Shifting continents, not behaviours: independent colonization of solitary and subsocial Anelosimus spider lineages on Madagascar (Araneae, Theridiidae)

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Introduction

Madagascar is a prominent biodiversity hotspot containing highly diverse, mostly endemic biota. The origin of the Madagascar biota is much debated, especially the relative roles of Gondwanan vicariance vs. Cenozoic dispersal (Yoder & Nowak 2006). A recent review across multiple lineages (Yoder & Nowak 2006) found that the most common pattern was a sister relationship of Malagasy fauna to taxa from the African continent, and that most Malagasy lineages were too recent to be explainable by vicariance. Examples of taxa that probably colonized via dispersal from Africa include a variety of organisms such as plants (Schaefer et al. 2009), freshwater crabs (Cumbersidge 2008), lizards (Raselimanana et al. 2009) and bats (Weyeneth et al. 2008). While there are also several examples of Gondwanan vicariance lineages in Madagascar (Janssen 2009).
et al., 2008), Cenozoic (up to 65 Ma) dispersal from Africa appears to have been a prominent biogeographical force shaping the Madagascar biota.

The spider genus Anelosimus Simon, 1891 (Theridiidae) is a model system for the study of sociality and its evolution, because the genus mostly contains species that range from temporarily (sub)social to permanently social (Avilés 1997; Agnarsson 2006; Lubin & Bilde 2007). Only a small number of Anelosimus species are solitary. The Central American Anelosimus pacificus Levi, 1956 has secondarily switched to solitary living (Agnarsson et al. 2006a). Other Anelosimus species that are suspected to be solitary based on preliminary evidence, such as web size and content (L. Avilés, pers. comm.) are all close relatives of A. pacificus, namely Anelosimus eticus and Anelosimus nigrescen from South America (Agnarsson 2005), and the European Anelosimus vitatus (IA pers. obs.) and likely also Anelosimus pulchellus, although we are aware of no data on its behaviour. Anelosimus is diverse in Madagascar and hitherto described species are all subsocial and monophyletic, hence forming a single Malagasy radiation (Agnarsson & Kuntner 2005).

Here, we report on the biology of two solitary Anelosimus species from northern Madagascar and Mayotte (an overseas department of France, forming a continuous island chain with the Comoro Islands, situated NW of Madagascar). We use a phylogenetic approach to determine the origin of these spiders. Specifically, we test two alternative hypotheses: (i) solitary behaviour evolved independently from (sub)social ancestors and thus represents a secondary reversal within Madagascar and the Comoros or (ii) a solitary lineage independently dispersed to Madagascar and the Comoros. A monophyletic Madagascar/Comoros clade that would include subsocial and solitary species treated here would support the first hypothesis, and a closer association of these species to other Old World Anelosimus would support the latter. We thus provide a better insight into the biogeography of Anelosimus spiders, and the evolution of behaviours, in Madagascar and neighbouring islands. We describe one new species, redescribe another, and also make taxonomic amendments to restore natural classification of Anelosimus.

Materials and methods

Solitary vs. social behaviour

Following prior work (Agnarsson et al. 2006a), we distinguish between solitary and social behaviour on the basis of cooperation. Many solitary theridiids show some degree of maternal care, beyond care of egg sacs (Avilés 1997; Agnarsson 2004; Lubin & Bilde 2007). However, in solitary species, juveniles are passive receivers of care and disperse from the natal nest at early instars, typically I–III, without contributing to the colony. In contrast, in all temporarily and permanently social species, juveniles stay in the natal nest until near or after adulthood. Older instars also actively cooperate and contribute to common colony tasks such as web spinning, prey capture and brood care. The webs of solitary and social species also differ in that the former are flimsier and typically less three dimensional (Fig. 1; see Results).

Observations

The two focal species, Anelosimus decaryi from mangrove forests of NE Madagascar and Mayotte (Fig. 2) and Anelosimus amelie sp. n. from lowland forest of Mayotte (Fig. 3), appeared common in their type habitats. Webs of A. decaryi were encountered at the tips of branches of small leaved mangrove species at the beachfront (Fig. 1). They occurred between Diego Suarez and Orangea, in the Diana region of Madagascar (S12°15.546'; E49°20.609', sea level, 3–4.iv.2008, coll. by I. Agnarsson and M. Kuntner), and on Plage Tahiti on the western coast of the island Mayotte (S12°51.817'; E43°06.657', sea level, 8.iv.2008, coll. by I. Agnarsson and M. Kuntner). Webs of A. amelie were found at the slope of Mt. Choungui, Mayotte (S12°56'43.872'; E45°7'19.1994, 200-m elevation, 8.iv.2008) in open canopy growth on tips of branches of lone trees. Webs were photographed and measured in the field, the contents of webs were examined. The ages or instars of juveniles were estimated based on their size, based on comparison of the instars to other Anelosimus species with similarly sized adult females.

Phylogenetics

Specimens were fixed in 95% ethanol. Voucher specimens were deposited at the National Museum of Natural History, Smithsonian Institution. We obtained sequences of mitochondrial (16S, COI) and nuclear (28S) loci from A. decaryi and A. amelie and added these species to the existing species level Anelosimus phylogeny based both on molecular and morphological data (Agnarsson 2006; Agnarsson et al. 2007). GenBank accession numbers of new sequences are: Anelosimus_amelie_Mayotte 16S: GQ980271, 28S: GQ980273, COI: GQ980276; Anelosimus_decaryi_Mayotte_AN03_16S: GQ980275, 28S: GQ980272, COI: GQ980277. The total dataset contained 70 individuals representing 25 Anelosimus species. The data matrix is available upon request from the first author. The molecular data were aligned and analysed using the same methods and settings as in the previous study (Agnarsson et al. 2007). In sum, for the protein coding gene COI, the alignment was trivial with no gaps implied. The other genes were aligned in CLUSTAL W (Thompson et al. 1997), followed by minor
manual editing in Mesquite (Maddison & Maddison 2009) to correct conspicuously misaligned blocks mostly near each end of the alignments. Based on sensitivity analyses of Agnarsson et al. (2007), we chose gap opening and gap extension costs of 24/6, resulting in a relatively compressed alignment for our analyses. We treated gaps as missing data (see Agnarsson et al. 2007, for justification). Bayesian analysis was performed using MrBayes V3.1.1 (Huelsenbeck & Ronquist 2001), using the GTR+Γ+I model for molecular data partitions (as chosen by ModelTest, see Agnarsson et al. 2007), and partitioning the data by source (morphology, 16S, CO1, 28S) and the protein coding CO1 also by codon position. Parameters were estimated independently for each partition [‘unlink statefreq = (all) revmat = (all) shape = (all) pinvar = (all)’]. The model employed six substitution types (nst = 6), with rates and proportion of invariant sites (rates = invgamma), and base frequencies, estimated from the data. For each analysis, four Markov chain Monte Carlo chains (one cold and three heated) were run for 10 000 000 generations, and the sample points of the first 5 000 000 generations were discarded as ‘burn-in’, after which the chain reached stationarity.

Parsimony analyses were conducted with NONA (Goloboff 1993). All matrices were analysed using a heuristic search with 10 000 random additions, keeping a maximum of 10 trees per iteration.

**Biogeography and sociality**

We used the phylogenetic results to test the two alternative hypotheses that (i) solitary behaviour evolved secondarily within Madagascar and the Comoros or (ii) that solitary and social lineages dispersed independently...
to Madagascar. For this, we used Fitch parsimony and maximum-likelihood ancestral character reconstruction (Pagel 1999), treating level of sociality and geographical distribution as discrete characters and optimizing them on the preferred phylogeny. For maximum-likelihood estimation, we used the Markov k-state 1-parameter model as implemented in Mesquite. Similar optimizations of geographical distribution as a discrete character (Fig. 5) have been used in prior biogeographical analyses (e.g. Ree & Smith 2008). Such methods seek ancestral areas for lineages that minimize subsequent dispersal or vicariance events needed to explain the current distribution of the lineage.

**Sequence divergence and lineage age estimation**

Intra- and interspecific sequence divergence was calculated in PHYLIP (Felsenstein, 2005) and used as a rough estimate of lineage age, assuming approximate rates of mitochondrial evolution of 2–3% per million years, following (Johannesen et al. 2007), for other social spiders. Currently available data only justify preliminary analyses of lineage age. More sequence data are currently being collected (Agnarsson laboratory) to allow more detailed lineage age estimation in *Anelosimus* and relatives worldwide, including fossil calibrations.
**Taxonomy**

Taxonomic methodology was detailed in (Agnarsson 2006). Specimens were examined under a Wild M-5A dissecting microscope. Illustrations were prepared using a Visionary Digital imaging system, the core components being a Canon 40D (Canon USA Inc. Lake Success, NY, USA) digital camera body and a K2 Infinity microscope equipped with Olympus (Olympus America Inc., Center Valley, PA, USA) metallurgical objectives. Successive images were combined with Helicon Focus 4.0, and thereafter minimally processed with Photoshop CS3 to adjust contrast, brightness, and to remove background blemishes. For photography, anatomical preparations were temporarily mounted as described in Coddington (1983). Measurements were made using an Infinity K2 long-distance microscope images processed in Photoshop CS3.

**Results**

**Observations**

The webs of most social *Anelosimus* species are similar, a dome-shaped sheet reinforced with leaves and above the sheet non-sticky aerial threads that intercept insects in flight (Agnarsson 2006; Aviles et al. 2001) (Fig. 1D). *Anelosimus decaryi* (Fig. 1A–C,E,F), and *A. amelie* (Fig. 3C), however, build webs that appear identical to those constructed by the solitary *A. pacificus* from littoral Central America (Agnarsson et al. 2006b). Typically, the web architecture is a three-dimensional silk mesh surrounding vegetation, with sticky droplets distributed throughout the mesh (Fig. 1B). Some webs included a basal, relatively planar, sheet that lacked sticky droplets and was reminiscent of subsocial species nests (Fig. 1C). Webs differed from *A. pacificus* in only sometimes containing a retreat. When a retreat was present, it consisted of two leaves sandwiched together using silk (Fig. 1E,F), as in *A. pacificus*, or alternatively, of a silk-enforced rolled leaf.

In the field, mostly solitary webs contained an adult female, an adult male or a single juvenile. We estimated the solitary juveniles to represent III or IV instars. Two webs contained a female and her young, but the young were very small, estimated to be first or second instars. These observations, while sparse, imply dispersal from the natal nest at an early ontogenetic stage, like in *A. pacificus*. As juveniles in social *Anelosimus* species typically start to contribute to the common tasks of the colony only after reaching instar III (Vollrath 1986), cooperative behaviour is likely absent in *A. decaryi* and *A. amelie*.

As in the coastal *Anelosimus kobi* from Asia, colour variation in *A. decaryi* is profuse (Fig. 2). *Anelosimus decaryi* and *A. amelie* lay globular white egg sacs (Figs 2B and 3A), which they may hide in the retreat or carry around in the chelicerae, as in the solitary *A. pacificus*. Most *Anelosimus* species in the Americas produce greyish egg sacs, while the solitary *A. pacificus* produces a white egg sac. African and Asian species also produce white egg sacs, indicating two lineages within *Anelosimus* that have switched from grey to white egg sacs.

Solitary behaviour in *Anelosimus* was first documented only recently, in *A. pacificus* (Agnarsson et al. 2006b). Preliminary data suggest solitary behaviour also occurs in its close relatives, the South American *A. ethicus* and *A. nigrescens* (L. Avilés pers. comm.). Our phylogeny suggests that *A. decaryi* and *A. amelie* belong to this same solitary lineage.

**Phylogenetics, biogeography and sociality**

Both Bayesian and parsimony analyses, irrespective of alignment, unequivocally place the new species as sister taxa (Figs 4 and 5). They nest within a clade containing all other known solitary *Anelosimus* species, including the Central American littoral species *A. pacificus* (Figs 4 and 5). Hence, a single reversal to solitary living is indicated in the common ancestor of this lineage. As suspected by Agnarsson & Kuntner (2005) based on morphological evidence these do not belong to the same lineage as the subsocial montane *Anelosimus* from Madagascar (Agnarsson & Kuntner 2005), which here are sister to *Anelosimus nelsoni* from South Africa, whose behaviour is unknown but presumed to be subsocial. This implies that, instead of a habitat and behavioural switch occurring within Madagascar, solitary and subsocial lineages arrived to Madagascar independently of one another and supports our dispersal hypothesis. Our results imply that *Anelosimus* originally diversified in the Americas, and that the lineage here described colonized Madagascar from the Americas. This result is strongly supported, the ’solitary Anelosimus clade’ is supported by posterior probability of 100%. This indicates that the placement of *A. amelie* and *A. decaryi* anywhere outside this clade, or of *Anelosimus may* and *Anelosimus sallee* within it, is a significantly worse explanation of the data than the current hypothesis, given the current data and the model. Similarly, the placement of the group *A. nelsoni* plus the two other Madagascar species, *A. may* and *A. sallee* sister to the large ‘eximius clade’ (Fig. 5), is strongly supported (97%). In the phylogeny, specimens of *A. decaryi* from Madagascar and Mayotte are sisters and are sister to the very similar *A. amelie* from Mayotte.

The phylogeny places the two included *Seycelloesa* Koçak & Kemal species deep within *Anelosimus*, *Seycelloesa* (along with the names it replaced, the unavailable homonyms Selinus Saaristo and Saaristoa Koçak & Kemal) is therefore synonymized with *Anelosimus* (see Discussion and Appendix 1).
Among the Anelosimus species here included, the maximum uncorrected mitochondrial sequence divergence was 26.9% (see Table S1, Supporting Information). Assuming a rate of evolution at 2–3% per million years, the base of Anelosimus can be estimated to be approximately...
9–13.4 Ma. We use the average value of 11.2 as our working estimate (Fig. 5). We note that although a crude estimation, the entire range indicates far younger age of these lineages than would be necessary to support a vicariance biogeographical scenario for *Anelosimus*. The sequence divergence between the solitary Malagasy species *A. amelie* and *A. decaryi* is about 4%, and that between the subsocial Malagasy species *A. may* and *A. sallee* about 5%. These are typical divergences between closely related *Anelosimus* species worldwide (Agnarsson, pers. obs.). In contrast, the divergence among the solitary and subsocial Malagasy species is about 16%, consistent with the hypothesis that the solitary Malagasy lineage is not derived from the subsocial Malagasy lineage. Maximum sequence divergence within the ‘solitary *Anelosimus* clade’ is about 18%, indicating that colonization of Madagascar by the solitary lineage took place at most 6–9 Ma.

**Discussion**

**Biogeography**

Our phylogeny supports the hypothesis that two *Anelosimus* lineages independently colonized Madagascar, one solitary and the other social. Our crude estimate of the age

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Fig. 5 A phylogenetic reconstruction of the geographical distribution of *Anelosimus* lineages. The base of the tree is roughly estimated to be dated around 11 Ma. Colours represent ancestral character optimization under parsimony of geographical distributions of lineages scored as discrete character states. Pie charts show maximum likelihood probabilities of ancestral distributions for nodes of interest. Origin and initial diversification of *Anelosimus* in the Americas is implied, with numerous subsequent dispersal events explaining colonization of other continents. There is clear scattering of solitary vs. subsocial *Anelosimus* lineages from Madagascar, as well as scattering of two mainland African lineages, implying dual dispersal to both landmasses. All *Anelosimus* species known to be solitary group together in a clade (the ‘solitary *Anelosimus* clade’ indicated by arrow (†)), which also contains three species of unknown behaviour. These we predict, based on these results, also to be solitary. Branches are proportional to their lengths, indicated in scale below the tree.
of *Anelosimus* suggests a range from 9 to 13.4 Ma, which even if loosely interpreted rules out vicariance explanations for broad biogeographical patterns in *Anelosimus*. Hence, two dispersal events to Madagascar and adjacent islands (Comoros) must be postulated. The closest living relatives of the highland *Anelosimus* lineage in Madagascar, represented in the phylogeny by *A. may* and *A. sallee*, is *A. nelsoni* from South Africa (Fig. 4). Cenozoic colonization of Madagascar from mainland Africa is hypothesized to be the main force shaping the Madagascar biota (Yoder & Nowak 2006; Weyeneth et al. 2008; Raselimanana et al. 2009; Schaefer et al. 2009). Thus, our observations fit this expected pattern. However, for the solitary coastal lineage we describe here, the closest living relatives are found in the Americas and in Europe (Fig. 4). This indicates dispersal over very long distances, that took place at most 6–9 Ma (see Table S1), and likely more recently given that the presence of this lineage on mainland Africa has not been ruled out (see below). Given the presence of *Anelosimus* on islands such as Madagascar, Mayotte, Seychelles (Saaristo 2006), Aldabra (Roberts 1983), they are clearly capable of long-distance dispersal. However, their absence on more isolated islands such as Reunion, Mauritius and Rodriguez (own data) indicates that dispersal to remote oceanic islands is uncommon in these spiders.

Currently, the knowledge of *Anelosimus* in Africa is very fragmented. We find it likely that the solitary lineage is present on the Eastern coast of Africa. We predict that this yet to be discovered lineage will be a close relative of the Malagasy solitary species. Strangely, the *Anelosimus* lineage that current knowledge suggests is the most diverse and abundant in Eastern Africa (Agnarsson & Zhang 2006), lacks representatives in Madagascar. Because the first author has examined large collections of *Anelosimus* from Madagascar without encountering any representatives of this lineage, we argue that their absence is real rather than reflecting poor knowledge. Instead, the lack of this diverse African lineage may reflect how haphazard colonization of islands is when long-distance dispersal events are very rare (Ricklefs & Bermingham 2008). Our results indicate that *Anelosimus* originally diversified in the Americas, with at least seven subsequent dispersal events to other continents (Fig. 5). We point out that although the current results do not strongly support the exact placement of the African/Asian clade (posterior probability of 0.64), there is no evidence suggesting it might be ‘basal’ to the American *Anelosimus rupununi/ Anelosimus lorenzo* clade and thus affect optimization of the genus origin. The sister relationship of the *A. rupununi* clade to the remaining *Anelosimus* was supported by 27 of 30 data partitions in the analyses of Agnarsson et al. (2007), including total evidence analyses, molecular and morphological data analysed separately, and by five of six molecular loci independently.
As is the case for Madagascar, two lineages independently reached Africa, the *A. nelsoni* group that includes a number of undescribed species (Agnarsson, unpublished), and the lineage represented in Africa by *Anelosimus dude* and *Anelosimus biglebowski*, which also occurs in Asia. Our results are likewise consistent with colonization of the Comoros from Madagascar (Fig. 5). This pattern is also seen, for example, in bats (Weyeneth *et al.* 2008). However, the current phylogeny contains fewer than half of the *Anelosimus* species, and is missing genetic data for several key species, such as *A. nelsoni*. Hence, more detailed understanding of the biogeographical history of the genus and timing of events requires better sampling of *Anelosimus* across the globe, a project that is ongoing.

**Colour variation**

Colour variation in *A. decaryi* is profuse (Fig. 2), as also recently documented in *A. kobi* from Malaysia, as well as *A. dude* and *A. biglebowski* from Africa (Agnarsson & Zhang 2006). Such colour variation can result from any number of factors ranging from diet to genes (see Oxford & Gillespie (1998), for review). Colour polymorphism is well studied in only very few theridiid species, such as the Hawaiian ‘happy face spider’, *Theridion grallator* Simon, 1900 (Oxford & Gillespie 1998, 2001), *Theridion californicum* (Oxford 2009) and *Enoplognatha* (Oxford 2005; Oxford & Gunnarsson 2006). While completely unknown, *Anelosimus* represents another promising lineage for understanding the mechanics of colour variation in theridiid spiders.
Dual colonization of Madagascar by Anelosimus spiders • I. Agnarsson et al.

Sociality
Our results support our second hypothesis explaining the existence of solitary and subsocial Anelosimus spiders on Madagascar and adjacent islands based upon independent colonization by two lineages. Thus, solitary littoral Malagasy species did not descend from Malagasy mountains and change their behaviour, but rather arrived from much further afar. Subsocial Malagasy Anelosimus probably colonized via Africa, and we predict that the solitary lineage did so also, although it has yet to be documented in Africa. Prior work suggests that while sociality in spiders frequently evolves and is beneficial in the short run (Bilde et al. 2007), at least in certain environments (Aviles et al. 2007, Jones & Riechert 2008), it may represent an evolutionary dead end (Agnarsson et al. 2006a; but see Johannesen et al. 2007). Reversing to solitary behaviour might represent a ‘way out’ from social dead end, however, our results imply that such shifts must be very rare, and that a shift from social to solitary behaviour happened only once in Anelosimus. The behaviour of several Anelosimus species is as yet unknown, but the phylogeny allows the prediction that behaviourally unknown members of the solitary clade such as Anelosimus misiones, Anelosimus inbandava and Anelosimus rabus, also are solitary.

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References


**Appendix 1**

**Taxonomy.**

Recent taxonomic work in Theridiidae can be largely characterized as the creation of new, often monotypic, genera through recategorization without any regard, or reference, to modern phylogenetics (Wunderlich 1992, 1995, 2008; Barrion & Litsinger 1995; Saaristo 2006; Yoshida 2007, 2008). This approach is unfortunate. Instead of using knowledge of phylogenetic affinities of new species to help place them, lack of such knowledge is used as the impetus to generate novel genera to accommodate each new species. Not only are such genera all but empty hypotheses (Platnick 1976), this practice can wreak havoc to natural classification of groups by rendering existing genera paraphyletic. In a recent extreme example (Saaristo 2006), nearly all species of theridiid spiders found on Seychelles islands were each placed in a new monotypic genus. These species included *Anelosimus placens*, which Saaristo transferred to a new monotypic genus *Selinus* Saaristo, 2006 (now *Seycellosa* Koçak & Kemal, see below). Wunderlich (2008) then subsequently transferred two similar European *Anelosimus* species to *Selinus*, *A. pulchellus* and *A. vittatus*. These changes ignored existing phylogenetic analyses clearly showing these species belong to...
Anelosimus (Agnarsson 2006). Here, a combination of molecular and morphological data again demonstrate that the transfer of these Anelosimus species to Selimus is invalid and flatly rejected on phylogenetic grounds (Fig. 4). Anelosimus pulchellus and A. vittatus nest deep within the genus. Furthermore, although A. placens has not yet been included in a phylogenetic analysis, it is clearly an Anelosimus based on morphological synapomorphies of the genus (Agnarsson, pers. obs.). In addition, Selimus Saaristo is likely not monophyletic because A. placens is, based on morphological similarity, more closely related to A. decaryi and A. amelie than to A. pulchellus and A. vittatus (Agnarsson pers. obs.). Therefore, here we synonymize Selimus Saaristo with Anelosimus and transfer A. placens, A. pulchellus, and A. vittatus back to Anelosimus (Appendix 1). Adding to this contorted taxonomical history, Selimus Saaristo, nota bene, is preoccupied by a jumping spider Selimus Peckham & Peckham, 1901. It was then subsequently erroneously replaced by Saaristoa Koçak & Kemal, 2008a; as Saaristoa is also preoccupied by a spider, the linyphiid Saaristoa Millidge, 1978. This was amended by the creation of a second replacement name Seycellocesa Koçak & Kemal, 2008b; here, Saaristoa Koçak & Kemal, 2008a and Seycellocesa Koçak & Kemal, 2008b are synonymized with Anelosimus. All this taxonomical conundrum was needless as there was never any reason, or rationale, to remove these species from Anelosimus.

Family THERIDIIDAE Sundevall, 1833
Genus Anelosimus Simon, 1891
Selimus Saaristo, 2006; an unavailable junior homonym of Selimus Peckham & Peckham, 1901, new synonymy (see above, and Fig. 4, for justification).
Saaristoa Koçak & Kemal, 2008a, a replacement name for Selimus Saaristo, itself an unavailable junior homonym of Saaristoa Millidge, 1978, new synonymy.
Seycellocesa Koçak & Kemal, 2008b, a replacement name for Saaristoa Koçak & Kemal, 2008, new synonymy.

Anelosimus decaryi (Fage, 1930)
Theridion decaryi Fage, 1930: 26, figs 1 and 2.
Anelosimus decaryi Agnarsson & Kuntner, 2005: 589 (transfer and synonymy) (Figs 6 and 7).


Diagnosis. Anelosimus decaryi can be distinguished from all other Anelosimus species, except A. amelie, by the shape of the embolus and embolic apophysis in the male, and by the internal female genitalia, including the trajectory details of the copulatory duct in the female (Figs 6–8). Anelosimus decaryi can be distinguished from A. amelie by smaller size, and the shape of the ridged tip of the embolic apophysis in the male, and by a less sclerotized epigynum in the female (Figs 6–8).

Male (from Orangea): Total length 2.97. Prosoma 1.45 long, 1.06 wide, 0.83 high, yellowish-brown, grey markings in centre and on rim. Sternum 0.72 long, 0.70 wide, extending between coxae IV, yellowish-brown, darker around rim. Abdomen 1.60 long, 1.19 wide, 1.18 high. Pattern as in Fig. 2M. Eyes subequal, diameter about 0.08. Leg I femur 2.05, patella 0.67, tibia 1.85, metatarsus 1.66, tarsus 0.77. Femur I about six times longer than wide, curved. Leg formula 1423. Leg base colour light, distal tips of joints dark red, especially on leg 1. Palp as diagnosed (Figs 6 and 7), with a prominent embolus bearing a characteristic embolic apophysis, strongly ridged distally.

Female (from Orangea): Total length 3.56. Prosoma 1.76 long, 1.31 wide, 0.88 high, yellowish-brown, centre and rim darker. Sternum 0.98 long, 0.81 wide, extending midway between coxae IV, yellowish-brown, darker around rim. Abdomen 1.89 long, 1.39 wide, 1.30 high, pattern as in Fig. 2. Eyes subequal, diameter about 0.11. Leg I femur 1.82, patella 0.79, tibia 1.83, metatarsus 1.64, tarsus 0.80. Femur I about 4.5 times longer than wide, curved. Leg formula 1423. Leg colour as in male. Epigynum as diagnosed (Fig. 6), with copulatory ducts spiralling partially around the spermathecae.

Natural history. See Results.

Anelosimus amelie Agnarsson, n. sp.

Holotype. Male, [FRANCE], Departmental collectivity of Mayotte, Comoros archipelago, slope of Mt. Choungui (S12°56′ 43.872 E45°7′19.1994, 200 m elevation, 8.iv.2008), collected by I. Agnarsson and M. Kuntner (National Museum of Natural History, Smithsonian Institution) (Fig. 8).

Paratype. Same data as for holotype, one female.
Other material. Same data as for holotype, about 20 specimens.

Etymology. The species is a patronym, a noun in apposition, after the senior author’s daughter, Amélie Melkorka.

Diagnosis. Anelosimus amelie can be distinguished from all other Anelosimus species except A. decaryi, by the shape of the embolus and embolic apophysis in the male, and by the internal female genitalia, including the trajectory of the copulatory duct in the female. It can be distinguished from A. decaryi by greater size, and the shape of the ridged tip of the embolic apophysis in the male, and by a more sclerotized epigynum in the female (Figs 6–8).

Male (holotype): Total length 2.83. Prosoma 1.49 long, 1.09 wide, 0.79 high, yellowish-brown, grey markings in centre and on rim. Sternum 0.79 long, 0.69 wide, extending between coxae IV, yellowish-brown, darker around rim. Abdomen 1.42 long, 1.15 wide, 1.14 high, truncated in front. Pattern as in Fig. 3. Eyes subequal, diameter about 0.09. Leg I femur 2.05, patella 0.67, tibia 2.04, metatarsus 1.59, tarsus 0.75. Femur I about 5.6 times longer than wide, curved. Leg base colour light brown, distal tips of joints on leg I and II red. Palp as diagnosed (Fig. 8).

Female (paratype): Total length 3.29. Prosoma 1.54 long, 1.16 wide, 0.85 high, yellowish-brown, centre and rim darker. Sternum 0.84 long, 0.77 wide, extending midway between coxae IV, yellowish-brown, darker around rim. Abdomen 1.79 long, 1.41 wide, 1.40 high, pattern as in Fig. 3. Eyes subequal, diameter about 1.10. Leg I femur 1.87, patella 0.69, tibia 1.88, metatarsus 1.50, tarsus 0.81. Femur I about 5.5 times longer than wide, curved. Leg formula 1423. Leg base colour light brown, distal joints red, especially leg I. Epigynum as diagnosed (Fig. 8).

Natural history. See Results.

Anelosimus placens (Blackwall, 1877) – comb. nov.
Theridion placens Blackwall, 1877: 13, pl. 2, fig. 10.
Seycellocesa placens Koçak & Kemal, 2008b: 8; Platnick, 2009.
See above for justification of transfer.

Anelosimus pulchellus (Walckenaer, 1802) – comb. nov.
Aranea pulchella Walckenaer, 1802: 208.
Selimus pulchellus Wunderlich, 2008: 362.
See above for justification of transfer.

Anelosimus vittatus (C. L. Koch, 1836) – comb. nov.
Theridion vittatum C. L. Koch, 1836: 65, fig. 217.
Selimus vittatus Wunderlich, 2008: 362, figs 450–452, 452a.
See above for justification of transfer.

Supporting Information
Additional Supporting Information may be found in the online version of this article:
Table S1 Uncorrected mitochondrial sequence divergence among the Anelosimus specimens for which we have mitochondrial data. Taxa from Madagascar are in bold, solitary taxa are marked with a blue fill.
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