

A New Species of *Croton* (Euphorbiaceae) from a Madagascan Lineage Discovered in Coastal Kenya

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Abstract—*Croton kinondoensis*, a new species from Kenya, is described and illustrated here with photographs. It is found in the sacred Kaya Kinondo Forest, one of the last remaining coastal forests patches in Kenya. Its morphology and systematic position based on ITS and *trnL-F* DNA sequence data clearly place it within the Adenophorus Group of *Croton*, a clade of ca. 15 species otherwise known only from Madagascar and the Comoros Archipelago. Its closest affinities appear to lie with *Croton mayottae*, from the island of Mayotte, and *C. menabeensis*, from northwestern Madagascar. This new species likely represents an independent dispersal of *Croton* from Madagascar to mainland Africa.

Keywords—*Croton kinondoensis*, endemic species, Kaya Kinondo Forest, phylogenetic analysis.

Croton L. is one of the biggest genera of flowering plants and the second largest genus in Euphorbiaceae, with an estimated 1300 species of trees, shrubs, herbs, and a few lianas (Govaerts et al. 2000; Frodin 2004; Berry et al. 2005; Caruzo et al. 2013). It has been traditionally classified in Euphorbiaceae and has remained there after the partitioning of the family into four families (Angiosperm Phylogeny Group III 2009). Baillon (1858) initially separated *Croton* into 20 sections, and Webster (1993) updated that system by recognizing 40 sections and several subsections in the genus. Van Ee et al. (2011) used molecular data to update Webster's (1993) sectional classification and showed that many of Webster's sections were polyphyletic. Their study focused mainly on the New World species, in which they recognized 31 sections, and they did not focus on the Old World species or sections. In a subsequent study of the Australian species of *Croton*, Van Ee et al. (2015) redefined some of the sections of *Croton* from Australasia, but they did not attempt to assign African and Madagascan species to sections. Subsequently, as part of an ongoing revision of the Western Indian Ocean Region (WIOR) species of *Croton*, Kainulainen et al. (2017) examined a number of glandular-leaved species from Madagascar and the Comoros archipelago; they placed the majority of these in the Adenophorus Group, an informal grouping named after one of its representatives, *Croton adenophorus* Baill.

Croton occurs mostly in tropical regions worldwide, with a few more representatives in subtropical and northern temperate areas. In the Neotropics, it has centers of diversity in Brazil, the West Indies, and Mexico (Burger and Huft 1995). In mainland Africa there are about 55 species (P. Barbera and R. Riina pers. comm.), with approximately 23 species known to occur in East Africa (Radcliffe-Smith 1987). Species of *Croton* can be easily recognized in the field by their indumentum of stellate or lepidote trichomes, leaves that turn orange at senescence, conspicuous petiolar or laminar glands, colorless or colored sap, unisexual flowers and anthers that are inflexed in bud (Berry et al. 2005; Haber et al. 2017).

During field investigations at the Sacred Kaya Kinondo Forest, a coastal forest in Kenya, we collected an unknown species of Euphorbiaceae. At first, the lead authors (VMN and MN) thought that it might be a species of *Mallotus* Lour., due to its shrubby habit and opposite, dentate leaves, but after preliminary molecular phylogenetic analyses, consultation of the literature on Madagascan *Croton*, and then enlisting the assistance of specialists on Western Indian Ocean *Croton* species (PEB and BvE), we found that the species belongs to *Croton*, although it bears little resemblance to any known species of *Croton* from continental East Africa (Radcliffe-Smith 1987). Its morphological characters are very similar to members of the Adenophorus Group (Kainulainen et al. 2017), which has been referred to as *Croton* sect. *Anisophyllum* Boivin ex Baill. (Baillon 1858). We describe this entity here as a new species, *Croton kinondoensis*, and provide contextual information on its affinities and biogeography.

MATERIALS AND METHODS

Specimens of the new species were first compared to other herbarium specimens deposited at the East Africa herbarium (EA), along with observations of living plants in the field. Once it was identified as potentially belonging to the Adenophorus Group, it was compared to specimens of species in that group from Madagascar and the Comoros Archipelago housed at, or on loan to, the University of Michigan Herbarium (MICH), including collections from K, MO, and P. Data on habit, habitat, distribution, and coordinates were taken from specimen labels and from notes taken during field investigations. Continuously updated collection information, and in some cases photographs, of all specimens used in this study are available at www.tropicos.org.

Taxon Selection—Haber et al. (2017) contains the most exhaustive phylogenetic analysis of *Croton* from Madagascar and continental Africa to date, and rather than add a few accessions to their matrix and repeat their analyses, our strategy for phylogenetic analysis here is to focus on taxa of the Adenophorus Group. Furthermore, several of the Adenophorus Group taxa included by Haber et al. (2017) were either not determined to species, or the determinations have changed since then (see www.tropicos.org for updated determinations of the specimens used in Haber et al. 2017). The taxon selection was guided by the results of Van Ee et al. (2015), Haber et al.

(2017), and Kainulainen et al. (2017) for the purpose of including taxa representing mainland East Africa and the Malagasy clade, with an emphasis on species belonging to the Adenophorus Group. ITS sequences from a total of 34 accessions of *Croton* were analyzed, of which nine were newly generated; *trnL-F* sequences from a total of 32 accessions were analyzed, of which seven were newly generated. Sequences of *trnL-F* were not obtained for the two accessions of *C. mayottae*: *Pascal 915* and *Barthelatt 225*. All additional sequences were downloaded from GenBank.

DNA Extraction, Amplification, and Sequencing—DNA was extracted from leaf fragments obtained from the holotype specimen *Ngumbau & Nyange SAJIT-V-0520* (HIB) using the Mag-MK Plant Genomic DNA extraction kit (Sangon Biotech, Shanghai) following the manufacturer's protocol. For Malagasy accessions, DNA was extracted using the DNeasy plant mini kit (Qiagen, Valencia, California) following the manufacturer's protocol. For phylogenetic inference, we selected the nuclear ITS region and the chloroplast *trnL-F* region, since they have been previously used for phylogenetic inference in Old World species of *Croton* (Van Ee et al. 2015; Haber et al. 2017). The ITS and *trnL-F* regions were amplified using the same primers (White et al. 1990; Taberlet et al. 1991) and the same PCR procedures as in Van Ee et al. (2015) and Haber et al. (2017). Sequence formatting and editing were conducted in Geneious v. 5.6.4 (Kearse et al. 2012).

Phylogenetic Inference—The program MAFFT v. 7.222 (Katoh and Standley 2013) was used for sequence alignment, with final matrix assembly being conducted in PAUP* v. 4.0a (Swofford 2003). The data were aligned into a two-partition matrix and analyzed with Bayesian inference (BI) in MrBayes v. 3.2.3 (Ronquist et al. 2012) on XSEDE (Townes et al. 2014) accessed through the CIPRES Science Gateway (Miller et al. 2010). Prior to performing the phylogenetic analyses, the separate ITS and *trnL-F* datasets were analyzed with MrModeltest v. 2.3 (Nylander 2004) to determine the best-fitting substitution model for each partition. The analyses were conducted under the selected models, setting the parameters that can be set in the XSEDE-CIPRES platform. In the combined analysis, the data were divided into two partitions (ITS and *trnL-F*), allowing the model parameters to be estimated separately for each partition.

Bayesian posterior probabilities (PP) were obtained from two runs of four chains each, heating parameter = 0.2, 100,000,000 generations, starting from random trees, default priors, sampling every 1000 generations, and discarding the first 30% of the sampled trees. Convergence of the Bayesian analyses was estimated by visually observing a plot of the generation vs. the log probabilities.

RESULTS

DNA Sequence Data—The newly generated ITS and *trnL-F* sequences, including *Croton kinondoensis*, are deposited in GenBank. GenBank accession numbers and details for all of the included accessions are provided in Appendix 1. The aligned, analyzed data matrices are deposited in Dryad (Ngumbau et al. 2020).

The ITS sequence of *Croton kinondoensis* differs from the most-similar ITS sequences included in these analyses (*Barthelatt 225* and *Pascal 915*, both *C. mayottae*) by two base pairs, and from that of *C. menabeensis* by three base pairs. The *trnL-F* sequence of *C. kinondoensis* differs from that of *C. menabeensis* by three base pairs (*trnL-F* sequences are not available from *Barthelatt 225* and *Pascal 915*). By comparison, the two varieties of *C. alabamensis* E.A.Sm. ex Chapm. for which multiple individuals of each were sampled by Van Ee et al. (2006) differ from each other's ITS sequences by three base pairs, and in their *trnL-F* sequences by four base pairs. In the divergence time estimates performed by Van Ee et al. (2006), the two varieties of *C. alabamensis* diverged less than two million years ago. Extrapolating from those findings, we hypothesize that *C. kinondoensis* represents a very recent dispersal from either northern Madagascar or the Comoros to mainland Africa.

Phylogenetic Inference—All analyses (combined, ITS, and *trnL-F*) recover *C. kinondoensis* within the Madagascan Adenophorus Group (Figs. 1, S1, S2) with high posterior probability (PP) support. The combined (Fig. 1) and ITS-only

(Fig. S1) analyses recover *C. kinondoensis* close to *C. menabeensis* and *C. mayottae*, although without strong support. In contrast, the *trnL-F*-only analysis (Fig. S2) does not recover these three species together. In regard to the phylogenetic relationships of *C. kinondoensis* and *C. menabeensis*, one notable difference between the three analyses is that the combined analysis recovers them within a group of northern Malagasy species with 94 PP (Fig. 1), ITS recovers them in an unresolved, unsupported position within the Adenophorus Group (Fig. S1), and *trnL-F* recovers them with 96 PP more closely related to a group of southern Malagasy species (Fig. S2).

One notable difference between the results presented here and those of Haber et al. (2017) is that the broader taxonomic sampling of Haber et al. (2017) recovered the Mongue Group, comprised of *C. mongue* and *C. goudotii*, sister to the Adenophorus Group, while in the results of the combined analysis (Fig. 1) and the ITS-only analysis (Fig. S1), these two species are embedded within the northern species of the Adenophorus Group. In the analyses of just *trnL-F* (Fig. S2), the Mongue Group is recovered in a polytomy together with members of the Adenophorus Group. Haber et al. (2017) included the chloroplast regions *matK* and *trnH-psbA* in addition to the ones we use here (ITS and *trnL-F*); it is our opinion that the observed differences between that study and the present one in regard to the phylogenetic relationship between the Adenophorus and Mongue Groups is due to the increased weight of the phylogenetic signal from ITS relative to that of the single chloroplast marker (*trnL-F*), along with differences in taxonomic sampling.

Another difference is that in Haber et al. (2017), *C. dichogamus* and *C. menyhartii* were recovered closely related to each other within WIOR clade 2, and *C. pseudopulchellus* was recovered distantly from them in WIOR clade 1. That pattern is consistent across all of the separate and combined analyses in Haber et al. (2017). Given that, Haber et al. (2017) considered *C. pseudopulchellus* an independent dispersal event from Madagascar to continental Africa. In our analyses, these three African species, *C. dichogamus*, *C. menyhartii*, and *C. pseudopulchellus*, group together as a clade, raising the possibility that they represent a single dispersal event from Madagascar to continental Africa. These three species are morphologically similar in having elliptic leaves with pinnate venation and lepidote scales on the abaxial surface, although *C. menyhartii* and *C. dichogamus* are more similar in their slightly cordate leaf base (vs. cuneate in *C. pseudopulchellus*). The phylogenetic relationships of these require further investigation, and the grouping recovered here may be an artifact of the narrower sampling.

TAXONOMIC TREATMENT

Croton kinondoensis G.W.Hu, V.M.Ngumbau & Q.F.Wang, sp. nov. TYPE: KENYA. Coast Province, Kwale County, Kaya Kinondo Forest, 04°23.508'S, 039°32.631'E, 5 m, 23 Jun 2018, V.M. Ngumbau & M. Nyange SAJIT-V-0520 (holotype HIB!; isotypes EA!, HIB!).

Croton kinondoensis shares key features of the Adenophorus Group of species from Madagascar and the Comoros and is most similar to *C. mayottae* and *C. menabeensis*; it differs from *C. mayottae* in its filiform, early deciduous stipules (vs. lanceolate, serrulate, and persistent), sessile acropetiolar glands (vs. stipitate), coarsely serrate leaf margins (vs. finely

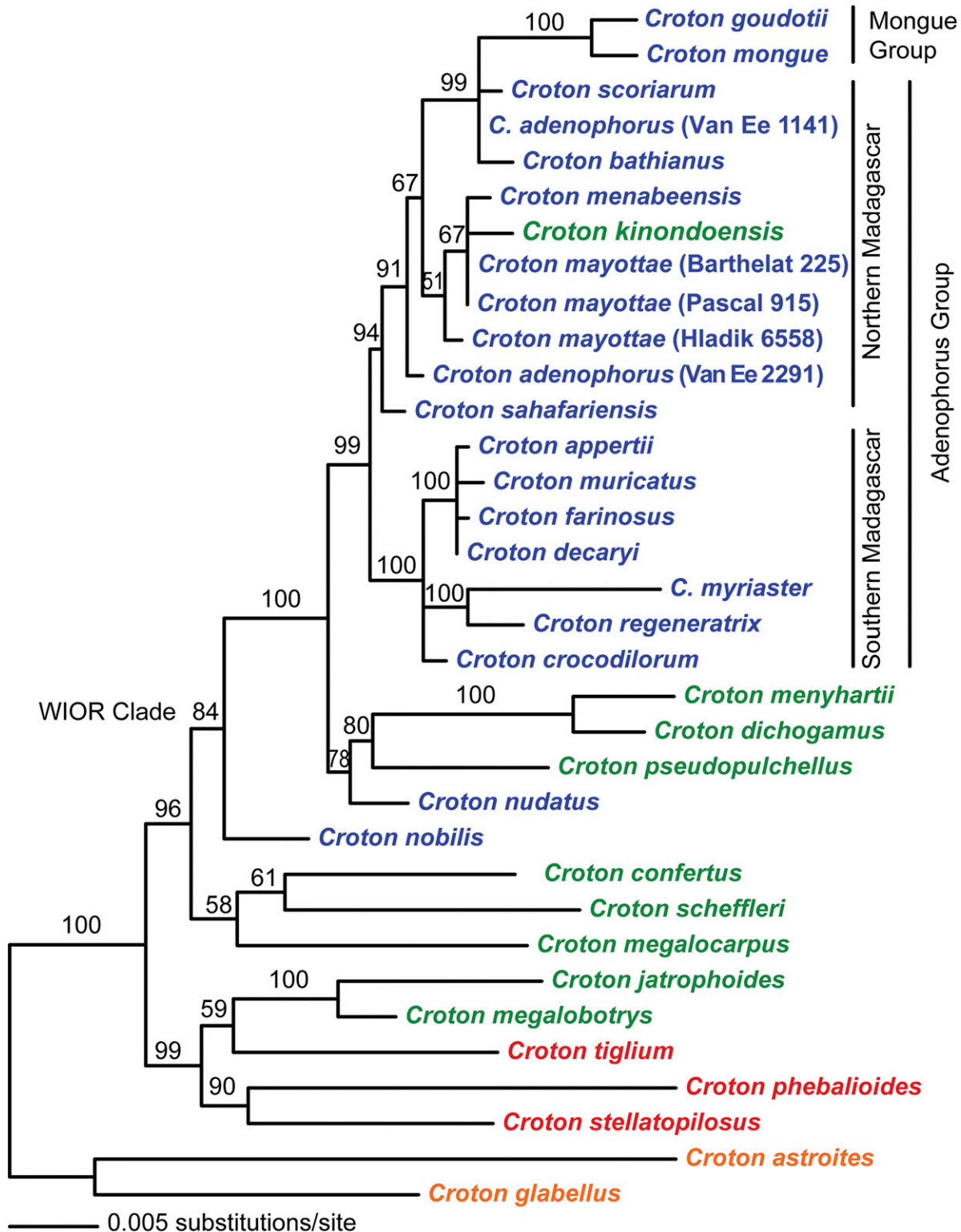


FIG. 1. Majority-rule consensus tree from the Bayesian MCMC inference of the combined ITS and *trnL-F* data. Bayesian posterior probabilities are given above the branches. Taxa belonging to the Adenophorus and Mongue groups are labeled and indicated by vertical lines to the right. Taxa in orange are from the New World, in red from Asia and Australia, in green from continental Africa, and in blue from Madagascar and the Comoro Islands.

denticulate), and abaxial laminar glands in the axils of the secondary veins where they branch from the midvein, along with domatia (vs. glands in the axils of the secondary and tertiary veins, without domatia), whereas it differs from *C. menabeensis* in its strongly cordate leaf bases (vs. rounded)

and abaxial glands as described above (vs. sparse glands in the axils of the secondary and tertiary veins).

Shrubs, 0.7–2 m tall, monoecious, with clear to orange latex. Branches with sparse, brown, stellate trichomes when young and glabrate, shiny, greyish-brown when mature. Stipules

filiform, 3–8 mm long, densely stellate, early deciduous. Leaves thinly chartaceous, opposite to subopposite; petioles 5–50 mm long, covered by black to brownish stellate trichomes, with two dark green to light brownish stipitate discoid acropetiolar glands at the junction with the lamina;

lamina ovate to oblong-ovate, 20–110(–120) × 15–65(–70) mm, base deeply cordate to cordate, apex acuminate to acute; margin irregularly serrate or coarsely serrate, adaxially stellate-pubescent when young to glabrescent when mature, abaxially black to brownish, densely stellate-pubescent when

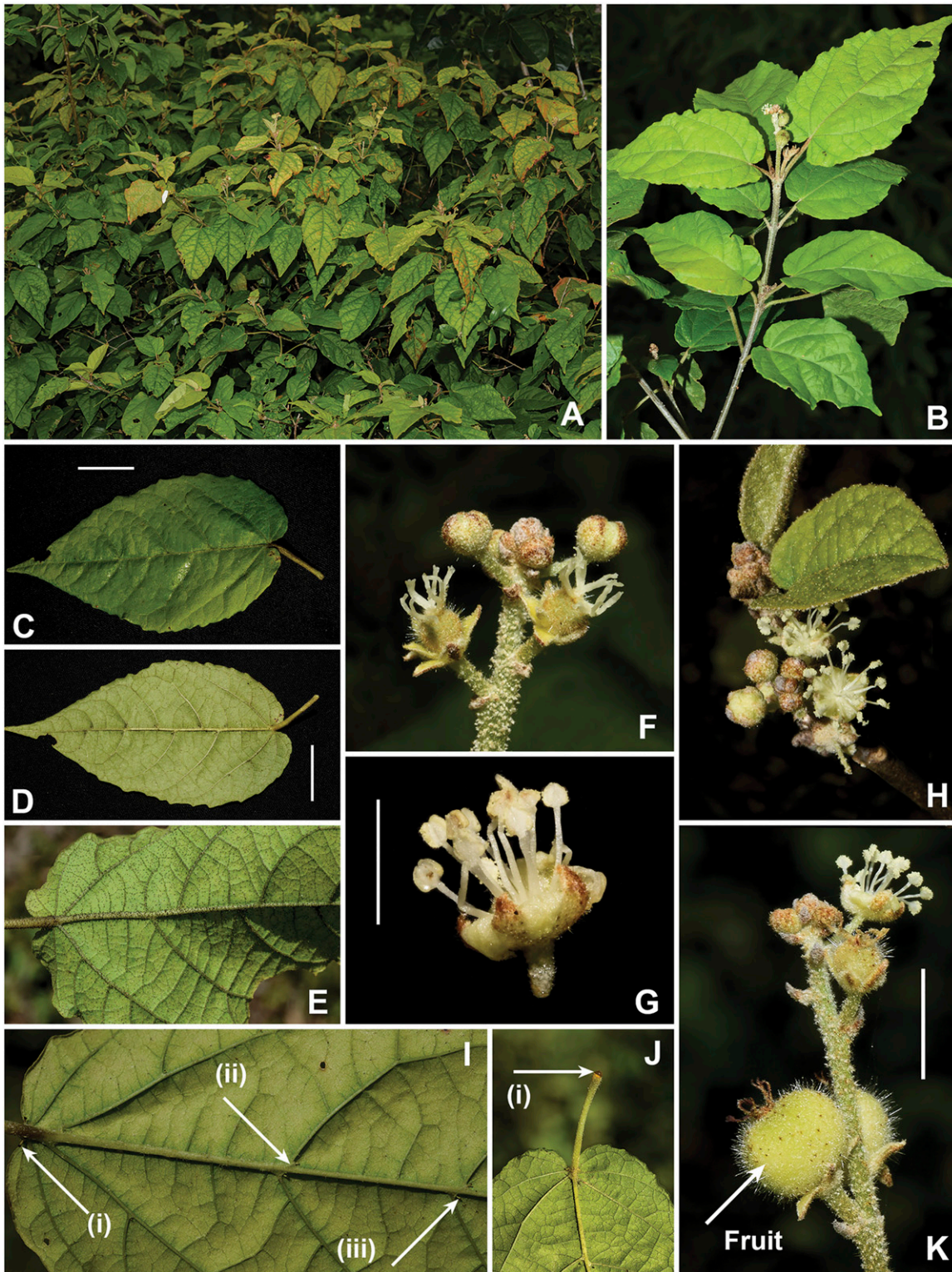


FIG. 2. *Croton kinondensis* G.W.Hu, V.M.Ngumbau & Q.F.Wang. A. Habit. B. Branch showing leaf arrangement. C. Adaxial side of leaf blade. D. Abaxial side of leaf blade. E. Black stellate trichomes. F. Inflorescence with pistillate flowers. G. Staminate flower. H. Inflorescence with staminate flowers. I. (i) Stipitate acropetiolar glands. (ii) Domatium. (iii) Axillary stipitate glands. J. (i) Orange latex. K. Inflorescence with both pistillate and staminate flowers. Scale bars: C–D = 2 cm, G = 2 mm, K = 0.5 mm. Photos by G. W. Hu and V. M. Ngumbau.

young, sparsely stellate when mature; (3–)5–7-veined from the base, lateral veins in 3–7(–9) pairs; the axil of each secondary vein branch from the midvein with a domatium and a stipitate discoid gland on the abaxial leaf surface up to $\frac{3}{4}$ of the leaf from the base; midrib and veins prominent beneath, slightly prominent above. Inflorescences terminal or axillary, raceme-like thyrses 15–40 mm long, unisexual or bisexual, bisexual inflorescences mostly consisting of pistillate flowers, with several staminate flowers at the apex; axis densely

stellate; bracts triangular-ovate, 1–2 mm long, densely stellate. Staminate flowers: pedicels 1.5–2 mm long, densely stellate; buds 2×1.5 mm, connate at the base; sepals 5, triangular-ovate, 2×1.5 mm, abaxially rusty stellate, adaxially glabrous, pale green; petals 5, oblong-elliptic, 2.5×2 mm, apex rounded, margin villous; stamens 12–16; filaments 1.5–2 mm long; anthers basifixed, elliptic. Pistillate flowers: pedicels 1–1.5(–2) mm long, brown pubescent; sepals 5, triangular-ovate, adaxially and abaxially pubescent,

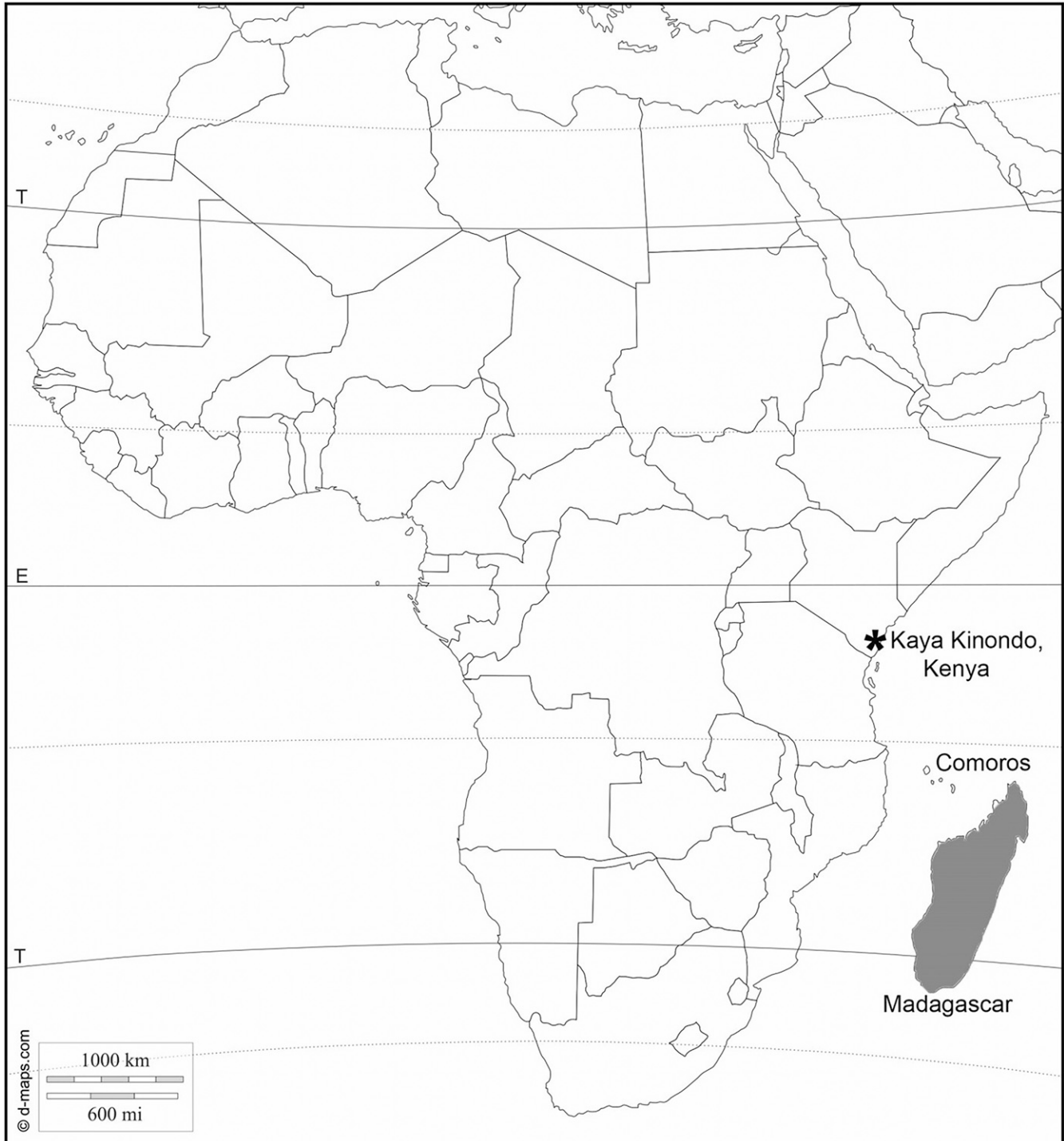


FIG. 3. Location of the Kaya Kinondo Forest in coastal Kenya, the only known locality of *Croton kinondoensis*. Madagascar and the Comoros Archipelago are also indicated, which is where the related species of the Adenophorus Group occur. We acknowledge use of the base map provided by d-maps.com (https://d-maps.com/carte.php?num_car=739&lang=en).

connate at the base, 1–1.5 × 0.7–1 mm, persistent; petals ca. 1.5 × 0.5 mm, often more reduced or absent; ovary subglobose to slightly trilobed; styles 3, 1.5–2 mm long, flattened, each bifurcating 2–4 times, for a total of 12 or more stigmatic tips, spreading, abaxially pubescent, adaxially glabrous, pale green, persistent. Capsules 5–6 mm wide, globose, stellate; endocarp woody, ca. 0.3 mm thick; columella 3–4 mm long. Seeds ellipsoid, 3–4 × 2–2.5 mm, testa glossy, brown. Figure 2.

Distribution and Ecology—So far this species is only known from the Sacred Kaya Kinondo Forest, which is located in Kwale County around Diani Beach (Fig. 3), which is within the Eastern Arc and Coastal Forests of Tanzania/Kenya biodiversity hotspot (Myers et al. 2000). *Croton kinondoensis* grows at the forest edge associated with *Mallotus oppositifolius* (Geiseler) Müll.Arg. (Euphorbiaceae), *Harrisonia abyssinica* Oliv. (Rutaceae), and *Fernandoa magnifica* Seem. (Bignoniaceae).

Phenology—Plants were found in flower and fruit from June to October.

Etymology—The species epithet ‘*kinondoensis*’ refers to its type locality within the Kaya Kinondo Forest.

Conservation Status—Given that this new taxon is presently known from only three collections from the Kaya Kinondo Forest, which is estimated at 30 ha in size (Robertson and Luke 1993), the application of any formula-based conservation assessment such as that of the IUCN (2017) will inevitably conclude that it is either highly endangered, or that there are not enough data to draw a firm conclusion. The limited ecological knowledge that we have about *C. kinondoensis* is that it is found at the forest edge, which is similar to many species of *Croton*, which are notorious elements of secondary and disturbed vegetation (Berry et al. 2005). It is therefore possible that some of the factors that are commonly thought of as worsening the conservation status of a species, such as anthropogenic habitat fragmentation, could actually benefit *C. kinondoensis*. The Kaya Kinondo Forest has been used as an example of successful community-based conservation (Nyamweru and Kimaru 2008). Therefore, although very small, the known population of *C. kinondoensis* is likely safe from immediate threats.

The restricted distribution and population size of *C. kinondoensis* is consistent with our hypothesis that it is a very recent arrival to coastal East Africa from either Madagascar or the Comoros. Even if it is ecologically very successful in Kenya, it is possible that not enough time has passed for it to further expand throughout suitable habitat on mainland Africa.

Additional Specimens Examined—Kenya.—COAST PROVINCE: Kwale County, Kaya Kinondo Forest, 4°39.27'S, 39°54.45'E, 1 Sep 2010, I. Malombe, N. Mwadime & K.I. Saidi 1647 (EA!); *ibid* loc., 5 m, 2 Oct 2018, Sino-Africa Joint Investigation Team (SAJIT) 007225 (HIB! EA!).

DISCUSSION

Based on morphological characters and a review of Baillon (1858), Leandri (1939), and Webster (1993), it is likely that this new species belongs to *Croton* sect. *Anisophyllum*, which is currently also referred to as the Adenophorus Group (Haber et al. 2017). This group was previously considered to be endemic to Madagascar and the Comoros Archipelago (Kainulainen et al. 2017). Characters that support *Croton kinondoensis* as a member of the Adenophorus Group include opposite leaves (Fig. 2B) with 3–7(–9) pairs of lateral veins and a deeply cordate base (Fig. 2C–E), stipitate and discoid acropetiole glands (Fig. 2E), stipitate glands in the axils of

the secondary veins on the abaxial leaf surface (Fig. 2I), a raceme-like thyrses inflorescence, and pistillate flowers with vestigial petals (Fig. 2F).

From the phylogenetic analyses performed based on ITS and *trnL-F* DNA sequences (Figs. 1, S1, S2), *Croton kinondoensis* is well nested within a group of species from Madagascar and Mayotte that belong to the Adenophorus Group, and this corroborates the morphological evidence. None of the species from mainland Africa that we sampled emerged close to *C. kinondoensis* (Fig. 1).

From our phylogenetic results, there is strong support that *Croton kinondoensis* is part of the Western Indian Ocean Region (WIOR) clade, and within it, it is part of the Adenophorus Group which was previously thought to be confined to northern Madagascar and the Comoros Archipelago (Kainulainen et al. 2017). The species that appear most closely related to *C. kinondoensis* are *C. mayottae* and *C. menabeensis*. *Croton mayottae* is endemic to the island of Mayotte, a French territory in the Comoros Archipelago, and *C. menabeensis* is restricted to northwestern Madagascar. These species are physically closer to the Kenyan coast than ones occurring in the south of Madagascar, and as such, they may indicate a possible dispersal route to Africa from Madagascar and the Comoros, most likely by ocean currents (Stankiewicz et al. 2006; Yoder and Nowak 2006; Ali and Huber 2010). The morphological differences among them are subtle, which is true for the characters that distinguish most species of the Adenophorus Group, which may indicate a relatively recent divergence.

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AUTHOR CONTRIBUTIONS

VMN and MN did field work and collected the holotype; G-WH, VMN, and Q-FW wrote the species description and the manuscript; NW and IM examined herbarium specimens and revised the manuscript; BvE performed data matrix assembly and phylogenetic inference, and revised the manuscript; PEB examined herbarium specimens, selected the taxon sampling for the phylogenetic analyses, provided the species diagnosis, and revised the manuscript.

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APPENDIX 1. GenBank accession numbers and specimen information for the accessions analyzed phylogenetically. The data are provided in the following order: taxon; locality; voucher; ITS; *trnL-F*.

New World outgroups: *Croton astroites* Dryand.; Puerto Rico; *Van Ee* 537 (WIS); EU586901; EU586955. *Croton glabellus* L.; Jamaica; *Van Ee et al.* 771 (MICH); EU477892; EU497719.

Old World: *Croton adenophorus* Baill.; Madagascar; *Van Ee et al.* 2291 (MICH); MN504415; MN504422. Madagascar; *Van Ee et al.* 1141 (MICH); KY039659; KY039937. *Croton appertii* Leandri; Madagascar; *Phillipson* 3699 (MO); KY039590; KY039868. *Croton bathianus* Leandri; Madagascar; *Van Ee et al.* 1140 (MICH); KY039586; KY039864. *Croton confertus* Baker; Oman; *Lawton* 2339 (K); KP878332; KP878417. *Croton crocodilorum* Leandri; Madagascar; *Van Ee et al.* 885 (MICH); MN504416; MN504423. *Croton decaryi* Leandri; Madagascar; *Van Ee et al.* 915 (MICH); KY039604; KY039882. *Croton dichogamus* Pax; Kenya; *Morawetz* 406 (MICH); KP878337; KP878421. *Croton farinosus* Lam.; Madagascar; *Van Ee et al.* 963 (MICH); KY039595; KY039873. *Croton goudotii* Baill.; Madagascar; *Van Ee et al.* 968 (MICH); KY039611; KY039889. *Croton jatrophioides* Pax; Tanzania; *Fahik* 20 (MO); KP878348; KP878427. *Croton kinondoensis* G.W.Hu, V.M.Ngumbau & Q.F.Wang; Kenya; *Ngumbau & Nyange SAJIT-V-0520* (HIB); MN504412; MN504420. *Croton mayottae* P.E.Berry & Kainul.; Mayotte; *Hladik* 6558 (P); MN504409; MN504418. Mayotte; *Barthelat, M'Changama & Sifary* 225 (P); MN504411; —. Mayotte; *Pascal* 915 (P); MN504414; —. *Croton megalobotrys* Müll.Arg.; South Africa; *Becker et al.* 1004 (MICH); KP878357; KP878430. *Croton megalocarpus* Hutch.; Tanzania; *Festo & Bayona* 549 (MO); KP878360; KP878431. *Croton menabeensis* Leandri; Madagascar; *Van Ee et al.* 2276 (MICH); MN504413; MN504421. *Croton menyhartii* Pax; South Africa; *Becker* 984 (MICH); KP878363; KP878434. *Croton mongue* Baill.; Madagascar; *Van Ee et al.* 974 (MICH); KP878368; KP878437. *Croton muricatus* Vahl; Madagascar; *Eboroke* 929 (MO); AY971201; AY971291. *Croton myriaster* Baker; Madagascar; *Van Ee et al.* 802 (MICH); KY039632; KY039907. *Croton nobilis* Baill.; Madagascar; *Van Ee et al.* 398 (MICH); HM044797; HM044778. *Croton nudatus* Baill.; Madagascar; *Van Ee et al.* 1104 (MICH); MN504417; MN504424. *Croton phebalioides* F.Muell. ex Müll.Arg.; Australia; *Ford* 2325 (QRS); KP878373; KP878442. *Croton pseudopulchellus* Pax; Tanzania; *Kayombo et al.* 4518 (MO); KP878381; KP878444. *Croton regeneratrix* Leandri; Madagascar; *Van Ee et al.* 1179 (MICH); KY039632; KY039910. *Croton sahafariensis* Kainul. & P.E.Berry; Madagascar; *Van Ee et al.* 2312 (MICH); MN504410; MN504419. *Croton scheffleri* Pax; Malawi; *Kathumba* 35 (MO); KP878388; KP878448. *Croton scoriarum* Leandri; Madagascar; *Van Ee et al.* 1120 (MICH); KY039646; KY039924. *Croton stellatopilosus* H.Ohba; Thailand; *Pooma* 98-101 (WIS); KP878391; KP878449. *Croton tigilium* L.; China; *Jin* 006 (MICH); KP878399; KP878454.