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RESEARCH ARTICLE

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Outbreaks of a native jewel beetle, *Agrilus grandis* (Coleoptera: Buprestidae), on commercial black wattle, *Acacia mearnsii*, plantations in South Africa

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In early 2024, an outbreak of an unknown wood-borer was observed in *Acacia mearnsii* De Wild (black wattle) compartments in the Midlands of KwaZulu-Natal, South Africa, causing symptoms of excessive resin production. Larvae uncovered beneath the bark were morphologically identified as a flathead borer, prompting urgent investigation due to the historically low impact of wood-borers on black wattle in South Africa. DNA sequencing of the COI and CytB regions of the larvae failed to yield conclusive matches, so infested logs were collected and the infesting insects reared, resulting in the emergence of three adult beetles. Morphological examination of the adults revealed them as being *Agrilus grandis* Gory & Laporte 1839, a native African jewel beetle. Comparison to historical specimens housed in the FABI Insect Reference Collection based at the University of Pretoria revealed a previous, unpublished outbreak of the same species in *Acacia mearnsii* in 1974. However, this is the first official report of *A. grandis* infestations on *A. mearnsii* in South Africa.

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INTRODUCTION

The Australian tree species *Acacia mearnsii* De Wild (black wattle) (Fabales: Fabaceae) is a key plantation species for South Africa's commercial forestry sector, accounting for approximately 110 000 hectares across the country, managed by commercial farmers, corporate growers and small-scale growers (Chan et al. 2015; Payn and Little 2017). Black wattle bark is an essential global source of tannins for the leather industry, and its timber supports various markets including construction, pulp, charcoal, and firewood (Chan et al. 2015; Lusizi et al. 2024). Despite its economic value, debates continue regarding its invasiveness and ecological consequences (Chan et al. 2015; Lusizi et al. 2024).

Pathogens have historically been the primary threat to black wattle plantations, with *Ceratocystis albifundus* M.J. Wingf., De Beer & M.J. Morris 1996 (Ascomycota: Ceratocystidaceae) causing the greatest documented damage (Roux et al. 2007; Heath et al. 2010). Other diseases, such as wattle rust, caused by *Uromycladium acaciae* (Cooke) P. Syd. & Syd. 1914 (Basidiomycota: Pileoliariaceae) and black butt, caused by various *Phytophthora* spp. (Oomycota: Pernosporaceae), occur occasionally but typically only have moderate impacts (Morris and Wingfield 1988; Roux and Wingfield 1997; McTaggart et al. 2015). Insect pests, including soil-borne cutworms (affecting young trees), and foliar pests such as wattle bagworm (Lepidoptera: Psychidae) and wattle mirid, *Lygidolon laevigatum* Reuter 1907 (Hemiptera: Miridae), are managed effectively, and serious outbreaks are rare (Payn and Little 2017; Hurley et al. 2023).

In early 2024, symptoms of excessive resin exudation were observed in black wattle compartments in the Midlands region of KwaZulu-Natal (Figure 1). Inspection revealed flathead borer larvae from the Buprestidae family (Coleoptera) tunneling beneath the bark. Few wood-borers are known to attack black wattle in South Africa (Hurley et al. 2023), making urgent identification of these larvae necessary.

MATERIALS AND METHODS

Sample collection, specimen rearing, and morphological identification

Field surveys were conducted in March 2024 at six sites in Melmoth, KwaZulu-Natal, where infestation signs first appeared (site 1: 28°32′27.86″ S, 30°47′22.652″ E, planted to three-month-old *A. mearnsii;* site 2: 28°37′41.52″ S, 31°20′39.48″ E, planted to one-year-old *A. mearnsii;* site 3: 28°19′6.24″ S, 31°13′12.719″ E, planted to one-year-old *A. mearnsii*; site 4: 28°38′28.68″ S, 31°22′42.239″ E, planted to one-year-old *A. mearnsii*; site 5: 28°37′18.12″ S, 31°19′56.999″ E, planted to 11-month-old *A. mearnsii*; and site 6: 28°37′7.68″ S, 31°35′21.48″ E, planted to 18-month-old *A. mearnsii*). Symptomatic stems were collected from trees at all of these locations and brought to the Forestry and Agricultural Biotechnology Institute (FABI), based at the University of Pretoria, South Africa for further analysis. Bark was peeled off the logs and larvae were manually extracted from feeding tunnels beneath the bark and preserved in absolute ethanol at –20 °C.

Selected stems were incubated in rearing cages at the FABI Biocontrol Centre and monitored for beetle emergence over six months, resulting in the recovery of three adult jewel beetles. These were submitted to the South African National Collection of Insects (ARC, Roodeplaat, Pretoria) for species identification.

Figure 1: Symptoms of excessive resin production observed on black wattle trees in the field caused by *A. grandis*.

Morphological features of both a larval and adult specimen were captured using a Zeiss Discovery V16 dissection microscope with an attached Zeiss Axiocam 512 color camera (Zeiss, Oberkocken, Germany). Focus stacked images were produced using HELICON FOCUS V.5 (HeliconSoft, Kharkiv, Ukraine).

DNA extraction and sequencing

DNA was extracted from a larval specimen using the MACHEREY-NAGEL NUCLEOSPIN TISSUE kit (Separations, Johannesburg, South Africa), following manufacturer's guidelines with the elution volume adjusted to 70 µL. PCR amplification targeted the Cytochrome oxidase 1 (COI–LepF1/LepR1 primers; Hebert et al. 2004) and Cytochrome B (CytB–CP1/CB2 primers; Harry et al. 1998; Jermiin and Crozier 1994) gene regions. Standard PCR conditions and touchdown annealing were used (Nel et al. 2025).

Amplicons were cleaned with EXOSAP-IT™ PCR Product Clean-up Reagent (ThermoFisher Scientific, Massachusetts, United States) and sequenced bidirectionally using the BIGDYE® TERMINATOR V3.1 CYCLE SEQUENCING KIT (ThermoFisher Scientific, Massachusetts, United States) protocol. Sanger sequencing was performed at the sequencing facility based at the University of Pretoria, South Africa, using an ABI PRISM®3500 GENETIC ANALYZER (Applied Biosystems, California, United States). Sequence quality was assessed using Sequence Scanner 1.0 and consensus sequences were manually assembled. Consensus sequences were deposited in GenBank (accession numbers PX870796 COI and PX898107).

RESULTS

Trees from all six sites visited showed similar symptoms, the most abundant being the occurrence of high amounts of resinous exudation (Figure 1). These exudations typically followed a spiraling pattern up the stem or along affected branches. Peeling of the bark in the locations of resin production revealed the presence of galleries filled with either resin or sawdust (frass).

Larval extractions from symptomatic logs collected across all study sites confirmed infestation by a single buprestid species. Each larva tunneled beneath the bark, leaving the spiral galleries (Figure 2A–C). Upon maturation, larvae doubled back on their tunnels, bored into the wood, and prepared for pupation (Figure 2D–E).

Three adult specimens were successfully reared from collected logs and emerged from D-shaped exit holes (Figure 2F). After successful recovery of these adults, the remaining logs were dissected and investigated. Post-rearing dissection showed non-emergent specimens that either died prior to pupation, or during the process. Low emergence of adults could be due to a need for live plant material or non-optimal rearing conditions.

The three adult specimens were submitted to the ARC for identification. Morphological analysis by Dr. Riaan Stals identified the adults as *Agrilus grandis* (Coleoptera: Buprestidae: Agrilini) (Figure 3). One of the submitted specimens was retained by the ARC to be maintained as a reference specimen in their National Collection of Insects (SANC-COLG-00023).

After interrogation of our DNA sequences against the NCBI and BOLD databases, it was found that no published DNA sequences for *A. grandis* were available. However, BLAST

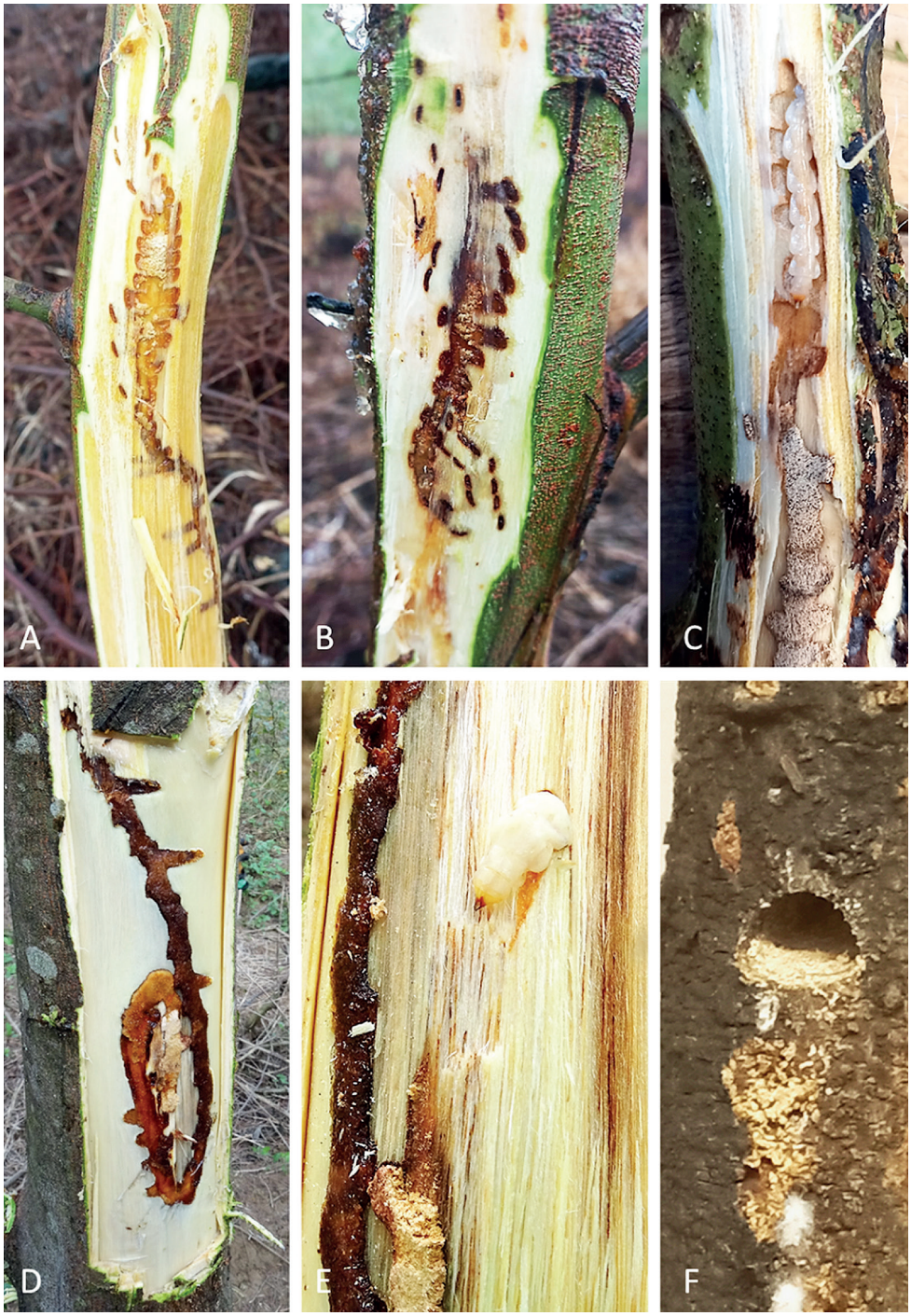

Figure 2: Larval tunneling of *A. grandis* beneath the bark of *A. mearnsii*. (A and B) Spiraling feeding tunnels exposed beneath the bark; (C) Exposed larva in its feeding tunnel; (D) Feeding tunnel doubling back; (E) Larva tunneling into the stem for pupation; (F) D-shaped emergence hole.

searches indicated that the newly generated sequences for both the COI and CytB regions were verified as most likely belonging to an *Agrilus* species. Comparison of our COI sequences to those in both BOLD and NCBI identified the closest matches both at 86% similarity to *A. ussuricola* Obenberger 1924, and an unknown *Agrilus* species, respectively.

DISCUSSION

This study is the first formal report of the native jewel beetle, *Agrilus grandis*, infesting commercial *Acacia mearnsii* plantations in South Africa. Identification relied on morphology, as DNA matches in public databases were inconclusive due to limited reference sequences available for regional species. New sequences submitted to GenBank will facilitate future identifications (Kelnorova et al. 2019; Ruzzier et al. 2023).

Buprestidae (jewel beetles) encompass over 15 000 species globally; many are wood-borers of economic concern to forestry (Evans et al. 2004; Muilenburg and Herms 2012; Ruzzier et al. 2023). Most species attack stressed or senescent trees, but some — such as those in the genus *Agrilus* — can seriously damage healthy hosts, particularly outside native ranges. *Agrilus* has been reported as the most speciose animal genus, with over 3 300 described species worldwide, and around 750 in Africa (Duan et al. 2024). Although several *Agrilus* species, such as *A. planipennis* Fairmaire 1880 (emerald ash borer), have caused major pest outbreaks elsewhere, native African species rarely do (Ruzzier et al. 2023; Duan et al. 2024).

The expansion of non-native tree plantations in South Africa has likely facilitated the host range shift seen in *A. grandis*. Historically, *A. grandis* was associated with *Albizia* species

Figure 3: Adult A. grandis specimen reared from *Acacia mearnsii*, scale = 2.0 mm.

(Bellamy et al. 1988); however, the increasing prevalence of black wattle forestry (a species in the same family as *Albizia*) appears to have prompted adaptation to a new, more abundant host. Host shifts are common in *Agrilus*, and their ecological flexibility makes them an important genus to monitor (Cipollini and Peterson 2018; Ruzzier et al. 2023; Duan et al. 2024).

Historical evidence showed *A. grandis* infested wattle in 1974 (WRI 1975) in the Paulpietersburg and Melmoth areas of KwaZulu-Natal, but outbreaks were never formally reported until now. Recent evidence confirms that the active outbreak has spread into parts of Mpumalanga, posing a widespread risk to plantations, especially for small-scale growers. However, it is unknown whether infestations can directly lead to tree mortality or facilitate entry of pathogenic fungi. This event highlights the need for regular pest monitoring and documentation. The spread of native wood-borers to non-native hosts may have significant implications for forestry management.

CONCLUSIONS

We document an outbreak of *Agrilus grandis* — a native jewel beetle — on *Acacia mearnsii* in two provinces in South Africa. Its expansion to a new host underscores important ecological consequences of non-native plantation forestry. We recommend enhanced monitoring, research on native wood-borers, and rapid outbreak reporting for effective future management. Gene sequences generated here will support ongoing surveillance of this emerging pest throughout the country. Surveys are ongoing to track the outbreak's distribution and assess beetle damage levels.

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