

plant disease

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DISEASE NOTES

First Report of the Root-Rot Pathogen, *Armillaria gallica*, on Koa (*Acacia koa*) and 'Ōhi'a Lehua (*Metrosideros polymorpha*) on the Island of Kaua'i, Hawai'i

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Koa (*Acacia koa*) and 'ōhi'a lehua (*Metrosideros polymorpha*) are the two most dominant native tree species in Hawai'i. Their populations are continuously decreasing, primarily because of forest disease (Dudley et al. 2007; Keith et al. 2015) and other biotic disturbances. In April 2015, *Armillaria* rhizomorphs were collected from woody hosts on the island of Kaua'i, Hawai'i. Based on somatic pairing tests, isolates were assigned to two genets or clones (Kōke'e-3 and Nu'alolo-2) of the same species. Subsequently, these two genets were identified as *A. gallica* on the basis of pairing against 18 tester isolates representing six North American *Armillaria* spp. and translation elongation factor 1 α (*tef1*) nucleotide sequences (GenBank accession nos. KX772408 for Kōke'e-3 and KX772409 for Nu'alolo-2). From 15 replications of somatic incompatibility tests, both genets showed reasonably high intraspecific compatibility (colorless antagonism) with three *A. gallica* tester isolates (average 62%), but low compatibility with closely related *Armillaria* spp. (average 1 to 31%). Sequences of *tef1* for both genets showed an identity of 98% (KF156775) and 97% (KF156772) to *A. gallica* with 99 to 100% coverage. In Hawai'i, *A. gallica* has been reported on the Big Island of Hawai'i on Monterey pine (*Pinus radiata*), loblolly pine (*P. taeda*), māmane (*Sophora chrysophylla*), and Methley plum (*Prunus* sp.) (Kim et al. 2010). This study identified four new host associations in Kaua'i, but only two of these hosts showed both signs and symptoms of root disease. Genet Kōke'e-3 comprised one isolate collected from a dying, mature koa tree in the west Pu'u ka Pele Forest Reserve (22°05'38.34" N, 159°41'27.42" W, elevation 876 m) approximately 1.45 km northwest of Lua Reservoir. The crown of the koa tree showed severe dieback (>75% dead) with decayed roots and flaccid/senescing leaves. Genet Nu'alolo-2 consisted of five isolates collected at the head of Nu'alolo trail (22°07'46.08" N, 159°39'35.82" W, elevation 1,124 m), approximately 5.07 km northeast of the Kōke'e-3 collection. These isolates were collected from koa and 'ōhi'a lehua with crown dieback/thinning and root decay, in addition to apparently healthy karaka nut

(*Corynocarpus laevigatus*; introduced from New Zealand) and 'āla'a (*Pouteria sandwicensis*; endemic in Hawai'i). Koa symptoms at Nu'alolo trail were similar to those associated with the Kōke'e-3 genet, except <25% of the crown was dead/dying at the time of collection. Above-ground symptoms on mature koa trees from each site were similar to koa-wilt disease caused by *Fusarium oxysporum* f. sp. *koae* (Dudley et al. 2007); however, the koa-wilt pathogen was not recovered from root samples from either tree. Interestingly, *A. gallica* genet Nu'alolo-2 was collected from diseased 'ōhi'a lehua (50 cm dbh), symptomless karaka nut, and symptomless 'āla'a, which were all growing in close proximity. *A. gallica* has a wide host range, it displays diverse ecological behaviors, and phylogenetic studies suggest it likely comprises a species complex (Kim et al. 2012). It can act as an opportunistic and/or primary pathogen (Brazee and Wick 2009), especially under stressors, such as climate change. Although *A. gallica* was isolated from multiple hosts in forests of Kaua'i and the Big Island of Hawai'i, continued surveys are needed to document distribution of *A. gallica* on diverse native and exotic tree species throughout the Hawaiian Islands, especially in relation to climate change.

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