from the Holotype
specimen and © T. Decaëns; CL= clitellum, CR= crop, GM= genital marks, GZ= gizzard, IN=
intestine, MP= male pore, NE= nephridia, SEP= septa, SP= spermathecae, SV= seminal
vesicles, TP= tubercula pubertatis.



311Fig. 4. – Pre-clitellar nephridia of *Flabellodrilus luberonensis* n. sp. © D.F. Marchán

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- 313

Genus Allolobophora Eisen, 1874

314 TYPE SPECIES. – *Enterion chloroticum* Savigny, 1826: 182

DIAGNOSIS. - Small-to-medium-sized species with green pigmentation (sometimes absent). 315 Prostomium epilobous, no transversal furrows. Setae closely paired. First dorsal pore in 4/5 316 317 (rarely 3/4, 5/6, 7/8). Male pores in 1/2 XV with well-developed porophores. Presence of spermatophores. Spermathecal pores in variable position and number between 7/8 and 10/11, 318 simple. Nephridial pores irregularly distributed (en solfège). Clitellum moderately posterior to 319 320 extremely posterior, starting between XXVIII and LXXIII and ending between XXXVI and LXXVIII. Calciferous glands in X-XV with diverticula in X. Typhlosole usually trifid 321 322 (sometimes bifid or with 4 lamellae). Variable number of simple spermathecae, usually three or four pairs. Four pairs of seminal vesicles in IX-XII. Nephridial bladders U-shaped (incurvate 323 and reclinate or proclinate). 324

325 INCLUDED SPECIES. -

- 326 *Allolobophora chlorotica* (Savigny, 1826: 182)
- 327 Allolobophora burgondiae Bouché, 1972: 272

- 328 Allolobophora icterica (Savigny, 1826: 182)
- 329 Allolobophora molleri Rosa, 1889: 3
- 330 Allolobophora moebii Michaelsen, 1895
- 331 *Allolobophora dubiosa* (Örley, 1881: 603)
- 332 *Allolobophora delitescens* n. sp.

DIVERSITY AND DISTRIBUTION. – The genus Allolobophora as redefined by Navarro et al. (2023) 333 334 comprises seven species natively distributed in the Iberian Peninsula, France, Morocco, Algeria, Italy, Belgium, Czech Republic, Germany, Romania, Switzerland, The Netherlands, 335 United Kingdom, Bulgaria, Croatia, Hungary, Moldova, Montenegro, Russia, Serbia, Slovakia, 336 337 Turkey and Ukraine. However, their geographic origin appears to be located between the Iberian Peninsula, Maghreb and the perialpine region (including France, Switzerland and the 338 Western Balkans). The species attributed to Heraclescolex Qiu & Bouché, 1998e in the genus 339 original description likely belong to Allolobophora and are mainly distributed in Portugal, 340 western Spain and Morocco. 341



343	FIG. 5. – Distribution of newly described Lumbricidae species, <i>Flabellodrilus luberonensis</i> n.
344	sp. and Allolobophora delitescens n. sp. (stars), and their closest relatives (circles) in Southern
345	France. All species within the genus Flabellodrilus n. gen. are represented.
346	
347	Allolobophora delitescens Gérard, Decaëns & Marchán n. sp.
348	(Figs. 6, 7)
349	TYPE MATERIAL Holotype. France • One adult specimen; Provence-Alpes-Côte d'Azur,
350	Var, 83830 Callas, in the soil; latitude/longitude: 43.573°N/6.530°E; elevation: 305 m asl; 28

November 2021; T. Decaëns, D. F. Marchán, S. Gérard, R. Della Vedova leg.; deposited at
MNHN (BOLD Sample ID: SG-0024).

Paratypes. France • One adult and one sub-adult specimens; same data as Holotype; deposited
as follow: one specimen at Eco&Sols (BOLD Sample ID: SG-0046), and one specimen at
MNHN (BOLD Sample ID: SG-0047).

ETYMOLOGY. – The species name is derived from the present participle of the latin verb *delitesco, is, ere*, which can be translated to the intransitive verb "to hide". This is a reference to the fact that Marcel Bouché did not find this species despite his sampling in 1968 at the type locality.

360 DESCRIPTION

361 *External morphology*. (Fig. 6A, 6B)

Body shape cylindrical. Body pigmentation absent. Average body length after ethanol fixation:

363 85 mm (range: 72 to 98 mm; n= 2 adult and 1 subadult specimens). Average body mass: 0.918

364 g (range: 0.639 to 1.197 g; n = 2). Average diameter: 4.7 mm (range: 4.6 to 4.7 mm; n= 2) in

the preclitellar region, 5.0 mm (range: 4.9 to 5.0 mm; n=2) in the clitellum, 4.5 mm (range: 4.1

to 4.8 mm; n= 2) in the postclitellar region. Average number of segments: 201 (range: 200 to
202; n= 2; 1 subadult specimen with 211 segments). Prostomium of closed epilobous type.
Setae closely paired. Setal arrangement aa:ab:bc:cd:dd = 11:1:6:1:29. Clitellum in (XXXV)
XXXVI–(XLVI) XLVII. Genital markings in intraclitellar in XXXVII–(XXXVIII) XXXIX.
Tubercula pubertatis: thin band in XL–XLVI. Male pores: one pair in XV. Ovipores: one pair
in 1/2 XIV, at 1 x ab dorsally from b. Spermathecal pores not visible. Nephridial pores not
visible.

373 Internal anatomy. (Fig. 6C, 7)

374 Septa: thickened from 6/7 to 10/11, otherwise membranous. Crop in XV-XVI. Muscular gizzard in XVII-XVIII, followed by a membranous pouch in XIX, with an average size (width 375 x length) of 3.80 x 2.25 mm. Calciferous glands: in X-XIV, forming two kidney-shaped lobes 376 377 in X. Esophagus-intestine transition in XV. Typhlosole start in XIX, forming five lamellae. Hearts: in VI-XI. Excretory apparatus: one pair of holonephridia per segment, nephridial 378 vesicles U-shaped (Fig. 7). Seminal vesicles: four pairs in IX-XII, smaller in IX-X, large 379 380 lobulated in XI-XII. Spermathecae: three pairs in 8/9, 9/10, 10/11, small globular and intraseptal, simple (a single case of a double spermathecae). 381

- ECOLOGY. *A. delitescens* n. sp. was found in a Mediterranean grassland, previously an olive
 tree orchard, surrounded by pine forests, at a low elevation (305 m asl).
- DISTRIBUTION. A. delitescens n. sp. is only known from its type locality, near the city of
 Callas, in the sedimentary basin north to the Esterel massif in the Var department (ProvenceAlpes-Côte d'Azur, France) (Fig. 5).
- REMARKS. *A. delitescens* n. sp. can be distinguished from its closest relatives *A. icterica* and *A. dubiosa* by the position of the clitellum, tubercula pubertatis and typhlosole type, and by its absence of pigmentation and smaller size in the latter case (Table 4).



390

FIG. 6. – *Allolobophora delitescens* n. sp.: A) External view of the anterior body; B) Lateral view of the
anterior body; C) Dissection of the anterior body. All images from the Holotype specimen and © T.

- 393 Decaëns; CL= clitellum, CR= crop, GM= genital marks, GZ= gizzard, IN= intestine, MP= male pore,
- 394 SEP= septa, SV= seminal vesicles, TP= tubercula pubertatis, TY= typhlosole.



396 FIG. 7. – Pre-clitellar nephridia of *Allolobophora delitescens* n. sp.. © D.F. Marchán.

395

- 397 TABLE 4. Main morphological characters distinguishing the newly described species *Flabellodrilus*
- 398 *luberonensis* n. sp., *Allolobophora delitescens* n. sp. and their closest relatives.

Characters	Flabellodrilu s luberonensis n. sp.	Flabellodrilus bartolii	Allolobophora Allolobophor delitescens n. icterica sp.		Allolobophor a dubiosa
Length	70–100 mm	60–120 mm	70–98 mm	70–90 mm	120–250 mm
N. segments	187–353	280–394	200–211	140–200	120–303
Weight	0.85–1.24 g	0.85–1.49 g	0.64–1.2 g	0.3–1.33 g	2.96–3.47 g
Pigmentation	Absent, dark spots	ıt, dark Brown- Absent Absent yellow, dark spots		Dark green to greenish brown	
Papillae	XI-XII, XVI– XXVIII, XXXIV	X, XI, XXXIII– XLIV	XXXVII, (XXXVIII), XXXIX	XI, XLIV, XLV	Unknown
Spermathecal pores	9/10, 10/11 double	9/10, 10/11 double	8/9, 9/10, 10/11 simple in c	(7/8)8/9, 9/10, 10/11 simple in c	8/9, 9/10, 10/11 simple in c
Clitelum	XXXII–XLII (XLIII)	XII–XLII (XXXIII) (XXXV) (XXXIII) III) XXXIV– XXXVI– XXXIV–XLIII XLIII (XLIV) (XLVI) XLVII (XLIV)		(XXXVI) XXXVII– XLVII (XLVIII)	
Tubercula pubertatis	XXXV-XL	(XXXV) XXXVI–XLI	XL–XLVI	(XXXV) XXXVI–XLII (XLIII)	(XLIII) XLIV–XLVII (XVIII)
Typhlosole	Four lamellae	Four lamellae	Five lamellae	Bifid	Bifid

24

	Nephridial bladders	Sigmoid, bag-like distension	Sigmoid, bag- like distension	U-shaped	U-shaped	U-shaped	
	Seminal vesicles	XI, XII	XI, XII	IX - XII	IX - XII	IX - XII	
	Spermathecae	Double, oval in X, XI	Double, oval in X, XI	Simple, intraseptal in 8/9, 9/10, 10/11	Simple, intraseptal to intracoelomic, in (VIII), IX, X, XI	Simple in 8/9, 9/10, 10/11	
399							
400		Family	HORMOGAST	FRIDAE Michae	elsen, 1900		
401	Genus <i>Vignysa</i> Bouché, 1970						
402	TYPE SPECIES	– Lumbricus te	res Dugès, 1828	8: 289			
403	DIAGNOSIS. –	Small-to-mediu	um-sized specie	es without cutar	neous pigmentatio	on. Prostomium	
404	prolobous. Trar	nsversal furrow	s on segments I	-II. Setae closel	y paired. Male por	es in 15/16 with	
405	well-developed	porophores.	Spermathecal p	pores in 9/10,	10/11, simple. N	ephridial pores	
406	aligned. Clitell	um between X	IV and XXIX ((1/2 XXX). Two	o gizzards in VI–	VII. Typhlosole	
407	lire or Y shape	ed. Two pairs	of spermatheca	e, disc shaped	or tubular. Two p	pairs of seminal	
408	vesicles in XI-	XII. Nephridia	l bladders fish-ł	nook shaped wit	h caeca from the	first segments.	
409	INCLUDED SPEC	CIES.—					
410	Vignysa teres (Dugès, 1828: 2	.89)				
411	Vignysa vedovinii Rota, 1994: 27						
412	Vignysa callasensis n. sp.						
413	DIVERSITY AND DISTRIBUTION This genus currently comprises three species occurring in						
414	South-Eastern	France, from	Montpellier (H	lérault, Occitan	ie) to the north	of Fréjus (Var,	
415	Occitanie), and from the Mediterranean Sea to the 44th north parallel (Fig. 8).						



FIG. 8. – Distribution of *Vignysa callasensis* n. sp. (star) and its closest relatives (circles) in
Southern France. All species of the genus *Vignysa* are represented.

416

420 Vign

Vignysa callasensis Gérard, Decaëns & Marchán n. sp.

421 (Figs. 9, 10, 11)

422 TYPE MATERIAL. - Holotype. France • One adult specimen; Provence-Alpes-Côte d'Azur,

423 Var, 83830 Callas, in the soil; latitude/longitude: 43.587°N/6.538°E; elevation: 340 m asl; 28

424 November 2021; T. Decaëns, D. F. Marchán, S. Gérard, R. Della Vedova leg.; deposited at

425 MNHN (BOLD Sample ID: DFM-1062).

426 Paratypes. France • 8 adult specimens; same data as Holotype; deposited as follow: 4
427 specimens at Eco&Sols (BOLD Sample ID: DFM-1061, DFM-1065, SG-0057, SG-0058), 4
428 specimens at MNHN (BOLD Sample ID: DFM-1064, DFM-1063; SG-0059, SG-0060).

429 Other material. France • 10 adult and 11 sub-adult specimens; same data as Holotype; 430 deposited at Eco&Sols.

- 431 ETYMOLOGY. The name of the species is derived from the city of Callas in the Var department
- 432 (Provence-Alpes-Côte d'Azur, France) where the type specimens were found.

433 DESCRIPTION

434 *External morphology*. (Fig. 9A, B)

Body shape cylindrical. Body pigmentation absent. Gut content visible in transparency. 435 Average body length after ethanol fixation: 95 mm (range: 82 to 150 mm; n= 9 adult 436 specimens). Average body mass: 0.984 g (range: 0.850 to 1.260 g; n= 11). Average diameter: 437 438 4.0 mm in the preclitellar region (range: 3.5 to 4.8 mm; n=11), 4.5 mm in the clitellum (range: 4.0 to 5.4 mm; n=11), 4.9 mm in the postclitellar region (range: 4.0 to 5.5 mm; n=11). Average 439 number of segments: 162 (range: 157 to 167; n= 7). Prostomium of prolobous type. Setae 440 closely paired. Setal arrangement aa:ab:bc:cd:dd = 18:2:8:1:25. Clitellum in XV-XXIII, 441 beginning unclear. Genital markings in XII-XIV and XX-XXIII, in ab. Tubercula pubertatis: 442 443 thin band in XVII-XXIII, more marked in XX-XXIII. Male pores: one pair in XV. Ovipores not visible. Spermathecal pores not visible. Nephridial pores not visible. 444

445 Internal anatomy. (Fig. 9C, D)

Septa: thickened from 7/8 to 9/10, otherwise membranous. Crop: missing. Gizzard: two globular gizzards in VI–VII, of 1.5 mm in diameter. Calciferous glands: absent. Esophagusintestine transition in XIII. Typhlosole start in XX or XXII, formed by a "Y" shaped large lamellae. Hearts: in VI–XI. Excretory apparatus: one pair of holonephridia per segment, nephridial vesicles boat-hook shaped (bent cecum) in preclitellar segments, open V shaped in the rest of the body. Seminal vesicles: two pairs in XI–XII, large and lobulated. Spermathecae: two pairs in IX–X (9/10, 10/11), intracoelomic, tubular and folded, simple.

ECOLOGY. – *Vignysa callasensis* n. sp. was found in a riparian grassland near La Risse stream,
at a low elevation (340 m asl).

- 455 DISTRIBUTION. *Vignysa callasensis* n. sp. was found near the city of Callas, in the sedimentary
 456 basin North to Esterel, in the Var department (Provence-Alpes-Côte d'Azur, France).
- 457 REMARKS. This species is the smallest species of the genus *Vignysa*: 0.850–1.260 g and 157–
- 458 167 segments versus 1.400–2.700 g and 205–232 segments for Vignysa teres (Bouché 1972;
- 459 personal data), and 3.500–4.800 g and 372–396 segments for Vignysa vedovinii (Rota 1994)
- 460 (see Table 5). It is also the easternmost species within the genus. Alive, it has a viscous texture
- 461 (Fig. 11) and tends to break easily. The absence of blood vesicles (the same as in *V. vedovinii*)
- 462 suggests that this trait is an apomorphy of *V. teres*.



FIG. 9. – *Vignysa callasensis* n. sp.: A) External view of the anterior body; B) Lateral view of the anterior
body; C) Dissection of the anterior body; D) Detail of the anterior body dissection showing the
spermathecae. All images from the Holotype specimen and © T. Decaëns; CL= clitellum, GM= genital
marks, GZ= gizzard, IN= intestine, MP= male pore, SEP= septa, SV= seminal vesicles, TP= tubercula
pubertatis, TY= typhlosole.



470 FIG. 10. – Pre-clitellar nephridia of *Vignysa callasensis* n. sp. © D.F. Marchán.



471

- 472 FIG. 11. Living specimen of *Vignysa callasensis* n. sp. © S. Gérard.
- TABLE 5. Main morphological characters distinguishing the newly described species *Vignysa callasensis* n. sp. and their closest relatives.

Characters	<i>Vignysa callasensis</i> n. sp.	Vignysa teres	Vignysa vedoninii
Length	88–150 mm	170–200 mm	110–130 mm
N. segments	160–163	205–232	372–396
Weight	0.85–1.26 g	1.4–2.7 g	3.5–4.8 g
Papillae	XII, XIV, XX–XXIII	(XIV) XV, XVI (XVII), XXII–XXV	XVI–XVIII, XXIV– XVII (XXVII, XXVIII)

Spermathecal pores	9/10, 10/11 simple	9/10, 10/11 simple	9/10, 10/11 simple
Clitelum	XV–XXIII	(1/2 XIII, XIV) 1/2 XIV–XXV	(XIV) XV–XXIX (1/2 XXX)
Tubercula pubertatis	(XVII) XX–XXIII	XXI–XXIV	XXIII, XIV–XXVII (XXVIII, XXIX)
Spermathecae	Simple, tubular in IX, X	Simple, tubular in IX, X	Simple, disc-shaped, in IX, X

476 **DISCUSSION**

477 TAXONOMY AND PHYLOGEOGRAPHY

Beyond its contribution to the knowledge of the earthworm fauna of France, our work
provides new insights into the understanding of the taxonomy and phylogeny of the genera *Allolobophora* and *Vignysa*.

The limits of the genus Allolobophora, and the number of species it contains, are still 481 not agreed upon in the literature. Depending on the authors, the genus comprises 69 species 482 (DriloBASE taxo), 51 species and subspecies (Blakemore 2008) or 57 species and subspecies 483 (Brown et al. 2023; Misirlioğlu et al. 2023). The relevance of the genus has also been and is 484 still highly discussed, Allolobophora being considered as a catch-all genus, and demonstrated 485 to be polyphyletic in phylogenetic trees (Navarro et al. 2023). Some authors proposed to 486 487 separate it between Allolobophora sensu stricto and Allolobophora sensu lato (Bouché 1972; Easton 1983; Csuzdi & Zicsi 2003). Marchán et al. (2021) elevated the subgenus Gatesona 488 proposed by Qiu & Bouché (1998a) to the genus level, and Popović et al. (2022) assigned 489 several Balkanic Allolobophora species to a redefined Cernosvitovia. Later, Navarro et al. 490 (2023) separated the genus Allolobophora into 4 distinct genera: Allolobophora, Panoniona, 491 Lucquesia Navarro et al., 2023 and Vosgesia Navarro et al., 2023. They also synonymised the 492 493 genus Heraclescolex with Allolobophora, and finally proposed to move Aporrectodea icterica 494 to the genus *Allolobophora*, a new taxonomic assignment which is strongly supported by our495 results.

496 Here, we propose to remove A. bartolii from the Allolobophora genus, and to assign it 497 to the new genus Flabellodrilus n. gen., along with the new species F. luberonensis n. sp.. This new cut within the genus Allolobophora, together with the previous revision by Navarro et al. 498 (2023), result in the restriction of the genus to seven species forming a monophyletic group and 499 corresponding broadly to the Allolobophora sensu stricto of Bouché (1972). The addition of A. 500 501 delitescens n. sp. further reinforce the monophyletic property of Allolobophora. These taxonomic acts and the phylogenetic analyses that support them highlight the artificial character 502 503 of the "catch-all" group Allolobophora sensu lato, which is progressively split into several small 504 genera generally comprising species of restricted geographical distribution. There are still 505 several Balkanic species of Allolobophora which likely belong to Cernosvitovia due to their morphological and biogeographic affinities (see Popović et al. 2022), but others such as 506 507 Allolobophora asconensis Bretscher, 1900, Allolobophora festae Rosa, 1892, Allolobophora marcuzzii Omodeo, 1952 or Allolobophora schneideri Michaelsen, 1900 (which are Italian 508 509 species) or the Caucasian Allolobophora pseudonematogena Perel, 1967, Allolobophora brunnecephala Kvavadze, 1985 and Allolobophora immaculata Omodeo and Rota, 1989 are 510 more controversial: a strong effort to include these species in molecular phylogenetic analyses 511 512 would allow to eliminate Allolobophora sensu lato once and for all.

The family Hormogastridae is endemic of Western Mediterranean region, being present only in Algeria, France, Italy, Malta, Spain and Tunisia with nine genera (Marchán *et al.* 2018 ; Rota *et al.* 2017). The genus *Vignysa* is endemic to South-Eastern France (Bouché 1972; Rota 1994) and comprises three species including the one described herein (Blakemore 2008; Brown *et al.* 2023; Misirlioğlu *et al.* 2023; DriloBASE taxo). All are restricted to France: *V. teres* occurs in several localities of the Hérault department (Occitanie), *V. vedovinii* has been found

in two localities of Bouches-du-Rhône and Var departments (Provence-Alpes-Côte d'Azur), 519 and V. callasensis n. sp. is known only from its type locality in the Var department (Fig. 8). The 520 distribution of the three species seems to be non-overlapping, but this will require further 521 occurrence data to be confirmed. The basal position of V. callasensis n. sp. in the DNA barcode 522 phylogenetic tree (Figure 2) indicates that the genus Vignysa could have originated in Provence, 523 a region that has been previously highlighted for its high rate of earthworm endemism (Bouché 524 1972; Marchán et al. 2020). However, this assumption should be treated with caution as it is 525 only based on a barcode tree whose topology reliability can be questioned. Analyses will need 526 to be strengthened by using multi-locus data and by including if possible other species in 527 528 neighboring genera before robust conclusions can be drawn.

529 DIVERSITY IN SOUTH-EASTERN FRANCE.

530 We describe here three new species and one new genus, which are, as far as we know, all endemic from South-Eastern France. We found these new taxa in a region previously 531 intensively sampled by M. Bouché (Bouché 1972). This underlines the remarkably high 532 earthworm diversity in this region, which already counted several endemic species before our 533 contribution (e.g. Aporrectodea balisa (Bouché, 1972); Cataladrilus porquerollensis Marchán 534 & Decaëns, 2020; Eumenoscolex pereli (Bouché, 1972); F. bartolii; Kritodrilus calarensis 535 (Tetry, 1944); Kritodrilus micrurus Zicsi & Csuzdi, 1999; Scherotheca dugesi (Rosa, 1895); 536 Scherotheca porotheca Bouché, 1972; Scherotheca portcrosana Marchán & Decaëns, 2020; 537 538 Scherotheca sanaryensis (Tetry, 1942) for Lumbricidae, together with Boucheona gallica (Rota, 1994) and the genus Vignysa). This supports the hypothesis of South-Western Europe 539 being the origin and the center of diversification of the family Hormogastridae (Marchán et al. 540 541 2018) and one of the center of diversification of the familie Lumbricidae (Omodeo & Rota 2008). It also highlights that South-Western Europe, and more especially of South-Eastern 542 France, can be considered as a biodiversity hotspot for earthworms. 543

These high levels of endemism and diversity of earthworm could be explained by the 544 geological and climatic history of the region. South-Eastern France is composed of a huge 545 variety of geological substrates, with various ages and composition (Chantraine et al. 1996). It 546 is composed of three main geological structures: (1) relics of the Variscan orogeny from late 547 Paleozoic (Esterel, Maures and Tanneron massifs), associated with late Paleozoic sediments; 548 (2) Mesozoic sediments and pre-Alps sedimentary massifs; and (3) Cenozoic sediment in the 549 Rhone and Durance basins. The whole structure is located between late Paleozoic mountains 550 (Central Massif in the West and North-West) and younger mountains from Mesozoic (Alps in 551 East, Pyrenees in South-West). This high diversity of geological substrates can explain a 552 553 complex evolutionary history, with different physico-chemical soil properties driving a 554 diversification of adaptive traits in earthworms. Mathieu & Davies (2014) also suggested that glaciations in the late Pleistocene acted as an environmental filter, with Southern France 555 providing habitat refuges for earthworm populations. 556

557 The discovery of three new species in that region was actually expected. M. Bouché carried a quite intensive sampling in the region, but he favored good spatial coverage over 558 intensive sampling at each locality (ECORDRE 0496 and ECORDRE 0503 were done the 559 same day together with 13 other sites, whereas ECORDRE 0527 was done together with 11 560 other sites (Bouché, 1972)). However, the non-detection of these species can also be explained 561 562 by their absence of the locality at that time. Earthworm can have a really patchy distribution, even at the very local scale, making them hard to collect. They could also have changed their 563 local distribution in response to climate and land use changes that have occurred over the past 564 565 five decades. Finally, they could be present at that time, but at a juvenile stage, making them undetectable without molecular analysis. 566

567 This highlights the importance of resampling previously surveyed localities when 568 seeking to establish species lists and discover potential new taxa, like the work of Marchán *et* *al.* (2023) in Corsica. Further studies should also aim at intensifying sampling in non-previously sampled localities in South-Eastern France, as for instance in the Saint-Baume mountain, the Plaine des Maures and the Esterel massif. Given the high diversity and the high proportion of species with narrow geographical distribution, this will undoubtedly result in the discovery of additional species new to science as has been the case in previous works in Port-Cros and Porquerolle Islands (Marchán *et al.* 2020), in Corsica (Marchán *et al.* 2023), and in southwestern France (Marchán *et al.* 2023).

576

577 CONSERVATION

The three species described in this work were found in open landscapes. Until more 578 specimens of these species are found, we can say they are open habitat specialists. This is the 579 case for many endemic species of South-Eastern France. For instance, A. balisa, C. 580 581 porquerollensis, E. pereli, K. micrurus, S. dugesi, S. porotheca and V. vedovinii are considered as strict open habitat specialists. Other species such as F. bartolii, K. calarensis, and V. teres, 582 even not being strict specialists, are mostly found in open habitats. The specialization to open 583 584 habitats from endemic species in the Mediterranean region is also observed in other taxa, such as birds (Blondel & Aronson 1999). 585

However, open landscapes are decreasing in the Mediterranean region. Since the middle 586 of the nineteenth century, the abandonment of traditional agro-pastoral practices and the 587 decrease of the use of wood for charcoal led most habitats to experience secondary successions 588 and the progressive afforestation of Mediterranean grasslands and scrublands (Barbero et al. 589 590 1990; Blondel & Aronson 1999; Chauchard et al. 2007). More recently, these habitats have also decreased in surface due to the expansion of housing urbanization in the second half of the 591 twentieth century, especially in South-Eastern France (Daligaux 2001; Baccaïni & Sémécurbe 592 2009). The type localities of the three new species, all open habitats (i.e. grasslands for V. 593

callasensis n. sp. and *A. delitescens* n. sp., garrigue for *F. luberonensis* n. sp.) have undergone
such a transition, visible from old (1950-1960) and current satellite pictures in Fig 12.

This historical decrease of open landscapes has led to a decrease in biodiversity, especially on rare and endemic species (Preiss *et al.* 1997; Blondel & Aronson 1999; Labaune & Magnin 2002; Höchtl *et al.* 2005). We can therefore argue that this open habitat loss at a fast pace represents a major threat on those newly described specialist species.

The threats these species are facing raise the question of their conservation. One of the 600 major tools for assessing the conservation status of a species is the IUCN red list. The species 601 602 described herein were only found in their type localities, in an already strongly sampled region. It can be an indication of small populations with a narrow distribution range. Thus, they match 603 604 the IUCN red list (IUCN Standards and Petitions Committee 2022) criterion D (very small 605 population size), especially criterion D2 (very restricted distribution) and first part of criterion B (small range area). However, the loss of the habitat where they were found and the 606 Mediterranean region being highly threatened by climate change (MedECC 2020) could be 607 608 indicators of their decline, matching the second part of criterion B (decline). We can then make the hypothesis that they face an extinction risk, and could be listed as Vulnerable species 609 610 according to the IUCN red list. More sampling should be conducted in their area to better know their repartition range and population size, since they are only known in their type localities. 611 Genetic diversity could also be measured to know if populations are fragmented, as it has been 612 613 done for Compostelandrilus cyaneus (Briones & Díaz Cosín, 1993) by Marchán & Domínguez (2022). 614



FIG. 12. – Satellite pictures around type localities of *Flabellodrilus luberonensis* n. sp., *Allolobophora delitescens* n. sp. and *Vignysa callasensis* n. sp. in the 1950-1965 period (left) and in 2022 (right).

618 (1950-1965 satellite pictures © IGN (Institut national de l'information géographique et forestière)
619 2022;© Google 2022).

620

621 CONCLUSION

The description of three new species in South-Eastern France in a resampling of Bouché's plots (Bouché 1972) highlights the tremendous diversity in this region, which could still host a high number of species yet to be discovered. In a region facing global change pressures like urbanization, habitat and land use changes and climate mutations, it also stresses that their conservation is not guaranteed and deserves consideration.

627 Moreover, these descriptions and the phylogenetic evidence on which they rely help to 628 better understand the systematics of the historically catch-all genera *Allolobophora*, and 629 improved our understanding of the diversity and distribution of the endemic genus *Vignysa*.

630 CONFLICT OF INTEREST

631 The authors do not have any conflicts of interest to declare.

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875 APPENDIX