United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
February 26, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Austropuccinia psidii***

Current APHIS regulatory status of pest: Quarantine only for Hawai'i

Hosts: **All taxa of Myrtaceae family**

Taxonomy and description of the pest:

Austropuccinia psidii is a rust pathogen classified in the Basidiomycota phylum, the Pucciniomycetes class, the Pucciniales order, and the Sphaerophragmiaceae family (Beenken, 2017). The genus has been newly erected and placed within the redefined family *Sphaerophragmiaceae* based on molecular evidences. Most of the literature for *Austropuccinia psidii* was written under the basionym *Puccinia psidii*.

A. psidii was first found on guava, *Psidium guajava*, in Brazil in 1884 (Winter, 1884). Since then, approximately 25 species of rust (mostly *Puccinia* or *Uredo*) have been described from Myrtaceae and are now considered synonyms of *A. psidii* (CABI, 2019; Hennen et al., 2005, Simpson et al., 2006; Walker, 1983). Simpson et al., (2006) described *Uredo rangelii* as a disctint species, based on two herbarium specimens from South and Central America. However, recent molecular analysis has revealed no distinction between "*U. rangelii"* from Australia and *A. psidii* from numerous collections in Brazil, Hawaii and Uruguay (CABI, 2019; Carnegie et al., 2010a; Pegg et al., 2014).

Common names for *A. psidii* diseases are guava rust, myrtle rust, eucalyptus rust, and ohia rust

(CABI, 2019).

Known distribution:

Austopuccinia psidii was first described from Brazil and is now widespread throughout Central and South America. It is present in Argentina, Australia, Brazil, China, Colombia, Costa Rica, Cuba, Dominica, Dominican Republic, Ecuador, El Salvador, Guatemala, Jamaica, Japan, Mexico, New Caledonia, Panama, Paraguay, Puerto Rico, South Africa, Trinidad and Tobago, United States, U.S. Virgin Islands, Uruguay and Venezuela (CABI, 2019; and references therein; Kawanishi et al., 2009; Simpson et al., 2006). Most recently, it was detected in Japan (Kawanishi et al., 2009), China (Zhuang and Wei, 2011), Australia (Carnegie et al., 2010), South Africa (Roux et al., 2013) and New Caledonia (Davar Nouvelle-Caledonie, 2014).

Within the United States, *A. psidii* is present in California, Florida, Hawaii, and the U.S. Virgin Islands (CABI, 2019; Uchida et al., 2006; Zambino and Nolan, 2012).

Biology of the pest:

A. psidii has a macrocyclic life cycle with distinct aecia, uredinia, telia, and basidia stages (Coutinho et al., 1998) and is considered autoecious (capable of completing its life cycle on species of Myrtaceae) (Figueiredo et al., 1984). However, attempts at basidiospore inoculation of Myrtaceae failed to provide unequivocal proof that the rust is autoecious (Morin et al., 2014). Simpson et al., (2006) suggested that *A. psidii* is heteroecious, with an alternate host yet to be found.

A. psidii teliospores have been reported from the field and laboratory on a range of hosts in both its native and introduced ranges (Alfenas et al., 2004; Aparecido et al., 2003; Carnegie and Lidbetter, 2012; Ferreira, 1983; Morin et al., 2012; Pegg et al., 2014; Pérez et al., 2011).

Urediniospores germinate in the presence of free water at temperatures between 15ºC and 25°C (Piza and Ribeiro, 1988; Ruiz et al., 1989a; Ruiz et al., 1989b; Ruiz et al., 1989c). Following germination, an infection peg directly penetrates the host, usually between two epidermal cells (Hunt, 1968). *A. psidii* pustules can mature to release spores in 10-12 days (Alfenas et al., 2003).

Low temperature (20°C), high nighttime relative humidity (80%), and high levels of airborne inoculum favor disease development (Blum and Dianese, 2001). *A. psidii* survives in moisture, including fog, dew, or the microclimate within a plant (CABI, 2019).

Signs and Symptoms:

A. psidii causes lesions on young, actively growing leaves and shoots, as well as on fruits and sepals (Coutinho et al., 1998). Lesions are brown to grey with masses of bright yellow or orange-yellow urediniospores. Occasionally, lesions have sori containing dark brown teliospores or a

mixture of the two spore types. Older lesions have purpling of their margins on leaves and shoots of many *Eucalyptus, Melaleuca* and *Callistemon* hosts. Lesions on fleshy fruits of *Eugenia, Psidium* and *Syzygium* may not have obvious margins due to their being covered with heavy spore masses when young, and rot caused by secondary pathogens as the fruits ripen. Severe rust disease in young trees may kill shoot tips, causing loss of leaders and a bushy habit (Glen et al., 2007). In the case of non- native *Syzygium jambos* in Hawai‘i, entire plants are eventually killed (Uchida and Loope, 2009, Loope, 2010).

Population structure:

Outside of Hawaii, different genotypes of *Austropuccinia psidii* were reported to occur in Brazil, Colombia, South Africa, Mexico, parts of southeast Asia, Oceania, Central America, the Caribbean and the continental United States (Beenken, 2017; Ross-Davis et al., 2014; Steward et al., 2018). Interestingly, in the introduced range the pathogen spread clonaly and largely single genotypes were present suggesting a high rate of clonal reproduction despite the presence of viable teliospores (Carnegie and Lidbetter, 2012; Ross-Davis et al., 2014; Steward et al., 2018). In addition, several, genotypes were identified that were uniquely associated with specific hosts (Aparecido et al., 2003; Graca et al., 2011; Graca et al., 2013). It is conceivable that contemporary populations of *A. psidii* are maintained solely via continued asexual reproduction (urediniospores) on its primarily nondeciduous Myrtaceae hosts and that mutation is the key process for the emergence of new genotypes (Graca, 2011; Graca et al., 2013; Zhong et al., 2011).

Movement and transmission:

A. psidii spreads rapidly because it produces large numbers of spores that can be dispersed over long distances by wind (CABI, 2019). The spores are known to survive up to three months, allowing ample opportunity for spread by wind, or animal vectors (birds, bats, possums, or insects). *A. psidii* is reportedly transported over short distances by honeybees (Carnegie et al., 2010b; Chapman, 1964). The pathogen also spreads through the movement of infected or contaminated planting material, contaminated equipment and tools, or contaminated clothing, shoes and other personal effects (CABI, 2019). *A. psidii* is not known to be seedborne.

It is believed that the introduction of *A. psidii* in California and Hawaii was due to live cut flower and nursery trade from Florida (CABI, 2019). It has been suggested that the pathogen can be introduced to Hawai‘i on Myrtaceae from anywhere in the world through the United States mainland (Loope, 2010). There is much geographic reshuffling of flowers and foliage among the far-flung firms in the trade, especially for bouquet making. Because of the difficulties of inspecting all plants entering Hawai’i and the presence of asymptomatic infections, the pathogen could potentially be introduced into Hawai’i from the continental US. *A. psidii* is a nonactionable and nonreportable pest in the continental United States.

Damage potential of pest:

A. psidii can have devastating impacts on the yield of young trees and saplings. The rust causes leaf deformity, defoliation, dieback, stunted growth, and death of various plant species.

In Brazilian guava plantations, *A. psidii* can cause production losses of up to 80-100% (Ferrari et al., 1997; Martins et al., 2011; Ribeiro and Pommer, 2004). On eucalyptus in Brazil, recurring outbreaks have had devastating impacts (Coutinho et al., 1998; Ferreira, 1983). A large outbreak on a Brazilian eucalyptus plantation in 1995 resulted in severe damage of 50% of plants (Furtado and Marino, 2003). Outbreaks continue to occur annually in plantations, but they have decreased in severity due to active disease management. Significant losses have also been reported in eucalyptus plantations in Uruguay (Telechea et al., 2003), and *A. psidii* has been found in young eucalyptus plantations in Australia, where it is not yet causing significant impact (Carnegie, 2015). The arrival of a new *A. psidii* strain in Jamaica in the early 1930s resulted in massive losses to the all-spice (*Pimenta dioica*) industry and the closing of oil distilleries in higher altitude areas (MacLachlan, 1938).

The main concern for Hawai‘i is for biodiversity, cultural, and economic issues, especially involving the state's overwhelmingly dominant endemic forest tree ‘Ōhi‘a, *Metrosideros polymorpha* (Loope 2010). ‘Ōhi’a comprises 80% of native forests statewide, providing stable watersheds and habitat for many Hawaiian forest birds and plants, including many endangered species. Additional native Hawaiian plant species in Myrtaceae include the endangered *Eugenia koolauensis* (nioi) and *Eugenia reinwardtiana*, both already severely damaged by *A. psidii*, as well as *Syzygium sandwicense* (’ohi’a ha), and four species of *Metrosideros* in addition to *M. polymorpha*. All these genera have been documented to be susceptible to *A. psidii* in Hawai‘i. Hawaiian nurseries growing ohia (*Metrosideros polymorpha*), can experience mortality as high as 10% even following regular fungicide application (Burnett et al., 2012). Most recently preliminary reports of damage to ōhi’a in Hawaii have ranged from mild to complete defoliation of trees on thousands of acres on the islands of Oahu and Molokai (Hauff, 2016; 2017).

The potential impact of foreign genotypes on ōhi’a in Hawaii was analyzed in a Brazilian study by Costa da Silva et al., (2014). In this study, Brazilian genotypes were tested on ōhi’a seedlings under artificial conditions (high inoculum, high moisture, and ideal temperatures). The study concluded that three of the five Brazilian genotypes tested were highly virulent on ōhi’a seedlings and could potentially devastate ōhi’a if introduced into Hawaii (Costa da Silva et al., 2014). The *A. psidii* genotype in Hawaii has caused mortality of ōhi’a trees in a commercial nursery when conditions are “extremely conducive for disease development” (e.g., nursery plants under mist irrigation and downwind of heavily infected plants) (Costa da Silva et al., 2014). These conditions are similar to the conditions described for the virulence study with the Brazilian genotypes (e.g., plants spray inoculated with uredinospores to the point of runoff, and transferred to a dark mist chamber for 24 hours before moving to a growth chamber) (Costa da Silva et al., 2014). Nevertheless, this data suggest that other genotypes of *A. psidii* from their native range

could possess greater fitness and be more aggressive than biotypes currently occurring in the introduced range and thus pose an increased threat to Myrtaceae species. This threat presents an elevated risk particularly for Hawai'i where Myrtaceae plant species dominate the native flora.

Additionally, of the approximately 200 species of non-native Myrtaceae that have been introduced in Hawai'i; about 10% of them have shown damage by *A. psidii* to date. Hawaii has documented significant damage on a non-native rose apple (*Syzygium jambos*). Damage to the Eucalyptus industry in Hawai'i from additional *A. psidii* strains could be very significant (Burnett et al., 2012).

Control:

Most of the current control of the rust worldwide is through the use of chemicals and active management in plantations to prevent the spread after an identified outbreak (CABI, 2019).

Recommended cultural control and sanitary measures include ensuring that clothing and equipment are clean and free of plant debris when moving between plantations (CABI, 2019). Infected plants should be carefully removed, sprayed with fungicide, and disposed of properly.

A range of fungicides with the following active ingredients are currently available to combat *A. psidii*: triadimenol, triforine, mancozeb, azoxystrobin, copper oxychloride and propiconazole (CABI, 2019). Chemicals may be used as preventative or curative measures and should be rotated to maintain usefulness and avoid pathogen resistance. Fungicides may be effective in nurseries, but field fumigation is considered impractical.

The relative levels of *A. psidii* resistance in various *Eucalyptus* spp. have been evaluated (Coutinho et al., 1998). This work is particularly relevant for industries reliant on myrtaceous species but does not resolve the impact that *A. psidii* disease has on biodiversity.

When discovered in Hawai'i in April 2005, *A. psidii* was already beyond eradication and within 4-8 months had spread by wind to all the major islands. Scientists in Hawai'i quickly noted in 2005 the distinctive host range of the Hawai'i rust population, which was dramatically different from the situation elsewhere (Beenken, 2017; Ross-Davis et al., 2014; Steward et al., 2018). For example, the *A. psidii* variant in Hawai'i did not affect common guava (*Psidium guajava*), the host on which the rust was originally described in Brazil in 1884. Also, inspectors of Hawai'i Department of Agriculture (HDOA) repeatedly intercepted *A. psidii* on decorative foliage of myrtle (*Myrtus communis*) from the U.S. mainland. This host is heavily infested in Hawai'i unlike eucalyptus species (foliage with attractive juvenile leaves) which appear to be resistant, indicating that myrtle foliage may have been the pathway for the disease into Hawai'i. If a new strain were to arrive in Hawai'i (presumably detectable only by a different host signature), it is extremely unlikely that it could be detected in time for even an effort at eradication.

This led to an initiative to marshal sufficient evidence from Hawai‘i’s experience and literature to justify rigorous effort to keep out new genetic strains (Loope and La Rosa, 2008; Loope, 2010). The Hawai‘i Board of Agriculture (HDOA) unanimously approved a 12- month interim rule banning importation of plants in the Myrtaceae family from “infested areas,” specified as South America, Florida, and California. The HDOA interim rule expired in August 2008. However, in 2018, as a proactive approach to eliminate the risk of introduction of new genotypes of *A. psidii*, a new rule was drafted by HDOA to establish a permanent state quarantine regulation to prohibit entry of all Myrtaceae taxa into Hawaii in domestic routes.

Known host range:

A.psidii is known to infect only members of the Myrtaceae (Graca et al., 2013). The host list of *A. puccinia* is extensive. A recent assessment lists 445 species in 73 genera of Myrtaceae as host of the rust (Giblin and Carnegie, 2014; see also CABI, 2019). However, the host list includes species identified to be susceptible after artificial inoculation (Carnegie and Lidbetter, 2012; Morin et al., 2012; Pegg et al., 2014; Sandhu and Park, 2013). Considering the diverse genera of the Myrtaceae being infected either naturally or during artificial inoculation experiments, it was suggested that all Myrtaceae are potential hosts of *A. puccinia*. Therefore some countries adopted a family wide prohibition. For example, New Zealand Ministry of Agriculture and Forestry (2011) concluded: “All species of the family Myrtaceae occurring in New Zealand must be considered potential hosts of *A. psidii*, because the fungus has demonstrated in both Australia and Hawai‘i that it finds new myrtaceous host species which were not known hosts previously.”

Most significant genera that are hosts of myrtle rust include the following:

Acca spp. (Carnegie and Lidbetter, 2012), *Acmena* spp. (Carnegie and Lidbetter, 2012), *Acmenosperma* spp. (Carnegie and Lidbetter, 2012), *Agonis* spp. (Carnegie and Lidbetter, 2012), *Allosyncarpia* spp. (Morin et al., 2012), *Angophora* spp. (Carnegie and Lidbetter, 2012), *Anetholea* spp. (Carnegie and Lidbetter, 2012), *Archirhodomyrtus* spp. (Carnegie and Lidbetter, 2012), *Arillastrum* spp. (Giblin and Carnegie, 2014), *Astartea* spp. (Carnegie and Lidbetter, 2012), *Asteromyrtus* spp. (Carnegie and Lidbetter, 2012), *Austromyrtus* spp. (Carnegie and Lidbetter, 2012), *Backhousia* spp. (Carnegie and Lidbetter, 2012), *Baeckea* spp. (Giblin and Carnegie, 2014), *Barongia* spp. (Giblin and Carnegie, 2014), *Beaufortia* spp. (Morin et al., 2012), *Callistemon* spp. (Carnegie and Lidbetter, 2012), *Calothamnus* spp. (Morin et al., 2012), *Calycorectes* spp. (Carnegie and Lidbetter, 2012), *Calytrix* spp. (Giblin and Carnegie, 2014), *Campomanesia* spp. (Carnegie and Lidbetter, 2012), *Chamelaucium* spp. (Carnegie and Lidbetter, 2012), *Choricarpia* spp. (Carnegie and Lidbetter, 2012), *Cloezia* spp. (Giblin and Carnegie, 2014), *Corymbia* spp. (Carnegie and Lidbetter, 2012), *Darwinia* spp. (Morin et al., 2012), *Decaspermum* spp. (Carnegie and Lidbetter, 2012), *Eremaea* spp. (Carnegie and

Lidbetter, 2012), *Eucalyptus* spp. (Carnegie and Lidbetter, 2012), *Eugenia* spp. (Carnegie and Lidbetter, 2012), *Gossia* spp. (Carnegie and Lidbetter, 2012), *Heteropyxis* spp. (Carnegie and Lidbetter, 2012), *Homoranthus* spp. (Giblin and Carnegie, 2014), *Hypocalymma* spp. (Carnegie and Lidbetter, 2012), *Kunzea* spp. (Carnegie and Lidbetter, 2012), *Lenwebbia* spp. (Carnegie and Lidbetter, 2012), *Leptospermum* spp. (Carnegie and Lidbetter, 2012), *Lindsayomyrtus* spp. (Giblin and Carnegie, 2014), *Lithomyrtus* spp. (Giblin and Carnegie, 2014), *Lophomyrtus* spp. (Carnegie and Lidbetter, 2012), *Lophostemon* spp. (Giblin and Carnegie, 2014), *Melaleuca* spp. (Carnegie and Lidbetter, 2012), *Metrosideros* spp. (Carnegie and Lidbetter, 2012), *Mitrantia* spp. (Giblin and Carnegie, 2014), *Myrcia* spp. (Carnegie and Lidbetter, 2012), *Myrcianthes* spp. (Carnegie and Lidbetter, 2012), *Myrciara* spp. (Giblin and Carnegie, 2014), *Myrrhinium* spp. (Carnegie and Lidbetter, 2012), *Myrtastrum* spp. (Giblin and Carnegie, 2014), *Myrtus* spp. (Carnegie and Lidbetter, 2012), *Osbornia* spp. (Morin et al., 2012), *Pericalymma* spp. (Carnegie and Lidbetter, 2012), *Pilidiostigma* spp. (Carnegie and Lidbetter, 2012), *Piliocalyx* spp. (Giblin and Carnegie, 2014), *Pimenta* spp. (Carnegie and Lidbetter, 2012), *Plinia* spp. (Carnegie and Lidbetter, 2012), *Psidium* spp. (Carnegie and Lidbetter, 2012), *Regelia* spp. (Carnegie and Lidbetter, 2012), *Rhodamnia* spp. (Carnegie and Lidbetter, 2012), *Rhodomyrtus* spp. (Carnegie and Lidbetter, 2012), *Ristantia* spp. (Carnegie and Lidbetter, 2012), *Sannantha* spp. (Giblin and Carnegie, 2014), *Sphaerantia* spp. (Giblin and Carnegie, 2014), *Stockwellia* spp. (Carnegie and Lidbetter, 2012), *Syncarpia* spp. (Carnegie and Lidbetter, 2012), *Syzygium* spp. (Carnegie and Lidbetter, 2012), *Thryptomene* spp. (Carnegie and Lidbetter, 2012), *Tristania* spp. (Carnegie and Lidbetter, 2012), *Tristaniopsis* spp. (Carnegie and Lidbetter, 2012), *Ugni* spp. (Carnegie and Lidbetter, 2012), *Uromyrtus* spp. (Carnegie and Lidbetter, 2012), *Verticordia* spp. (Morin et al., 2012), *Waterhousea* spp. (Carnegie and Lidbetter, 2012), and *Xanthostemon* spp.(Carnegie and Lidbetter, 2012).

Proposed Action under NAPPRA:

The importation of Myrtaceae plants for planting genera, excluding seeds, and excluding cut flowers and greenery, that are hosts of ***Austropucccinia psidii***, are not authorized pending pest risk analysis (NAPPRA) **from all countries when destined to Hawaii:**

All taxa of Myrtaceae family

Potential risks posed by cut flowers and greenery of Myrtaceae will be addressed by APHIS under separate regulations.

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Plants for Planting Quarantine Pest Evaluation Data Sheet
May 06, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: **Black currant reversion virus**

Hosts: ***Ribes***

Taxonomy and description of the pest:

Black currant reversion virus (BRV) is the current species name for the causal agent of black currant reversion disease (Lemmetty et al., 1997; Susi, 2004). BRV is a *Nepovirus* in the Secoviridae family. Black currant reversion associated virus (BCRV or BRAV) is a synonym of BRV (Susi, 2004).

Known distribution:

Austria (Thresh, 1970), Belarus (Gryshanovich, 1976), Czech Republic (Pribylová et al., 2002; Zulge et al., 2018), Denmark (Thomsen et al., 1991), England (Thresh, 1970), Estonia (Tiits, 1969), Finland (Bremer and Heikinheimo, 1979; Zulge et al., 2018), France (Putz, 1970), Germany (Krczal, 1976; Thresh, 1970), Hungary (Nyerges et al., 2001), Latvia (Zulge et al., 2018), Lithuania (Zulge et al., 2018), Netherlands (Jones, 2000; Thresh, 1970), New Zealand (Wood and Langford, 1998; Zulge et al., 2018), Poland (Thresh, 1970; Zulge et al., 2018), Russia (Jones, 2000; Zulge et al., 2018), Scotland (Zulge et al., 2018), Sweden (Zulge et al., 2018), and Switzerland (Thresh, 1970).

This pest is not known to occur in the United States.

Biology of the pest:

Black currant reversion disease was first described in the Netherlands over 100 years ago (Jones, 2000) and has since been recorded in virtually all parts of the world where black currant (*Ribes nigrum*) and other *Ribes* species are grown. The causal agent of the disease remained elusive until recently, partly because the effects of the virus were confused with damage caused by the disease-transmitting vector, the eriophyid gall mite *Cecidophyopsis ribis* (Adams and Thresh, 1987).

During late spring and early summer, *C. ribis* disperse from infested black currant buds as they open. Some mites move into new buds of the parent plant and some may be carried on the bodies of birds or insects, but the majority are spread by wind (Jones, 2000). Those that arrive at susceptible plants form galls and cause sterility of buds (Adams and Thresh, 1987). Eriophyid mites have short stylets that allow them to feed in the epidermal cells of plants, where they may acquire or transmit viruses or virus-like agents (Jones, 2000). *C. ribis* mites transmit BRV in a non-persistent or semi-persistent manner to the epidermal cells of black currant.

After BRV infection, symptoms in plants often take one or two years to develop and appear on only one or two branches. Several more years may pass before infection extends to all branches of infected plants (Jones, 2000). Two forms of the disease have been identified: the common European (E) form and the severe (R) form, which is restricted to Eastern Europe, Scandinavia and countries of the former Soviet Union (Jones, 2000). The two disease forms differ in severity of symptoms but have similar rates of progression(Adams and Thresh, 1987).

BRV movement within the plant is slow and erratic, affecting symptom expression (Jones, 2000). Most black currant cultivars affected by either form of the disease have fewer leaves than uninfected plants, and the leaves may be flatter, smaller, with fewer marginal serrations, fewer main veins and smaller basal sinuses (Adams and Thresh, 1987). In some black currant cultivars and alpine currant (*Ribes alpinum*), leaves may develop a chlorotic line-pattern or a veinal oak-leaf pattern (Jones, 2000).

The most reliable symptoms of BRV infection occur in flower buds as they open in early spring. The E form of the disease causes a marked decrease in the hair density on the flower buds and an increased intensity of bud color (Jones, 2000). In addition to these symptoms, plants afflicted with the R form usually have flowers with ten instead of five petals and further increased intensity of pigmentation. These plants exhibit elongated styles and lack stamens (Adams and Thresh, 1987). Flower buds affected by either form of black currant reversion disease are usually sterile, resulting in a severe loss in berry production (Lemmetty et al., 1997). In red currant, leaf and flower symptoms are much less noticeable than those in black currant making diagnosis difficult (Adams and Thresh, 1987). Black current reversion disease diagnostic capacity was recently improved with

development of a reliable, RT-PCR-based test for BRV (Dolan et al., 2011).

The physiological factors underlying the differences in symptom severity between the E and R forms of the disease have not been characterized. Analyses of nine BRV isolates from six different countries indicated 94-99% sequence identity (Lemmetty et al., 2001). Some BRV isolates carry satellite RNA, which may be related to the R form of the disease, but the effect of the satellite RNA on symptom development is not yet understood (Susi, 2004).

Movement and transmission:

BRV is transmitted by the eriophyid gall mite *Cecidophyopsis ribis* (Adams and Thresh, 1987).
BRV is not seed-transmitted (Jones, 2000).

Damage potential of pest:

Black currant reversion disease is the most important viral disease for black currant crops, causing substantial losses in production (Jones, 2000; Krczal, 1976). Likewise, the gall mite vector of BRV is regarded as the most damaging pest of black currant crops worldwide (Jones, 2000). Because of the serious damage caused by these organisms, black currant cultivation has ceased in some parts of New Zealand and Europe (Jones, 2000; Krczal, 1976).

All of the main commercial black currant cultivars in Western Europe are susceptible to BRV (Adams and Thresh, 1987). Neither BRV nor its vector are present in North America giving local growers an advantage over their European counterparts (Barney, 2000).

In the early 1900s, United States federal and state governments outlawed the growing of currants and gooseberries because the bushes serve as hosts for white pine blister rust (*Cronartium ribicola*), a fungus that is lethal for many pine trees (Anonymous, 2013). Prior to the ban, the United States produced 7.6 million quarts of currants annually (Sen, 2009). The federal ban was rescinded in 1966. New York modified its ban in 2003, allowing commercial growers and home gardeners to legally grow *C. ribicola*-resistant black currant cultivars. This prompted a renewed interest in black current production (Sen, 2009). Quarantine measures should be in place to protect the burgeoning black currant industry.

Several *Ribes* species are native to the United States, where they are valuable as ornamental plants, food and cover for wildlife, and tools for erosion control (Pfister and Sloan, 2008)

Control:

Only certified healthy material should be planted. Galled and/or diseased plants should be removed and burned in addition to adjacent symptomless plants (Jones, 2000).

Chemical control measures are aimed at eliminating the mite vector. Systemic acaricides, such as Endosulfan (Nielsen, 1987), may be applied during the main mite dispersal period, but these chemicals are banned in some countries and their success requires the accurate timing of applications to coincide with mite dispersal (Jones, 2000). This may be difficult to achieve because of the differences in the opening time of buds down the length of the branches of a bush.

Sources of resistance both to BRV and its mite vector have been identified in *Ribes* germplasm, and are being employed in breeding programs in Europe (Jones, 2000; Mazeikiene et al., 2017; SCRI, 2013).

Known host range:

Ribes alpinum (Adams and Thresh, 1987), *R. aureum* (Zulge et al., 2018), *R. bracteosum* (Thresh, 1970), *R. fasciculatum* var. *chinense* (Zulge et al., 2018), *R. fragrans* (Zulge et al., 2018), *R. glutinosum* Benth. x *R. nigrum* L. (Thresh, 1970), *R. nigrum* (Susi, 2004), *Ribes nigrum* var. *pauciflorum* (Zulge et al., 2018), *R. rubrum* L. var. *pubescens* (Thresh, 1970), and *R. spicatum* (Susi, 2004).

Hosts confirmed by artificial inoculation: *Chenopodium amaranticolor*, *C. murale*, *C. quinoa*, *Nicotiana benthamiana*, *N. clevelandii*, *N. debnyi*, *N. occidentalis* (Lemmetty et al., 1997).

Current APHIS Regulations for hosts:

Ribes: All propagules except seeds are NAPPRA from Europe and New Zealand. Must enter Postentry Quarantine from all other countries, except Canada, Europe, and New Zealand.

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, that is a host of **Black currant reversion virus**, is not authorized pending pest risk analysis (NAPPRA) **from all countries except Canada**:

Ribes

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
March 04, 2019

In order to prevent the introduction of quarantine pests into the United States, the U.S. Code of Federal Regulations 7 CFR §319.37-4 (2018) allows the U.S. Department of Agriculture Animal and Plant Health Inspection Service (APHIS) Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Brevipalpus chilensis*** (Baker, 1949)

Order (Family): Trombidiformes (Tenuipalpidae)

Common names:
Grape flat mite
Chilean false red mite of grapes
False red vine mite
Falsa arañita de la vid [Spanish]

Hosts: ***Actinidia, Ampelopsis, Annona, Antirrhinum, Apium, Catalpa, Catharanthus, Cestrum, Chrysanthemum, Citrus, Convolvulus, Crataegus, Cydonia, Diospyros, Dysphania, Ficus, Garcinia, Jasminum, Ligaria, Ligustrum, Malus, Pelargonium, Plantago, Prunus, Pyrus, Rubus, Strongylodon, Vinca, Vitis***

Known distribution of pest:

Known world distribution: *Brevipalpus chilensis* is native to Chile (Gonzalez, 1958, 1989; Jeppson et al., 1975; Prado, 1991). It was first identified on lemon from Chile intercepted at New York in 1933, while other original specimens had been collected on *Vitis vinifera* in Chile in 1909 (Baker, 1949). It has also been reported in Argentina (Prado, 1991) and India (Ghai and Shenhmar, 1984; Nagesha Chandra and Channabasavanna, 1979), although other sources (Childers and Rodrigues, 2011; Gonzalez, 1989, 2006) state that it is restricted to Chile.

Distribution in the United States, including control measures in place: Currently *B. chilensis*

does not occur in the US (Childers and Rodrigues, 2011), however it is a cause for quarantine treatments of fresh fruit shipments from Chile, including fig, grapes, kiwi, baby kiwi, citrus and cherimoya (USDA APHIS, 2015).

Biology of pest:

Brevipalpus chilensis is a small flat mite in the family Tenuipalpidae, colloquially referred to as the false spider mites (Childers and Rodrigues, 2011). The genus *Brevipalpus* contains five of the most important economic pests within the family including *B. chilensis* (Childers and Rodrigues, 2011). The *Brevipalpus chilensis* life cycle is haplodiplontic (Childers and Rodrigues, 2011) and they may reproduce through parthenogenesis, especially in the second and third generations where few males are produced (Gonzalez, 1958). Mites in the Tenuipalpidae family have four active stages of development, each interrupted with a sessile quiescent stage (chrysalis) (Childers and Rodrigues, 2011). Eggs and chrysalis stages are attached strongly to the plant surface (Childers and Rodrigues, 2011). *Brevipalpus* mites do not produce webbing, but motile stages can be difficult to remove even when using alcohol washes (Childers and Rodrigues, 2011). Adult *B. chilensis* mites are small; female average length including the rostrum is 406 µ and 211.8 µ wide, while males are smaller, 312 µ long by 158.6 µ wide. Eggs are a pale red with longitudinal striae measuring 14 µ by 9.8 µ (Gonzalez, 1958). Fertilized females overwinter in cracks and crevices along the stem of the host (Gonzalez, 1958; Jeppson et al., 1975). In Chile, oviposition begins in September or October (spring in the Southern Hemisphere) on buds, shoots, or the underside of leaves, and the eggs may take 6-20 days to hatch (Gonzalez, 1958). Generation time averages 25.3 days (18-59 days), with three to six generations occurring during the year depending on temperature and humidity (Gonzalez, 1958; Herrera Villamil, 1958; Jeppson et al., 1975).

Damage potential of pest:

Brevipalpus chilensis is described as a serious and very destructive pest in its native range (Jeppson et al., 1975; Loeb et al., 2015), with 20% losses reported in some areas (Gonzalez, 1958). It is considered one of the primary arthropod pests of grapevines in Chile (Gonzalez, 1958; Klein Koch and Waterhouse, 2000). Mites feed on the lower surface of the leaves and new shoots (Gonzalez, 1958; Jeppson et al., 1975). Damage is most notable on leaves where discoloration from feeding precedes abscission and new growth is reduced, with the highest level of damage to vineyards occurring in the spring (Gonzalez, 1958; Jeppson et al., 1975). Production of grapes decreases (Loeb et al., 2015) and the resulting wine has a lower alcohol content (Gonzalez, 1983). Wine grapes experience significant damage from *B. chilensis*, whereas most cultivars of table grapes do not (Gonzalez, 2006). Many other *Brevipalpus* mites vector plant viruses, however it is not known whether *B. chilensis* possesses this ability (Childers and Rodrigues, 2011).

The mite has also been observed naturally attacking what may be considered secondary hosts, including citrus, privet, almond, fig, chrysanthemum, geranium, morning-glory, bindweed, custard apple, peppervine, celery, wormseed, periwinkle, persimmon, apricot, raspberry, kiwi, apple, quince, and pear (individual references cited under "Host-Plant Species" below). There is no evidence that any of these suffer economically significant damage, but they may still pose a risk of serving as an import pathway for this pest (for example, the interception on Chilean citrus in New York that led to the original naming of this species (Baker, 1949)). Clover and beans have been used to rear *B. chilensis* in the laboratory (Gonzalez, 1958; Herrera Villamil, 1958), but there is no evidence of these plants serving as hosts in the field.

Means of Movement and Dispersal:

Due to their small size and slow movement, natural dispersal of *Brevipalpus* mites on their own is inefficient (Childers and Rodrigues, 2011). Usually, dispersal between plants is via plant-to-plant contact, wind (aerial), or animals (phoretic) (Childers and Rodrigues, 2011). Long-distance movements generally require human transport, such as in trade of live plants and the plant parts listed in the following table.

Plant parts liable to carry the pest	Pest stages	Borne internally or externally?	Visibility of pest or symptoms
Fruit	All	Externally	Pest difficult to see with naked eye, light microscope generally required
Leaves	All	Externally	Pest difficult to see with naked eye, light microscope generally required
Stems/shoots/trunk/ branches/bark	All	Externally	Pest difficult to see with naked eye, light microscope generally required

Control:

Ionizing radiation combined with cold storage has been shown to be a potentially effective method of quarantine treatment of grapes for *B. chilensis* with 90% mortality for adults (Castro et al., 2004). Irradiation treatment has been approved for treatment of *B. chilensis* on all imported fruits and vegetables (USDA APHIS, 2015). Fumigation followed by cold storage also effectively controls the mite on grapes, apples, and other fresh fruits (Horn, 2012), and is approved for treatment of *B. chilensis* on apple, apricot, grape, kiwi, peach, nectarine, pear and quince fruits (USDA APHIS, 2015). A soapy water/wax treatment has been approved for imported fresh limes, and cherimoya from Chile by the USDA PPQ, as well as methyl bromide fumigation for citrus, grape, kiwi, baby kiwi and fig fruits (USDA APHIS, 2015).

Host-Plant Species:

Scientific and selected common names verified in EOL and GRIN databases, unless specified otherwise.

Actinidia chinensis (Actinidiaceae) (Klein Koch and Waterhouse, 2000)

Synonym(s): none

Common name(s): kiwi fruit (Klein Koch and Waterhouse, 2000), golden kiwifruit, Chinese gooseberry

Actinidia deliciosa (Actinidiaceae) (Gonzalez, 2006)

Synonym(s): *A. chinensis* var. *deliciosa*, *A. chinensis* var. *hispida*, *A. latifolia* var. *deliciosa*

Common name(s): kiwi (Castro et al., 2004; Gonzalez, 1983, 1989, 2006; Prado, 1991), kiwifruit, Chinese gooseberry

Note: occasional host, in kiwis near grape vineyards, light infestations on the underside of leaves, but at very low level due to abundance of trichomes (Gonzalez, 1989); in plantations near grapevine cultivation (Castro et al., 2004; Gonzalez, 1983); after wine grapes and privet, kiwi can be found with the largest populations of this mite, between the trichomes on the underside of the leaves (300-400 per leaf), females overwinter in the scar left by the petioles, cleaning trichomes from the fruits leads to capture of many mobile stage individuals, but even with high populations, damage to the plant or fruit is not seen (Gonzalez, 2006)

Ampelopsis sp. (Vitaceae) (Gonzalez, 1958, 1983, 1989, 2006)

Synonym(s): *Ituterion* sp., *Nekemias* sp.

Common name(s): hiedra trepadora [Spanish] (Gonzalez, 2006), peppervine

Note: secondary host (Gonzalez, 1989); very abundant on *Ampelopsis* (Gonzalez, 1983)

Annona cherimola (Annonaceae) (Gonzalez, 1958, 2006)

Synonym(s): *A. acutifolia*, *A. odorata*, *A. pubescens*, *A. tripetala*

Common name(s): chirimoyo [Spanish] (Gonzalez, 1958, 1983, 1989; Prado, 1991), chirimoya [Spanish] (Gonzalez, 2006), cherimoya (Castro et al., 2004), custard-apple

Note: occasional host, found only on the leaves, at low density, almost never on the fruits (Gonzalez, 1989); very common on cherimoya (Gonzalez, 1983)

Antirrhinum sp. (Plantaginaceae) (Gonzalez, 1983, 2006)

Synonym(s): none

Common name(s): cartucho [Spanish] (Gonzalez, 2006), snapdragon

Note: very abundant on *Antirrhinum* (Gonzalez, 1983)

Apium graveolens (Apiaceae) (Gonzalez, 1958)

Synonym(s): *A. celleri*, *A. decumbens*, *A. dulce*, *A. integrilobum*, *A. lobatum*, *A. lusitanicum*, *A. maritimum*, *A. palustre*, *A. rapaceum*, *A. vulgare*, *Celeri graveolens*, *Carum graveolens*, *Helosciadium graveolens*, *Petroselinum vulgare*, *Selinum graveolens*, *Seseli graveolens*, *Sium apium*, *Sium graveolens*

Common name(s): apio [Spanish] (Gonzalez, 1958), celery, celeriac, marsh parsley, smallage

Catalpa speciosa (Bignoniaceae) (Gonzalez, 1983, 2006)
Synonym(s): *C. bignonioides* var. *speciosa*
Common name(s): catalpa (Gonzalez, 1983, 2006), Indian-bean, catawba, cigartree

Catharanthus roseus (Apocynaceae)
Synonym(s): *Vinca rosea* (Gonzalez, 2006), *Ammocallis rosea, Lochnera rosea*
Common name(s): pervinca [Spanish] (Gonzalez, 2006), Madagascar periwinkle, old-maid, periwinkle, rosy periwinkle, vinca

Cestrum parqui (Solanaceae) (Gonzalez, 1983, 2006)
Synonym(s): *C. bolivianum, C. conglomeratum, C. ellipticum, C. foetidissimum* var. *pallidisimum, C. jamaicense* var. *parqui, C. lorentzianum, C. mandonii, C. pubens, C. salicifolium, C. virgatum*
Common name(s): palqui [Spanish] (Gonzalez, 1983, 2006), Chilean jessamine, Chilean cestrum, green cestrum, green poison-berry, willow leaf jessamine

Chrysanthemum sp. (Asteraceae) (Gonzalez, 1958, 1983, 2006)
Synonym(s): *Arctanthemum* sp., *Dendranthema* sp.
Common name(s): chrysanthemum (Castro et al., 2004; Jeppson et al., 1975), manzanillon [Spanish] (Gonzalez, 1958), crisantemo [Spanish] (Gonzalez, 2006)
Note: very abundant on *Chrysanthemum* (Gonzalez, 1983)

Citrus aurantium (Rutaceae) (Gonzalez, 1958)
Synonym(s): *C. amara, Citrus* x *aurantium, C. bergamia, C. bigarradia, C. vulgaris*
Common name(s): naranjo agrio [Spanish] (Gonzalez, 1958), Seville orange, sour orange, bitter orange

Citrus limon (Rutaceae) (Klein Koch and Waterhouse, 2000)
Synonym(s): *C. abyssinica, C. inaequalis, Citrus* x *limon, C. limonum, C. medica* var. *limon*
Common name(s): lemon (Castro et al., 2004; Klein Koch and Waterhouse, 2000), limonero [Spanish] (Gonzalez, 1983, 1989, 2006; Prado, 1991), limon agrio [Spanish] (Gonzalez, 2006)
Note: primary host (Gonzalez, 1989); very common on lemon trees (Gonzalez, 1983)

Citrus reticulata (Rutaceae) (Klein Koch and Waterhouse, 2000)
Synonym(s): *Citrus* x *aurantium* fo. *deliciosa, Citrus* x *aurantium* var. *tachibana, C. aurantium* subsp. *suntra, C. chachiensis, C. chrysocarpa, C. daoxianensis, C. deliciosa, C. depressa* var. *vangasay, C. erythrosa, C. madurensis* var. *deliciosa, C. mangshanensis, C. nobilis, C. ponki, C. poonensis, C. succosa, C. suhuiensis, C. sunki, C. tachibana, C. tangerina, C. tankan, C. unshiu, C. vangasay, C. vangasy, C. voangasay*
Common name(s): tangerine (Klein Koch and Waterhouse, 2000), clementina [Spanish] (Gonzalez, 2006), mandarin orange, clementine, Unshu orange
Note: small populations in the pedicel area at low levels which do not affect the fruit, low populations in foliage as well (Gonzalez, 2006)

Citrus sinensis (Rutaceae) (Klein Koch and Waterhouse, 2000)

Synonym(s): *C. aurantium* var. *sinensis, C. macracantha, Citrus* x *sinensis*

Common name(s): orange (Castro et al., 2004; Klein Koch and Waterhouse, 2000), naranjo [Spanish] (Gonzalez, 2006; Prado, 1991), sweet orange, navel orange, Valencia orange, blood orange

Convolvulus arvensis (Convolvulaceae) (Gonzalez, 1958, 1983, 2006)

Synonym(s): *C. ambigens, C. auriculatus, C. hastatus, C. longipedicellatus, Strophocaulos arvensis*

Common name(s): bindweed (Jeppson et al., 1975), morning-glory (Jeppson et al., 1975), correvuela [Spanish] (Gonzalez, 1958), correhuela [Spanish] (Gonzalez, 1983, 2006), field bindweed, corn bind, corn lily, creeping jenny

Note: this weed can harbor important populations of the mite in vineyards (Gonzalez, 1983)

Crataegus sp. (Rosaceae) (Herrera Villamil, 1958)

Synonym(s): *Mespilus* sp.

Common name(s): hawthorn

Cydonia oblonga (Rosaceae) (Klein Koch and Waterhouse, 2000)

Synonym(s): *C. communis, C. cydonia, C. europaea, C. maliformis, C. sumboshia, C. vulgaris, Pyrus cydonia, Pyrus-Cydonia cydonia, Sorbus cydonia*

Common name(s): quince (Klein Koch and Waterhouse, 2000), membrillo [Spanish] (Gonzalez, 1983; Prado, 1991)

Diospyros kaki (Ebenaceae) (Klein Koch and Waterhouse, 2000)

Synonym(s): *D. chinensis*

Common name(s): persimmon (Klein Koch and Waterhouse, 2000), caqui [Spanish] (Prado, 1991), kaki (Gonzalez, 1989), Japanese persimmon

Note: occasional host (Gonzalez, 1989)

Dysphania ambrosioides (Chenopodiaceae)

Synonym(s): *Chenopodium ambrosioides* (Gonzalez, 1958, 2006), *C. integrifolium, C. obovatum, C. retusum, C. suffruticosum, Ambrina ambrosioides, Teloxys ambrosioides*

Common name(s): paico [Spanish] (Gonzalez, 1958, 2006), Mexican-tea, Jerusalem-tea, Spanish-tea, wormseed, wormseed goosefoot

Ficus benghalensis (Moraceae)

Synonym(s): *F. indica* (Gonzalez, 2006), *F. umbrosa, Urostigma benghalense*

Common name(s): higuera [Spanish] (Gonzalez, 2006), banyan tree, banyan fig, East Indian fig tree

Ficus carica (Moraceae) (Gonzalez, 1958; Klein Koch and Waterhouse, 2000)

Synonym(s): *Caprificus insectifera, C. leucocarpa, C. oblongata, C. pedunculata, C. rugosa, C. sphaerocarpa, F. albescens, F. caprificus, F. colchica, F. colombra, F. communis, F. deliciosa, F. dottata, F. globosa, F. hypoleuca, F. hyrcana, F. kopetdagensis, F. latifolia, F. leucocarpa, F. macrocarpa, F. neapolitana, F. pachycarpa, F. pedunculata, F. polymorpha, F. praecox, F. regina, F. rugosa, F. silvestris, F. burdigalensis*
Common name(s): fig (Jeppson et al., 1975; Klein Koch and Waterhouse, 2000), higuera [Spanish] (Gonzalez, 1958, 1983, 1989; Prado, 1991), common fig
Note: occasional host (Gonzalez, 1989)

Garcinia sp. (Clusiaceae) (Nagesha Chandra and Channabasavanna, 1979)
Synonym(s): *Ochrocarpos* sp., *Ochrocarpus* sp., *Rheedia* sp., *Tsimatimia* sp., *Xanthochymus* sp.
Common name(s): saptree, mangosteen

Jasminum angustifolium (Oleaceae) (Nagesha Chandra and Channabasavanna, 1979)
Synonym(s): *Nyctanthes angustifolia*
Common name(s): jasmine
Note: observed on flower stalk, calyx and petals, all stages noted (but no males) (Nagesha Chandra and Channabasavanna, 1979)

Ligaria cuneifolia (Loranthaceae)
Synonym(s): *Psittacanthus cuneifolius* (Gonzalez, 2006), *Loranthus cuneifolius, Loranthus montevidensis, Phrygilanthus cuneifolius, Psittacanthus peruanus*
Common name(s): quintral del espino [Spanish] (Gonzalez, 2006)

Ligustrum japonicum (Oleaceae) (Jadue et al., 1996)
Synonym(s): *L. coriaceum*
Common name(s): Japanese privet, wax leaf privet
Note: mites obtained from *L. japonicum*, kept on individual *Ligustrum* leaves *in vitro* (Jadue et al., 1996)

Ligustrum sinense (Oleaceae) (Castro et al., 2004; Gonzalez, 1958, 1983, 2006)
Synonym(s): *L. indicum, L. microcarpum, L. stauntonii, L. villosum, Phillyrea indica*
Common name(s): Chinese privet (Castro et al., 2004), ligustrina [Spanish] (Gonzalez, 1958, 1983, 1989, 2006), Chinese ligustrum
Note: secondary host, one of the most common hosts, small leaf can hold about 100 mites (Gonzalez, 1989); among the most infested host plants of ornamental interest (Gonzalez, 2006); very abundant on privet (Gonzalez, 1983)

Malus pumila (Rosaceae) (Gonzalez, 2006)
Synonym(s): *M. domestica* (Klein Koch and Waterhouse, 2000), *M. communis, M. dasyphylla, M. niedzwetzkyana, M. paradisiaca, M. praecox, M. sylvestris, Pyrus malus, P. niedzwetzkyana, P. praecox, P. pumila*
Common name(s): manzano [Spanish] (Gonzalez, 1983, 2006; Prado, 1991), apple (Klein Koch and Waterhouse, 2000), paradise apple

Note: low infestations on both sides of leaves with no apparent damage (Gonzalez, 2006)

Pelargonium sp. (Geraniaceae) (Gonzalez, 1958, 1983, 2006)
Synonym(s): none
Common name(s): geranium (Jeppson et al., 1975), cardenal [Spanish] (Gonzalez, 1958, 2006), pelargonio [Spanish] (Gonzalez, 2006), cardinal flower (Castro et al., 2004)
Note: very abundant on *Pelargonium* (Gonzalez, 1983)

Plantago lanceolata (Plantaginaceae) (Gonzalez, 2006)
Synonym(s): *P. lacustris, P. sinuata*
Common name(s): siete venas [Spanish] (Gonzalez, 2006), llanten [Spanish] (Gonzalez, 2006), ribwort plantain, buckhorn plantain, English plantain, narrow-leaf plantain, ribgrass

Prunus armeniaca (Rosaceae) (Klein Koch and Waterhouse, 2000)
Synonym(s): *Armeniaca limeixing, A. manshurica, A. vulgaris, P. mandschurica*
Common name(s): apricot (Klein Koch and Waterhouse, 2000), damasco [Spanish] (Gonzalez, 2006; Prado, 1991), Siberian apricot, wild apricot, apricot tree
Note: stone fruits practically not colonized but females and eggs may be found in the pedicel cavity of the fruits at very low population densities (Gonzalez, 2006)

Prunus dulcis (Rosaceae)
Synonym(s): *P. amygdalus* (Gonzalez, 1958), *Amygdalus amara, A. communis, A. dulcis, A. fragilis, A. sativa, Druparia amygdalus, P. communis*
Common name(s): almond (Jeppson et al., 1975), almendro [Spanish] (Gonzalez, 1958; Prado, 1991), sweet almond, bitter almond

Prunus persica (Rosaceae)
Synonym(s): *Amygdalus persica, Cerasus vulgaris, Persica platycarpa, Persica vulgaris, Prunus daemonifuga, Prunus vulgaris*
Common name(s): durazno [Spanish] (Gonzalez, 2006), nectarino [Spanish] (Gonzalez, 2006), peach, nectarine (var. *nucipersica*)
Note: stone fruits practically not colonized but females and eggs may be found in the pedicel cavity of the fruits at very low population densities (Gonzalez, 2006)

Pyrus communis (Rosaceae) (Klein Koch and Waterhouse, 2000)
Synonym(s): *Pyrus* x *amphigenea, P. asiae-mediae, P. balansae, P. bourgaeana, P. caucasica, P. domestica, P. elata, P. medvedevii, P. pyraster, P. sativa*
Common name(s): pear (Klein Koch and Waterhouse, 2000), peral [Spanish] (Prado, 1991)

Rubus idaeus (Rosaceae) (Klein Koch and Waterhouse, 2000)
Synonym(s): *Batidaea idea, B. strigosa* subsp. *itascica, B. vulgaris, R. frambaesianus*
Common name(s): raspberry (Klein Koch and Waterhouse, 2000), frambuesa [Spanish] (Prado, 1991), red raspberry

Strongylodon macrobotrys (Fabaceae) (Nagesha Chandra and Channabasavanna, 1979)
Synonym(s): *S. megaphyllus, S. warburgii*
Common name(s): jadevine, emerald creeper

Viburnum sp. (Adoxaceae) (Gonzalez, 1983, 2006)
Synonym(s): *Actinotinus* sp., *Oreinotinus* sp.
Common name(s): viburno [Spanish] (Gonzalez, 2006), viburnum
Note: very abundant on *Viburnum* (Gonzalez, 1983)

Vinca sp. (Apocynaceae) (Gonzalez, 1958, 1983)
Synonym(s): none
Common name(s): pervinca [Spanish] (Gonzalez, 1958), periwinkle
Note: very abundant on *Vinca* (Gonzalez, 1983); Gonzalez may be referring to *Vinca rosea*, listed under the preferred synonym *Catharanthus roseus* above

Vitis vinifera (Vitaceae) (Gonzalez, 2006; Klein Koch and Waterhouse, 2000)
Synonym(s): none
Common name(s): grape (Klein Koch and Waterhouse, 2000), grapevine (Jeppson et al., 1975), wine grape (Castro et al., 2004), vid [Spanish] (Gonzalez, 1989, 2006; Prado, 1991), vid vinifera [Spanish] (Gonzalez, 1958, 1983), European grape, table grape, wild grape
Note: primary host, red wine grape varieties can be found with up to 1500 mites per leaf, table grape varieties are rarely affected except when grafted on red wine grape rootstock (Gonzalez, 1989); principally on wine grapes and some cultivars of table grape (Gonzalez, 1983)

Species with unclear taxonomy, listed as hosts for *B. chilensis*:

Ribes georgianus (Grossulariaceae) (Gonzalez, 1983, 2006)
Common name(s): la zarzaparrilla [Spanish] (Gonzalez, 1983), ribes (Gonzalez, 2006), currant, gooseberry?
Note: *R. georgianus* not found in EOL or GRIN databases

Current APHIS Regulatory Status of Hosts:

The importation of the following plants for planting genera that are hosts of *Brevipalpus chilensis* are currently regulated under the following quarantines:

***Diospyros* spp.:** All propagules except seeds are Postentry Quarantine from all countries except Canada.

Garcinia livingstonei, G. mangostana, G. dulcis: All propagules except seeds are Postentry Quarantine from all countries except Canada

Jasminum: All propagules except seeds are NAPPRA from Belgium, Germany, India, Philippines, United Kingdom, and Postentry Quarantine from all other countries except Canada.

Ligaria: All propagules prohibited from all countries under 7CFR 330

Ligustrum: All propagules except seeds NAPPRA from Europe and Postentry Quarantine from all other countries except Canada

Rubus fruticosus, (R. plicatus,) R. moluccanus: are federal noxious weeds. All propagules are prohibited from all countries under 7CFR 360

Proposed Action under NAPPRA:

The importation of the following plants for planting genera, excluding seeds and excluding cut flowers and greenery, that are hosts of ***Brevipalpus chilensis***, are not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Ampelopsis
***Cestrum (C. laevigatum* is a NAPPRA weed)**
Diospyros
Dysphania
Plantago
Strongylodon

The importation of the following plants for planting genera, excluding seeds and excluding cut flowers and greenery, that are hosts of *Brevipalpus chilensis*, are not authorized pending pest risk analysis (NAPPRA) **from all countries except those listed after the genus**:

Antirrhinum	Canada, Colombia, Costa Rica, France, Guatemala, Indonesia, Israel, Netherlands
Apium	Canada
Catharanthus	Costa Rica, Guatemala, India, Japan
Convolvulus	Costa Rica, Israel, Kenya, Mexico, Uganda
Garcinia	Thailand
Jasminum	Canada
Ligustrum	Canada
Vinca	Brazil, Canada, Colombia, Costa Rica, Dominican Republic, El Salvador, Ethiopia, Guatemala, Israel, Japan, Kenya, Mexico, Netherlands

Already regulated under NAPPRA:

The importation of all propagules except seeds of the following plants for planting genera that are hosts of *Brevipalpus chilensis* are already regulated under **NAPPRA** and are therefore not listed here again:

Actinidia, Annona, Catalpa, Chrysanthemum, Citrus, Crataegus, Cydonia, Ficus, Malus, Pelargonium, Prunus, Pyrus, Rubus, Viburnum, Vitis

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
April 22, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: **Chickpea chlorotic dwarf virus (CpCDV)**

Hosts: ***Beta, Capsicum, Cicer, Datura, Gossypium, Lens, Solanum* (*Lycopersicon*), *Nicotiana, Phaseolus, Pisum, Sesbania, Vicia, Xanthium***

Taxonomy and description of the pest:

Chickpea chlorotic dwarf virus (CpCDV) is a plant pathogen in the Family Geminiviridae, Genus Mastrevirus. Alternate names for CpCDV include *Chickpea chlorotic dwarf geminivirus, Chickpea chlorotic dwarf monogeminivirus, Chickpea chlorotic dwarf mastrevirus, Chickpea chlorotic dwarf Pakistan virus* (CpCDPV), and *Chickpea chlorotic dwarf Sudan virus* (CpCDSV).

Geminiviruses have a propensity to evolve through recombination, which may support new host adaptability (Akhtar et al., 2014). Early reports of different CpCDV isolates were based on vector transmission, host symptoms, and visualization of geminate virus particles (Thomas et al., 2010), all of which could be confounded by inconsistency and/or cross-reactions with other viruses. Serological reactions, including DAS-ELISA and tissue-blot immunoassays (Farzadfar et al., 2008) have been used with good results, but specificity is an issue as the dicot-infecting Mastreviruses cross-react serologically (Horn et al., 1993; Liu et al., 1997). It was not until complete or partial genome sequences became available that the diversity among isolates was revealed (Farzadfar et al., 2008;

Thomas et al., 2010). CpCDPV and CpCDSV are closely related to *Bean yellow dwarf virus* (BeYDV), but these three viruses are all distinct from one another, forming discrete clades on a phylogenetic tree. Interestingly, analysis of partial sequence data showed that CpCDV-Syria was actually a chickpea isolate of BeYDV. Sequence analysis also suggested that there has been extensive inter- and intra-strain recombination that contributed to the diversification of this virus (Kraberger et al., 2015).

Known distribution:

Mastreviruses have as yet been identified only in the Old World, including western and south-central Asia and northern Africa (Akhtar et al., 2014; Thomas et al., 2010). Countries in which CpCDV has been reported include Egypt (Kumari et al., 2006), Ethiopia (CABI and EPPO, 2005), India (Horn et al., 1994; Horn et al., 1993), Iran (Akhtar et al., 2014; Farzadfar et al., 2008), Iraq (Kumari et al., 2006), Pakistan (Horn et al., 1994; Horn et al., 1993), Sudan (Hamed and Makkouk, 2002), Syria (Kumari et al., 2004), and Yemen (Kumari et al., 2006).

Biology of the pest:

Chlorotic dwarf disease symptoms in chickpea include overall stunting of the plant, shortened internodes, leaf lamina reduction, bushiness, tissue brittleness, and vascular discoloration at the collar (Horn et al., 1993; Kanakala et al., 2013). Indiginous 'Desi' varieties also show leaf reddening, while the introduced kabuli types may show yellowing (Horn et al., 1993). If infected early in the season (prior to flowering), plants rarely produce pods, declining and dying rapidly with yield losses reaching 75-100% (Horn et al., 1995). If diseased plants are few and they are scattered in a densely planted field, Horn et al. (1995) indicate that neighboring plants may compensate in production, but this phenomenon is not observed consistently. The detection of multiple isolates of CpCDV, and of CpCDV and other viruses, such as CpRLV, from a single field suggest that mixed infections are possible (Thomas et al., 2010).

Transmission and dissemination of the pest:

Reported insect vectors include the leafhopper species: *Orosius orientalis* Matsumura (India and Pakistan) (Horn et al., 1994) and *Orosius albicinctus* Distant (Syria) (Kumari et al., 2004). However, Fletcher et al. (2017) demonstrated that *O. orientalis* is restricted to Oriental, Palaearctic and Australian regions and concluded that reports of the species in India, Israel and Turkey were actually *O. albicinctus.* The latter species also is a natural vector of chickpea phyllody in India and Pakistan and of sesame phyllody in several countries (Akhtar et al., 2011). The minimum acquisition and inoculation access periods for CpCDV were both under 2 minutes, and the minimum latent period under 2 hours (Horn et al., 1994), suggesting that secondary spread within a crop can occur readily, potentially allowing in-plant titers to reach high levels. Males and females

transmitted at the same rate. The mode of transmission was persistent; the virus was not lost after molting and most individuals were able to transmit for life (Horn et al., 1994). However, the virus apparently did not multiply in the vector; rather its titer decreased over time (Horn et al., 1994). Experimentally, *O. albicinctus* transmitted the pathogen to 40-80% of exposed plants, depending on how the insects acquired the virus (Akhtar et al., 2011).

A different leafhopper, *Neolimnus aegyptiacus*, was mentioned by Hamed and Makkouk (2002) as a vector associated with chickpea stunt in Sudan, but it is unclear whether their reference to this species was connected to CpCDV or to other viruses contributing to stunting in this host.

CpCDV is transmissible by grafting (Farzadfar et al 2008), but not mechanically (Brunt et al., 1997; Farzadfar et al., 2008). There are no reports of seed transmission.

Damage potential of pest:

Chickpeas, as well as lentils, faba beans and various other pulse crops, rich in vegetable protein, are major components of the diets of residents of the Indian subcontinent as well as North Africa and the Middle East, where they are also important cash crops (Kanakala et al., 2013; Kraberger et al., 2015). In addition, germinated chickpea seeds have significant medicinal value and soaked grains and husks are fed to livestock. In India alone, chickpeas are grown over 7.1 million hectares and yield 5.75 million tons per year (Kanakala et al., 2013).

CpCD is the most important biotic stress for chickpea cultivation around the world (Kanakala et al., 2013). If infected early in the season (prior to flowering) plants rarely produce pods, declining and dying rapidly; yield losses can reach 75-100% (Horn et al., 1995). CpCDV is only one of several viruses affecting chickpea and related hosts in the same areas of the world. For example, others having similar host ranges and symptoms (all contributing to a general condition known as stunting) include the Luteoviruses *Bean leafroll virus* (BLRV), *Soybean dwarf virus* (SbDV) and *Chickpea luteovirus* (CpLV) as well as the Polerovirus *Beet western yellows virus* (BWYV) (Kumari et al., 2006); *Legume yellows virus* and *Subterranean clover red leaf virus* cause similar symptoms on chickpea in California, U.S.A. (Kumari et al., 2006). However, in numerous instances CpCDV was the most frequent of the stunting viruses and was considered to be the primary cause of the symptoms.

Control:

In Sudan, early sown fields allowed to become weedy sustained greater stunt incidence than did late sown fields kept free of weeds (Hamed and Makkouk, 2002), likely because the weeds, which survive throughout the year, served as virus reservoirs. Longer intervals

of irrigation (over 10 days) at this site were associated with greater leafhopper activity, while persistent humidity reduced it. The authors noted that disease spread declined after mid-November sowing when temperatures dropped, perhaps because vector activity declined under those conditions.

The development of CpCDV-resistant cultivars is likely the most sustainable approach for disease management (Kanakala et al., 2013). Current evaluation of virus resistance is based primarily on naturally infected field plants. Until recently, screening for disease resistance in chickpea cultivars was hampered by the lack of efficient and reliable methods to conduct field inoculations (use of the vector is cumbersome and inconsistent) or to measure disease severity (no objective scoring system had been developed). However, Kanakala et al. (2013) developed an *Agrobacterium*-mediated delivery of viral genomic DNA into selected chickpea cultivars and proposed a quantitative disease scoring system. In Sudan, chickpea cv. Shendi was more resistant than cv. ICCV-2 (Hamed and Makkouk, 2002), indicating that there may be sources of resistance to the virus. In Pakistan, the native "desi" chickpea varieties sustained less disease than did the non-native "kabouli" types (Kanakala et al., 2013).

Known host range:

Beta vulgaris (Farzadfar et al., 2008), *Capsicum annum* (Akhtar et al., 2014), *Cicer arietinum* (Horn et al., 1995), *Datura stramonium* (Brunt et al., 1997), *Gossypium* spp. (Manzoor et al., 2014), *Lens esculenta* (Horn et al., 1995), *L. culinaris* (Horn et al., 1995), *Lycopersicon esculentum* (Brunt et al., 1997), *Nicotiana benthamiana* (Brunt et al., 1997), *N. glutinosa* (Brunt et al., 1997), *N. tabacum* (Brunt et al., 1997), *Phaseolus vulgaris* (Horn et al., 1995), *Sesbania bispinosa* (Nahid et al., 2008), *Vicia faba* (Horn et al., 1995), *Pisum sativum* (Horn et al., 1995), and *Xanthium strumarium* (Mubin et al., 2012).

Plants were infected by the use of inoculative *O. orientalis* or by graft transmission experimentally to a range of species in the families Chenopodiaceae, Fabaceae, and Solanaceae; symptoms were similar to those in chickpea (Farzadfar et al., 2008).

Current Regulatory Status of Hosts:

The importation of the following plants for planting genera that are hosts of Chickpea Chlorotic Dwarf Virus, are already regulated under NAPPRA.

Cicer, Capsicum, Gossypium, Lens, Nicotiana, Phaseolus, Pisum, Solanum (Lycopersicon), Sesbania, Vicia

Datura: Per Federal Order effective August 6, 2014 All propagules except seeds prohibited from Albania, Algeria, Argentina, Austria, Bahrain, Belgium, Benin, Bolivia, Brazil, Bulgaria, Burkina Faso, Canary Islands, Cape Verde, Cayman Islands, Chile,

Colombia, Costa Rica, Cote D'Ivoire, Cyprus, Czeck Republic, Denmark, Ecuador, Egypt, Estonia, Finland, France, Gambia (The), Germany, Ghana, Greece, Guinea, Guinea-Bissau, Hungary, Iraq, Ireland, Israel, Italy, Jordan, Kenya, Kosovo, Kuwait, Latvia, Liberia, Libya, Lithuania, Luxembourg, Mali, Malta, Morocco, Netherlands, Niger, Nigeria, Palestinian Authority (West Bank), Panama, Paraguay, Peru, Poland, Portugal (including the Azores), Romania, Russia, Saudi Arabia, Senegal, Sierra Leone, Slovakia, Slovenia, South Sudan, Spain, Sweden, Switzerland, Syria, Togo, Tunisia, Turkey, United Kingdom (all regions), Ukraine, Uruguay, Venezuela, Western Sahara. **NAPPRA from India; Postentry Quarantine from all other countries.**

Proposed Action under NAPPRA:

The importation of the following plants for planting genera, excluding seeds and excluding cut flowers and greenery, that are hosts of **Chickpea Chlorotic Dwarf Viru**s is not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Beta
Datura
Xanthium

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
May 16, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Elm mottle virus*** **(EMoV)**

Hosts: ***Hydrangea, Philadelphus, Syringa, Ulmus***

Taxonomy and description of the pest:

Elm mottle virus (EMoV) is a viral pathogen of elm, hydrangea and lilac and a member of the Bromoviridae family and *Ilarvirus* genus. Synonyms for the virus include *Hydrangea mosaic virus* (Jones and Scott, 2004; Scott et al., 2003), *Lilac streak mosaic virus* (Jones et al., 1987), and *Lilac white mosaic virus* (Schmelzer, 1969; Scott et al., 2003).

Known distribution:

Germany (Schmelzer, 1969) and the United Kingdom (Scotland)(Jones and Mayo, 1973; Schmelzer, 1969).

Based on reported leaf symptoms, EMoV may also be present on elm in Bulgaria, the Czech Republic, England, and the former USSR (Schmelzer et al., 1966; Scott et al., 2003).

This pathogen is not known to occur in the United States.

Biology of the pest:

Viruses in the *Ilarvirus* genus mainly infect woody plants, with transmission by seed and pollen (Hull, 2002). *Ilarvirus* species are divided by serological methods, with EMoV belonging to sub-group 2, which includes *Asparagus virus-2* (AV-2), *Citrus leaf rugose virus* (CiLRV), *Citrus variegation virus* (CVV), and *Tulare apple mosaic virus* (TAMV)(Scott et al., 2003). There is evidence that members of the *Ilarvirus* genus are harbored in native plant species, with occasional infections in crop species (Scott et al., 2003). Based on this, there has been speculation that elm—a long-lived tree—harbors EMoV, and this relationship is a precursor to *Ilarvirus* spp. infecting asparagus, citrus and spinach (Scott et al., 2003).

Vectors for EMoV are as yet unidentified (Scott et al., 2003). EMoV belongs to the alpha-like superfamily of viruses, with a tripartite, positive-sense, single-stranded RNA genome (Scott et al., 2003). Its coat protein (or the subgenomic mRNA that encodes it) is required for replication, with other *Ilarvirus* coat proteins able to functionally substitute for it (Hull, 2002).

EMoV is associated with ringspot and line-pattern symptoms in elm leaves, with artificially inoculated seedlings kept in a heated greenhouse remaining asymptomatic (Jones and Mayo, 1973; Schmelzer, 1969). In mechanically inoculated *Forsythia intermedia* and *Syringa vulgaris*, systemic chlorotic or white mosaic ringspots occur (Jones and Scott, 2004). In artificially inoculated experimental indicator hosts, other symptoms include faint chlorotic local lesions and mosaic or mottle in systemic leaves (*Chenopodium quinoa*); necrotic local lesions with necrotic or chlorotic spots in systemic leaves (*Nicotiana megalosiphon*); and necrotic local lesions and small rings without systemic infection (*Phaseolus vulgaris* and *Vigna sinensis*) (Jones and Scott, 2004).

EMoV virions are not enveloped. They are quasi-isometric elongated to isometric nucleocapsids that are 25-30nm in diameter (Jones et al., 1987).

Movement and transmission:

Ilarvirus Elm mottle virus is transmitted by pollen and seed in elm (Hull, 2002; Jones and Scott, 2004). The virus is readily sap-transmissible to many herbaceous plants, many of which are systemically infected and develop symptoms. Infectivity is maintained after protease treatment (Jones et al., 1987). There are no known vectors of EMoV (Scott et al., 2003), with aphids failing to transmit to test plants after access to infected plants (Schmelzer, 1969).

In *Ulmus glabra*, EMoV is seedborne to 20% (Jones and Mayo, 1973) and detected in infected *Syringa vulgaris* pollen (Schmelzer, 1969). Dodder (*Cuscuta californica* or *C. subinclusa*) does not transmit EMoV (Schmelzer, 1969).

Damage potential of pest:

American elm (*Ulmus americana* var. *americana*) is found throughout the eastern United States, including in the Dakotas, Kansas, Oklahoma, Texas, and the Gulf Coast over to Florida (Coladonato, 1992). *U. americana* var. *floridana* is restricted to eastern North Carolina to the central Florida coastal plains). Although elm wood is not durable, it is used as a veneer in furniture, in the manufacture of various wood products, and as fuel wood. Elm is also an important part of the environment, with birds and small animals feeding on its flowers, fruit and seeds. Elm is used for windbreaks and erosion control.

Until its populations were decimated by Dutch elm disease, American elm was a valued ornamental tree for landscaping in many parts of the country (Anonymous, 2000).

No information about the economic costs associated with EMoV disease in Europe is available.

Control:

Effective control is best achieved through the use of virus-tested planting material (CABI, 2017).

Known host range:

Hydrangea macrophylla (Jones and Scott, 2004); *Philadelphus* (Schmeltzer, 1974), *Syringa vulgaris*, *Ulmus carpinifolia*, *U. glabra* (Jones and Scott, 2004; Schmelzer, 1969); and *U. minor* (Jones and Scott, 2004).

66 plant species from 22 families, including many members of the Chenopodiaceae, Leguminoseae, and Solanaceae, were confirmed as hosts by artificial inoculation with EMoV (Schmelzer, 1969).

Current APHIS Regulations for hosts:

***Hydrangea*:** All propagules except seeds are NAPPRA from Japan; and Postentry Quarantine from all countries except Japan and Canada.

Ulmus: All propagules except seeds are NAPPRA from all countries except Canada; seeds are NAPPRA from Europe.

Philadelphus: All propagules except seeds are NAPPRA from Europe; must enter Postentry Quarantine from all countries except Canada and Europe.

Syringa: All propagules except seeds are NAPPRA from Europe except Netherlands; from Netherlands needs Phytosanitary certificate with AD for plant parasitic nematodes

capable of transmitting European nepoviruses, including, but not limited to, the Arabis mosaic nepovirus. Must enter Postentry Quarantine from all countries except Canada and Europe (except Netherlands).

Syringa vulgaris: Needs to meet *Phytophthora ramorum* conditions of entry from Canada, Netherlands, and other countries; then enter Postentry Quarantine from all countries except Canada and Europe.

Proposed Action under NAPPRA:

The importation of the following plants for planting genera, excluding seeds, and excluding cut flowers and greenery, that are hosts of **Elm mottle virus**, are not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Philadelphus

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, that is a host of **Elm mottle virus**, is not authorized pending pest risk analysis (NAPPRA) from **all countries except those listed after the genus:**

Syringa	Canada

The importation of all propagules except seeds of the following plants for planting genera that are hosts of **Elm mottle virus** are already regulated under NAPPRA and are therefore not listed here again:

Hydrangea, Ulmus

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
Aug 26, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-2a allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: **Euonymus yellow mottle associated virus (EuYMaV)**

Hosts: *Euonymus bungeanus*

Taxonomy and description of the pest:

Euonymus yellow mottle associated virus (EuYMaV) is a plant pathogen in the *Alphaflexiviridae* family and *Potexvirus* genus and the causal agent of yellow mottle disease in *Euonymus bungeanus*, an ornamental tree that is widely planted in gardens in Shenyang of Liaoning Province, China (Yang et al., 2019).

Known distribution:

China (Yang et al., 2019).

This pathogen is not known to occur in the United States.

Biology of the pest:

Potexviruses, are single-stranded RNA, positive-strand viruses characterized by non-enveloped flexuous filaments (470-580 × 13 nm). A typical potexvirus genome is monopartite, 5.9-7.0 kb in size, contains a 5′ cap structure and a 3′ poly(A) tail, and encodes five proteins: RNA-dependent RNA polymerase (RdRp), triple gene block (TGB 1, 2, and 3) proteins, and the coat protein (CP) (ICTV, 2011).

EuYMaV was isolated from *E. bungeanus* showing yellow mottle leaf disease. Transmission electron microscopy of symptomatic leaf samples showed typical flexuous filaments approximately 500 nm in length and 13 nm in diameter (Yang et al., 2019).

Analysis of the EuYMaV genome revealed that it is 6,784 nt, including a 74-nt 5′ untranslated region (UTR) and a 476-nt 3′ UTR. Like that of a typical potexvirus, the EuYMaV genome contains five ORFs (Yang et al., 2019). ORF1 encodes a 1,351-aa RdRp. ORF2 encodes a 248-aa TGB1, which was predicted to contain a viral_helicase 1 domain reported to play multiple roles in viral RNA replication (Morozov and Solovyev, 2015; Rikkonen et al., 1994). ORF3 encodes a 114-aa TGB2 protein containing a Plant_vir_prot superfamily domain that is predicted to be involved in viral movement (Verchot-Lubicz et al., 2010), and ORF4 encodes an 83-aa TGB3. ORF5 encodes a 271-aa CP (Yang et al., 2019).

Pairwise percent identity analyses revealed that the EuYMaV complete genome sequence, 3′-UTR, and TGB1 share nucleotide and amino acid identity with euonymus yellow vein associated virus (EuYVAV). EuYMaV is most similar to pepino mosaic virus (PeMV) in the 5′-UTR; white clover mosaic virus (WCMV) in the RdRp and TGB3; citrus yellow vein clearing virus (CYVCV) in TGB2; and cymbidium mosaic virus (CyMV) in CP (Yang et al., 2019). Phylogenetic analyses placed EuYMaV in a group with other potexviruses. Based on its morphology and degree of sequence similarity and phylogenetic clustering with previously reported potexviruses, EuYMaV was proposed as a distinct species in the genus *Potexvirus* (Yang et al., 2019).

Although little other specific information is available on EuYMaV, which was discovered very recently, the *Potexvirus* type strain, *Potato virus X* (PVX), has been extensively characterized as a model system for the group (Batten et al., 2003; Martelli and Rubino, 2012; Verchot-Lubicz et al., 2007).

Movement and transmission:

No information has been published on the dissemination of EuYMaV. Most *Potexvirus* spp. occur in high concentrations within their host plant cells, and all examined to date are mechanically transmitted. Contaminated worker hands or clothing, cutting tools, and small mammals have all been reported as mechanisms for the spread of various potexviruses. PVX is also spread by contact between infected and healthy plants (Martelli and Rubino, 2012); whether this occurs with EuYMaV is not known. A small number of potexviruses have been reported to be transmitted by aphids, but this phenomenon may have been due to encapsulation by associated luteoviruses or to the presence of a helper virus (Martelli and Rubino, 2012). Most *Potexvirus* spp. are not seed transmitted, but two that infect legume species have been reported to move through seed at a low rate (Martelli and Rubino, 2012).

Damage potential of pest:

No information about the damage potential of EuYMaV is available. Further investigation is needed to confirm the relevance of the virus to the disease (Yang et al., 2019)

The pathogen's only known host, *Euonymus bungeanus* (winterberry euonymus), is native to China and used in the United States for landscape (Brand, n. d.).

Control:

No information about control of EuYMaV is available. In general, virus-free seed and planting material should be used, and strict hygienic measures should be observed.

Known host range:

Euonymus bungeanus (Yang et al., 2019).

Current Trgulatory Status of Host:

***Euonymus*:** Is Not Authorized Pending Pest Risk Analysis (NAPPRA) from Europe and Japan; and must enter Postentry Quarantine program from all other countries except Canada, Europe, and Japan.

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, that is a host of Euonymus yellow mottle associated virus is not authorized pending a pest risk analysis ((NAPPRA)) **from all countries, except those listed after the plant genus:**

Euonymus	**Canada**

References:

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
January 14, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-2a allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: **Hop stunt viroid (HSVd)**

Hosts: ***Citrus, Cucumis, Ficus, Fortunella, Galinsoga, Gynura, Hibiscus, Humulus, Malus, Morus, Pistacia, Prunus, Punica, Pyrus, Vitis, Ziziphus***

Taxonomy and description of the pest:

Hop stunt viroid (HSVd) is a pathogen in the *Pospiviroidae* family and *Hostuviroid* genus and the causal agent of hop stunt disease.

Alternate names for HSVd include Citrus cachexia viroid (Diener et al., 1988), Citrus viroid II (Diener et al., 1988), Cucumber pale fruit viroid (van Dorst and Peters, 1974), Dapple plum viroid (Sano et al., 1989), and Peach fruit disease viroid (Sano et al., 1989). Alternate names for HSVd disease include cucumber pale fruit, citrus xyloporosis (Diener et al., 1988), citrus cachexia (Reanwarakorn and Semancik, 1999), gummy bark of sweet orange (Önelge et al., 2004), citrus yellow corky vein (Roy and Ramachandran, 2003), split bark disease of sweet lime (Bagherian and Izadpanah, 2010), dapple disease of peach and plum (Sano et al., 1989), and degeneracion of apricot (Amari et al., 2007).

Known distribution:

Algeria, Argentina, Australia, Brazil, Canada, China, Colombia, Cyprus, Czech Republic, Ecuador, Egypt, Finland, France, Germany, Greece, Iran, Israel, Italy, Jamaica, Japan, Jordan, Korea, Lebanon, Libya, Morocco, New Zealand, Philippines, Portugal, Saudi Arabia, Serbia, Slovenia, South Africa, Spain, Sudan, Suriname, Syria, Thailand, Tunisia, Turkey, Trinidad and Tobago, the United States (Arizona, California, Florida, Texas, and Washington), Uruguay, and Yemen (CABI, 2017; EPPO, 2001; Parkinson and Reed, 2013).

HSVd presence in the United States is restricted to Arizona, California, Florida, Texas and Washington (CABI, 2017).

Biology of the pest:

Viroids, the smallest infectious pathogens known, are composed of a short strand of circular, single-stranded RNA but lack the protein coat of viruses (Diener, 1981). All currently described viroids are residents of higher plants, in which they may cause disease or not. HSVd is 294-303 nt in length depending on the host and the isolate (Ohno et al., 1983). Over 600 HSVd sequences have been deposited in the DDBJ/GenBank/EMBL sequence databases (Hataya et al., 2017). The quasi-rod-like form of this viroid consists of five domains; its central conserved region is similar to that of *Pospiviroids* and *Cocadviroids*, and a terminal conserved hairpin structure is similar to that in *Cocadvioids* (Flores et al., 1997). HSVd lacks ribozyme activity, and its RNA replicates via an asymmetric, rolling circle model (Flores et al., 2005). Isolates have been grouped into a variety of sequence variants or sub-species level clades from different host species (Lafontaine et al., 1999); one scheme included five such groups: Plum, Hop, Citrus, P-H/Cit3 and P_C clades (Amari et al., 2001). Additional taxonomic variants have recently been described (Elbeaino et al., 2012; Jo et al., 2017; Zhang et al., 2012), but a recent review organized the variants into just three major groupings: plum-type, grape/hop-type and citrus-type (Hataya et al., 2017). Considerable genetic diversity can be present among HLVd variants within a single host plant. For example, Gazel et al. (2008) identified five new sequence variants in naturally infected apricot, plum and peach trees in Turkey, and Jo et al. (2017) identified 11 distinct variants of 70 HSVd genomes obtained from unique apricot and plum trees in Korea. HSVd isolates from Tunisian clementines and figs, characterized phylogenetically, fell into two groups: a cachexia strain from the citrus group and a recombinant citrus-plum type group (Gorsane et al., 2010); evidence suggests that these variants have spread rapidly in the region. Furthermore, 382 non-redundant HSVd variants were discerned among all known (572) HSVd sequences (Jo et al., 2017).

The pathogen was first recognized in the 1940s in hop plants originating from Japan, giving rise to its name (Yamamoto et al., 1973). Since then, HSVd has been reported in a wide range of herbaceous and woody hosts in which the infection seems to be latent (such as grapevine, apricot, pear, and tomato) or may induce associated symptoms such as with hop stunt, citrus cachexia, and dapple fruit of plum and peach (Ragozzino et al., 2004). Symptoms on hops vary substantially with the cultivar; in one study yield was reduced by 14%, 34% and 62% in cvs. Cascade, Willamette and Glacier, respectively, while cv. Nugget had no visual symptoms or growth reduction (Kappagantu et al., 2017). Physical symptoms include plant stunting due to shortened internodes (often not obvious until 3-5 years after infection); curling, chlorotic and small upper leaves; leaves drooping from the base; yellow-green basal foliage; and yellow speckles on leaf veins (Sano et al., 1989). Limited production of bine hooks hampers the normal climbing habit of the plant (Sano, 2003). Infected hop plants may flower 8-10 days earlier than healthy plants, produce fewer and smaller cones having fewer lupulin glands, reducing yield by 50% and lowering alpha and beta acids 50-70% compared to healthy plants (Pethybridge et al., 2008; Yamamoto et al., 1973). Symptoms are often more severe in warm climates (Sano, 2003; Sano et al., 1989). Cucumbers infected with the viroid (pale fruit disease) may be stunted and display shriveled flowers, chlorotic and rugous leaves and small, pale, pear-shaped fruits (Sano, 2003). Citrus plants affected by cachexia disease are stunted and chlorotic with gummy deposits and pitting of the bark (Reanwarakorn and Semancik, 1999). Dapple fruit disease of stone fruits (plum and peach) is characterized by irregular red blotching and an irregular surface on young fruits, as well as delayed fruit maturity and a hard flesh texture (Sano, 2003). A recent, comprehensive table of HSVd host plants, diseases and symptoms, viroid variants and sequence types, and associated references is provided by Hataya et al. (2017).

HSVd also can be present in mixed infections with other pathogens, including other viroids, being reported in a co-infection with the *Citrus exocortis viroid* (*Pospoviroid*) in symptomless grapevines in Brazil (Eiras et al., 2006). Other viroids of hops exist; one that differs significantly from HSVd in physical and biological properties was reported in commercial hop production sites in Spain (Pallás et al., 1987), while *Hop latent viroid* (HpLVd) has been found in the Pacific Northwest region of the U.S. (Eastwell et al., 2018).

Movement and transmission:

HSVd is transmitted over short distances by mechanical means, facilitated by farm operations such as ‘stringing’ (attaching the climbing hop vines to cords for support) and basal growth control (cutting with sickles or scissors), resulting in down-row movement (Pethybridge et al., 2008; Sasaki et al., 1989; Yamamoto et al., 1973). Long-distance movement is primarily through

infected propagation material. Hop is clonally propagated via rooted cuttings or rhizomes, and HSVd can be spread by such propagation of infected plants (Eastwell and Nelson, 2007). Seed transmission has been reported (Luigi et al., 2010; Parkinson and Reed, 2013), but it was not clear whether the source was infected pollen, and pollen transmission to tomato also was noted (Kryczyński et al., 1988). No insect vector has been reported, and attempts to transmit the viroid through soil or via aphids failed; however, the viroid was shown to move through dodder (CABI, 2017).

Damage potential of pest:

Hops are the flowers of the perennial, dioecious hop plant (*Humulus lupulus*), which is grown commercially for its strobiles (cones) that produce resins, oils and polyphenols—particularly alpha acids—used primarily in making beer, to which they add substance stability and characteristic bitterness and aroma (Pethybridge et al., 2008).

The United States is the second largest producer of hops in the world; in 2015, about 17,658 ha were planted to the crop (Kappagantu et al., 2017). Within the U.S., Washington State accounts for about ¾ of the production. HSVd was first reported from commercial plantings of hops in the state of Washington in 2004 (Eastwell and Nelson, 2007), with symptoms of chlorosis and reduced plant vigor. About 17% of hop plants tested in Washington were shown to be infected. Since hops is a perennial crop, with individual plants productive for as long as 20 years, vigilance is needed to minimize disease threats.

HSVd is a serious disease in hops. Outbreaks in Japan in the 1940s-50s caused reductions of 25-50% in bine length, cones/bine, cone weight and alpha acid content (Hataya et al., 2017). In other circumstances, losses have reached as much as 65% (Brown and Sirrine, 2012). Since opportunities for long-distance spread are relatively small, and infectivity of HSVd in infected hop cones and leaves remaining in the field post-harvest is lost after three months (Yaguchi and Takahashi, 1984), infections may be restricted to the vicinity of the site of introduction except where moved during trade or by shared machinery. Effective management programs play a major role in minimizing the impacts of this pathogen. In cucumbers, HSVd-incited pale fruit disease has led to economic losses in greenhouse-grown crops (van Dorst and Peters, 1974). In citrus, cachexia disease is particularly problematic in mandarins and their hybrids as well as *Citrus macrophylla* (Hataya et al., 2017). Dapple fruit disease of plum and peach has caused serious commercial losses, particularly in sensitive cultivars, in Japan, Korea and Italy (Sano et al., 1989).

Losses in other susceptible crops, such as cucumber and stone fruits, due to HSVd may be

associated with effects of the viroid on the availability of produce for fresh market and processing. The viroid is of significant phytosanitary importance, especially for the production of healthy propagating material of fruit tree crops (Papayiannis, 2014).

Control:

Currently, detection and diagnosis of HSVd is primarily by molecular-based tools including polyacrylamide gel electrophoresis (Duran-Vila et al., 1986), molecular hybridization (Fonseca, 1996) and reverse transcription polymerase chain reaction (RT-PCR) (Osman et al., 2017; Papayiannis, 2014). The pathogen is unevenly distributed throughout the host plant (Hataya et al., 2017), so sampling strategies should take this into account.

The primary means of managing HSVd is through a variety of cultural practices (Eastwell et al., 2018; Eastwell and Sano, 2009; Singh et al., 2003). The use of planting stock certified to be free of viroids is recommended; clean rootstock is available from the Clean Plant Network at http://healthyplants.wsu.edu/hop-program-at-cpcnw/. Growers should plant where hops have not been grown before or in fields where all hop plants have died out.

General sanitation practices include working in or harvesting plots in which disease is present only after other plots have been addressed. Equipment should be cleaned well before moving between yards, particularly early in the season, by washing to remove plant debris, sterilizing with a bleach solution, then rinsing with clean water. Removal of basal vegetation late in the season should be by chemical rather than mechanical means to reduce risk of transmission. Contact herbicides should be used to set training dates and weak shoots should be removed in the spring to avoid use of mechanical mowers that could transmit the viroid. Plants that are severely stunted or yellowed should be rogued. Growers should wait at least one season after infected plants are removed before replanting to hop to ensure that all infected hop plants have been eliminated.

Little information is available on the existence of hops cultivars or other plants that carry resistance to the viroid. In one study, variable levels of susceptibility were identified among 26 apricot cultivars, but none had acceptable levels of resistance (Rubio et al., 2015).

The use of cold therapy in combination with chemotherapy in shoot tip cultures of infected peach and pear was reported to eliminate HSVd from the plants, suggesting that this could be a viable management approach (El-Dougdoug et al., 2010).

Known host range:

Citrus clementina, *Citrus limettioides*, *Citrus limon*, *Citrus limonia*, *Citrus macrophylla*, *Citrus reticulata*, *Citrus sinensis*, *Citrus unshui*, *Citrus volcameriana*, *Citrus x paradisi*, *Cucumis sativa*, *Ficus carica*, *Fortunella* spp., *Galinsoga quadriradiata*, *Gynura aurantiaca*, *Hibiscus rosa-sinensis*, *Humulus lupulus*, *Malus domestica*, *Malus sylvestris*, *Morus alba*, *Pistacia vera*, *Prunus armeniaca*, *Prunus avium*, *Prunus domestica*, *Prunus dulcis*, *Prunus persica*, *Prunus salicina*, *Prunus undulata*, *Punica granatum*, *Pyrus communis*, *Vitis vinifera*, and *Ziziphus jujuba* (Hataya et al., 2017; Plantwise, n. d.).

Current APHIS Regulatory Status of Hosts:

The importation of the following plants for planting genera that are hosts of Hop Stunt Viroid are currently regulated under the following quarantines:

***Humulus*:** All propagules except seeds must enter Postentry Quarantine Program from all countries.

***Pistacia*:** All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada.

Proposed Action under NAPPRA:

The importation of the following plants for planting genera, excluding seeds, and excluding cut flowers and greenery, that are hosts of **Hop stunt viroid**, are not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Galinsoga, Humulus, Pistacia

The importation of the following plants for planting genera, excluding seeds, and excluding cut flowers and greenery, that are hosts of Hop stunt viroid, are not authorized pending pest risk analysis (NAPPRA) **from all countries, except those listed after the genus**:

Cucumis	Canada, Netherlands
Gynura	Dominican Republic, Guatemala

The importation of the following plants for planting genera that are hosts of Hop stunt viroid are already regulated under NAPPRA and are therefore not listed here again:

Citrus, Ficus, Fortunella, Hibiscus, Malus, Morus, Prunus, Punica, Pyrus, Vitis, Ziziphus

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
April 25, 2019

In order to prevent the introduction of quarantine pests into the United States, the U.S. Code of Federal Regulations 7 CFR §319.37-4 (2018) allows the U.S. Department of Agriculture Animal and Plant Health Inspection Service (APHIS) Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Myrtaspis syzygii* (Takagi, 1999)**

Order (Family): Hemiptera (Diaspididae)
Synonyms: *Chionaspis syzygii* (Takagi, 1985)
Common names: None

Hosts: ***Syzygium***

Known Distribution of pest:

Known world distribution: *Myrtaspis syzygii* is an established pest in Asia, recorded in India (Varshney et al., 2015), and Nepal (Takagi, 1985).

Distribution in the United States: *M. syzygii* is not known to be present in the United States.

Biology of the pest:

M. syzygii is an armored scale insect reported to feed on the leaves and twigs of *Syzygium spp.* host plants (Takagi, 1985). Additional data on feeding behavior and life history are not available. In Diaspididae scale insects, nymphal stages of both sexes and adult females can inflict damage by feeding on the sap and cellular tissues of host plants (Miller and Davidson, 2005). The following description of Diaspididae life stages is based on reports by Miller and Davidson (2005), and Henderson (2011). Most Diaspididae species produce less than 100 eggs per female. There are two immature nymphal instars and an adult stage in females, and four immature instars

and an adult stage in males. Nymphs and adult females create a protective scale cover, separate from the body, consisting of wax, shed skins, and other compounds. Adult males are winged, lack mouthparts, and are typically small and short lived. For *M. syzygii*, information regarding the overwintering stage, if any, and the number of generations per year, is not available.

The feeding behavior and general biology of *M. syzygii* has not been reported; however, it is likely to be similar to other Diaspididae, as reported by Miller and Davidson (2005), and Henderson (2011). The first instar nymphs of Diaspididae, also known as the crawler stage, are moderately active and disperse over a short distance in search of a favorable feeding spot, then insert their mouthparts into the plant to feed. After attachment, the nymphs and adult females of all Diaspididae are immobile and remain attached to the plant by their mouthparts, continuing to feed on the sap and tissues of the host plant. Unlike other scale insects, Diaspididae do not produce honeydew. Adult males do not feed.

Damage Potential of pest:

Specific damage reports for *M. syzygii* are not available. Other Diaspididae pests damage host plants by injecting toxic saliva and sucking nutrients, which weakens the plants and can cause necrotic spots and other injury (Miller and Davidson, 2005). Severely infested leaves and stems can become chlorotic, resulting in potential leaf drop, twig dieback, and eventual host plant death (Miller and Davidson, 2005). Unlike other scale insects, Diaspididae do not produce honeydew; consequently, there is no potential damage associated with sooty mold fungus (Henderson, 2011).

Means of movement and dispersal:

The long-range dispersal of *M. syzygii* is likely due primarily to human-assisted movement of infested plant materials. Diaspididae armored scale insects are commonly intercepted at US ports of entry (Evans and Dooley, 2013). The natural spread potential of all Diaspididae is minimal. Immature stages are either immobile or move a very short distance, and adult females are immobile (Miller and Davidson, 2005). Adult males can fly; however, distances are likely to be short (Miller and Davidson, 2005). First instar nymphs may occasionally be blown passively by wind a short distance (Henderson, 2011).

Plant parts liable to carry the pest	Pest stages	Borne internally or externally?	Visibility of pest or symptoms
Leaves	Egg, nymph, adult (female)	Externally	Immobile nymphs and adult females; waxy scale covering late instar nymphs and adult females
Twigs	Egg, nymph, adult (female)	Externally	Immobile nymphs and adult females; waxy scale covering late instar nymphs and adult females

Control:

Import risk-mitigation options: Detection can be made by visual inspection of leaves and twigs using a hand lens. There are no currently published recommended import risk mitigation

procedures specifically for *M. syzygii*. The USDA APHIS PPQ Treatment Manual (2016) prescribes methyl bromide fumigation at Normal Atmospheric Pressure for host plants of scale insects in general.

Host-Plant Species:

Scientific and selected common names verified in EOL and GRIN databases, unless specified otherwise.

Syzygium cumini (Myrtaceae) (Takagi, 1985)

Synonyms: *Caryophyllus jambos, Eugenia cumini, E. jambolana, Myrtus cumini,* S. *jambolanum*

Common names: jambolan, Java-plum, Malabar-plum, Portuguese-plum, rose-apple

Notes: Female adults and immature exuvial casts collected from leaves and twigs, and male nymphs collected from leaves during a field survey (Takagi, 1985)

Syzygium jambos (Myrtaceae) (Takagi, 1985)

Synonyms: *Eugenia jambos*

Common names: jambos, Malabar-plum, rose-apple

Notes: Female adults and immature exuvial casts collected from leaves and twigs, and male nymphs collected from leaves during a field survey (Takagi, 1985)

Syzygium nervosum (Myrtaceae) (Takagi, 1985)

Synonyms: *Cleistocalyx nervosus, C. operculatus* (Takagi, 1985), *Eugenia operculata, E. paniala, S. operculatum*

Common names: Daly River satin-ash

Notes: Female adults and immature exuvial casts collected from leaves and twigs, and male nymphs collected from leaves during a field survey (Takagi, 1985)

Current APHIS Regulatory Status of Hosts:

***Syzygium* spp.** All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada

Proposed Action under NAPPRA:

The importation of the following genus of plants for planting, excluding seeds, and excluding cut flowers and greenery, which is a host of ***Myrtaspis syzygii*** is not authorized pending a pest risk analysis ((NAPPRA)) **from all countries**:

Syzygium

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
May 01. 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Neopestalotiopsis macadamiae*** and ***Pestalotiopsis macadamiae***

Hosts: ***Macadamia***

Taxonomy and description of the pest:

Neopestalotiopsis macadamiae and *Pestalotiopsis macadamiae* are fungal plant pathogens of the Sordariomycetes class, Xylariales order, and Amphisphaeriaceae family and causal agents of dry flower disease of macadamia (Akinsanmi et al., 2017).

Known distribution:

Australia (Akinsanmi et al., 2017).

Neither *N. macadamiae* nor *P. macadamiae* is known to occur in the United States.

Biology of the pest:

Macadamia trees (*Macadamia integrifolia*, *M. tetraphylla*, and hybrids) are grown in commercial plantations in tropical and subtropical regions around the world. Macadamia fruit is a dehiscent pericarp (the husk) that encloses a shell and an edible cream-colored kernel (the embryo). The fruits are derived from flowers borne on racemes (inflorescences) that are susceptible to blights caused by a number of pathogens (Drenth et al., 2009; Manicom, 2003; Zentmyer, 1962). Raceme blights caused by various pathogens may be distinguished based on well-known symptoms. Dry flower, a new

disease of macadamia racemes, was discovered in Australia in 2009 (Akinsanmi et al., 2017). Unlike other raceme blights of macadamia caused by *B. cinerea* (Holtzmann, 1963) and *C. cladosporioides* (van den Berg et al., 2008), the new disease was characterized by the dry appearance of the diseased racemes, infection at all stages of raceme development, and diseased, easily dislodged flowers (Akinsanmi et al., 2017).

Additionally, necrotic blight symptoms appear on infected flowers and sometimes on the rachis from early bloom to full anthesis (Akinsanmi et al., 2017). Within a few days of infection, immature buds or florets may become blighted, turn brown to dark brown, and remain attached to the green rachis. At later stages of inflorescence development, the floral parts became blighted. Necrotic flower parts may remain attached to the rachis or are easily dislodged when shaken (Akinsanmi et al., 2017).

N. macadamiae and *P. macadamiae* were ultimately identified as responsible for the dry flower disease observed in Australian macadamia orchards (Akinsanmi et al., 2017). The pathogens were consistently isolated from flowers with blight symptoms, rachises with necrotic symptoms, and dieback at the distal end of diseased macadamia racemes.

Akinsanmi et al. (2017) provided a thorough description of *N. macadamiae* and *P. macadamiae* anatomy. Both pathogens elaborate spore-producing conidiophores organized into conidiomata. *N. macadamiae* conidiomata are pycnidial in culture on PDA, globose, 200–500 mm diameter, solitary or aggregated in clusters, pale yellow brown, and exude dark brown slimy conidial droplets. *N. macadamiae* conidiophores are septate or reduced to conidiogenous cells. They produce conidia (spores) that are fusiform to narrowly ellipsoidal, straight or curved, (23–) 24–28 (–29) × (6–) 6.5–7.5 (–8) mm, 4-septate. The apical cells of the conidia are subcylindrical, 4–6 mm long, hyaline, smooth, thin-walled, with 3 (rarely 2) apical tubular unbranched filiform flexuous appendages (24–) 25–30 (–32) mm. The basal cells are conic with a truncate base, 3–6 mm, hyaline, smooth, thin walled, with a simple appendage 3–7 mm long. The three median cells of the conidia are doliiform, 14–18 mm, versicolored, and olivaceous brown, smooth. The septum between the median cell and fourth cell from the base is dark brown and thickened. The second cell from base is pale brown and 3.5–6 mm long. The third cell is medium to dark brown, 4.5–7 mm long, and the fourth cell is medium brown and 4–6.5 mm long.

P. macadamiae conidiomata are pycnidial in culture on PDA, globose, 200–400 mm diameter, solitary or aggregated in clusters, pale yellow brown, and exude dark brown slimy conidial droplets. The conidiophores are septate and sparsely branched or reduced to conidiogenous cells, up to 40 mm long, hyaline, and smooth. *P. macadamiae* conidia are fusiform to narrowly ellipsoidal, straight or curved, (18–) 18.5–22 (–25) × (5.5–) 6–6.5 (–7) mm, and four-septate. The conidial apical cells are conical, 2.5–5 mm long, hyaline, smooth, thin-walled, with 3 (rarely 2) apical tubular unbranched filiform flexuous appendages (12–) 14–21 (–24) mm. The basal cells are conic with a truncate

base, 3–5 mm, hyaline to subhyaline, smooth, thin-walled, with a simple appendage 3–7 mm long. The three median cells of the conidia are doliiform, 12–15 mm, concolored or the lower median cell is slightly paler than the other two cells, and olivaceous brown. The septa are darker than the rest of the cell, and smooth. The second cell from the base is 3–6 mm long, the third cell is 3.5–5 mm long, and the fourth cell is 4–6 mm long (Akinsanmi et al., 2017).

Movement and transmission:

The dried racemes of infected macadamia trees may persist in the tree canopy, where they may serve as a source of inoculum in the following growing season (Akinsanmi et al., 2017). No other information about the movement and transmission of *N. macadamiae* and *P. macadamiae* is available.

Pestalotiopsis species are commonly isolated as endophytes or plant pathogens, and many of these species persist as saprobes on dead leaves, bark, and twigs (Maharachchikumbura et al., 2014). Some other *Pestalotiopsis* species have been isolated from seeds (Douanla-Meli and Langer, 2009; Gure et al., 2005; Meon and Nik, 1988; Tagne and Mathur, 2001). *Neopestalotiopsis* species have been isolated from various plant hosts, soil, and as saprobes in leaf litter and other materials (Maharachchikumbura et al., 2014).

Damage potential of pest:

Dry flower of macadamia was first observed in an orchard in the Bundaberg production region of Queensland, Australia in 2009. Nutrient deficiencies were assumed to be the cause, but continued incidence of the disease over multiple seasons suggested a biotic origin. In the 2011–12 production season, dry flower resulted in complete crop failure in an orchard, and during the 2012–13 season, affected orchards suffered 10 to 30% yield loss (Akinsanmi and Drenth, 2013). A preliminary report associated the new disease with *Pestalotiopsis* spp. (Akinsanmi and Drenth, 2013), and ultimately, *N. macadamiae* and *P. macadamiae* were identified as responsible for the outbreaks (Akinsanmi et al., 2017).

In the United States, macadamia trees are grown in California, Florida, and Hawaii. The farm value for the 2017–18 cropping season was $53.9 million (net, wet-in-shell basis) in Hawaii alone (NASS, 2018). If *N. macadamiae* or *P. macadamiae* were to become established within the U.S., they could significantly damage the commercial tree nut industry. Further study is necessary to determine whether either of these pathogens has the potential to cause significant yield losses in other economically important crops.

Control:

No information about control of *N. macadamiae* or *P. macadamiae* is available.

Known host range:

Macadamia integrifolia (Akinsanmi et al., 2017).

Current Regulatory status of host:

***Macadamia* spp:** All propagules except seeds must enter Postentry Quarantine from all countries except Canada

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, that is a host of ***Neopestalotiopsis macadamiae***, is not authorized pending pest risk analysis (NAPPRA) **from all countries**:

Macadamia

References:

Akinsanmi, O. A., and A. Drenth. 2013. Emergence of *Pestalotiopsis* species as the causal agent of raceme blight and dieback of macadamia. Page 82 In 19th Australas. Plant Pathol. Conf., Auckland, New Zealand.

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Douanla-Meli, C., and E. Langer. 2009. *Pestalotiopsis theae* (*Ascomycota, Amphisphaeriaceae*) on seeds of *Diospyros crassiflora* (*Ebenaceae*). Mycotaxon 107:441-448.

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Gure, A., K. Wahlström, and J. Stenlid. 2005. Pathogenicity of seed-associated fungi to *Podocarpus falcatus in vitro*. Forest Pathol. 35(1):23-35.

Holtzmann, O. V. 1963. Raceme blight of macadamia in Hawaii. Plant Dis. Rep. 47:416-417.

Maharachchikumbura, S. S. N., K. D. Hyde, J. Z. Groenewald, J. Xu, and P. W. Crous. 2014. *Pestalotiopsis* revisited. Stud. Mycol. 79:121-186.

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capsici in naturally infeted chili seed. Pertanika 11(3):341-344.
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Plants for Planting Quarantine Pest Evaluation Data Sheet
February 27, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Peronophythora litchii***

Hosts: ***Dimocarpus*** **(synonym:** ***Euphoria), Litchi***

Taxonomy and description of the pest:

Peronophythora litchii (synonyms: *Phytophthora litchii* and *Peronospora litchii*) causes fruit rot, root rot or downy blossom blight in lychee (*Litchi chinensis*) and longan (*Euphoria longana*). *P. litchii* is considered a transitional species between the genera *Phytophthora* and *Peronospora* because it exhibits characteristics of both Pythiaceae and Peronosporaceae families (Ko et al., 1978). Recent sequencing of the *P. litchii* genome suggested that the organism is a *Phytophthora* pathogen that in the process of acquiring downy mildew–like (Peronosporaceae) genomic and morphological features (Ye et al., 2016).

Known distribution:

China (Chi et al., 1984), India (Butani, 1977), Papua New Guinea (Arentz, 1986), Taiwan (Ann et al., 2012), Thailand (Kraturisha et al., 1995), and Vietnam (Vien et al., 2001). In Japan, *P. litchii* was isolated from diseased fruit imported from Taiwan, but the pathogen has not been reported on crops in Japan (CABI, 2012; Kobayashi et al., 1986).

This pest is not known to occur in the United States.

Biology of the pest:

P. litchii causes a downy blight (synonym: brown blight) on lychee – a disease that occurs frequently in several subtropical regions of Asia and has been recognized for many years (Wang et al., 2010). Symptoms of *P. litchii* infection are often severe and may appear on the flowers, panicles, leaves, fruit or roots of infected plants. The pathogen was recently discovered on symptomatic longan seedlings that had emerged in a lychee orchard in Taiwan, implicating longan as a potential source of inoculum for downy blight of lychee (Ann et al., 2012). The pathogen causes significant losses both in the field and post-harvest (Wang et al., 2010).

Symptoms of *P. litchii* infection include blight, necrosis, lesions, flecking, and streaks on inflorescence (CABI, 2012). Diseased flowers often appear brown and covered with white masses of sporangia and sporangiophores. Fruits may have watery brown spots or black lesions. Panicles, leaves and new shoots may exhibit necrosis and withering (Wang et al., 2010). In periods of heavy rain, the infected tissues of young and ripe fruits, pedicels and leaves may turn brown and die (CABI, 2012).

P. litchii is a facultative necrotrophic plant pathogen that produces a cottony aerial mycelium composed of colorless, aseptate, irregularly branched hyphae (CMI, 1989). In the presence of water (flooding), asexual reproduction is initiatied and sporangia develop from the mycelial hyphae. *P. litchii* sporangiophores produce 5-30 lemon-shaped sporangia simultaneously. The sporangia have distinct, flattened apical papilla used to release bi-flagellate, kidney-shaped zoospores in water (CMI, 1989). The zoospores are highly motile, and their movement is directed in response to environmental signals (e.g., plant host exudate) (CABI, 2012). *P. litchii* cyst formation has not yet been reported. Upon arrival at surface-water films on aerial plant parts, zoospores infect host tissues directly. Mycelia then grow inside the host tissues, producing more sporangia and repeating the asexual cycle (the multiplication phase) (CABI, 2012). In the sexual phase, the mycelium produces gametes. Fertilization results in an oospore, which germinates to produce hyphae or a sporangium (Ann and Ko, 1980). Repeated cycles of sporangia and zoospores lead to build-up of inoculum. Laboratory studies indicate that the incubation period is brief and temperature dependent, varying from 1 day at 25°C to 3 days at 18°C (Chi et al., 1984).

Movement and transmission:

Transmission of *P. litchii* is not well documented. The *P. litchii* inouculum source has not been defined, but the pathogen probably persists as oospores or dormant mycelia in soil or plant debris (CABI, 2012). Once a primary infection has been established, secondary dispersal likely occurs when rain splashes zoospores or whole sporangia from infected flowers and fruits to uninfected ones (CABI, 2012). Water is required for *P. litchii* dispersal and pathogenesis, making disease worse in areas of high rainfall and high humidity.

Damage potential of pest:

World production of lychee is estimated to be around 6 to 6.5 million tons, with more than 95% of the world cultivation occurring in Asia (Evans and Degner, 2005; NAFED, 2012). The major lychee producing countries are India, China, Taiwan, Thailand, South Africa, Madagascar and Australia. In the United States (Florida, Hawaii and California), total annual production of lychee fruit is estimated at 433 tons (Evans and Degner, 2005). At an average seasonal price of $3 per pound, the crop would be worth an estimated $2.6 million (Crane and Mossler, 2008). Production of longan is estimated to be 1.4 million pounds in the United States. At an average seasonal price of $2.00 per pound, the crop would be worth an estimated $2.8 million (Crane and Mossler, 2008).

Introduction of *P. litchii* would likely have significant impact on United States lychee and longan production. The pathogen is a major problem for growers in Asia. Downy blight is considered one of the most serious diseases of fruit crops in China (Chi et al., 1984). In a 2000 outbreak of lychee downy blight in Vietnam, the disease significantly reduced the appearance of affected fruit, resulting in a 25-35% reduction in the price received by farmers (Vien et al., 2001).

Control:

Control measures for lychee downy blight rely on the integration of cultural methods with the use of fungicides (Wang et al., 2010). To reduce inoculum levels, growers are encouraged to remove dead branches and diseased leaves and fruit. The canopy may be sprayed with copper oxychloride in winter and copper sulfate in spring. Metalaxyl, fosetyl-Al and mancozeb are effective when applied during flower and fruit development (Menzel, 2002). Pretreatment with fungicides before pathogen infection is a key factor in controlling the disease (Huang et al., 2013). During the last decade, chemical control of lychee downy blight in Asia has been based mainly on the use of dimethomorph, a carboxylic acid amide fungicide (Wang et al., 2010).

A recent study established the efficacy of nested-PCR and LAMP (Loop-mediated isothermal amplification)assays for detection of *P. litchii* (Li et al., 2016).

Known host range:

Euphoria longana (Ann et al., 2012) and *Litchi chinensis* (Chi et al., 1984).

Hosts confirmed by artificial inoculation: *Carica papaya, Luffa cylindrica, Solanum lycopersicum* (Chi et al., 1984).

Current APHIS Regulatory Status of Hosts:

Dimocarpus: All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada.

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, that is a host of ***Peronophythora litchi***, is not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Dimocarpus (*syn*: Euphoria)

The importation of the following plants for planting genus that is a host of *Peronophythora litchi* is already regulated under NAPPRA and is therefore not listed here again:

Litchi (Lychee)

References:

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Ann, P.-J., J.-N. Tsai, and H.-R. Yang. 2012. First report of leaf and stem downy blight of longan seedlings caused by *Peronophythora litchii* in Taiwan. Plant Dis. 96(1224).

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Chi, P. K., S. P. Pang, and R. Liu. 1984. On downy blight of *Litchi chinensis* Sonn: The pathogen and its infection process (In Chinese). Acta Phytopathologica Sinica 14:113-119.

CMI. 1989. CMI descriptions of pathogenic fungi and bacteria No. 974: *Peronophythora litchii*. Mycopathologia 106:189-190.

Crane, J., and M. Mossler. 2008. Crop profile for lychee and longan in Florida. Florida IBM, 10 pp.

Evans, E. A., and R. L. Degner. 2005. Recent developments in world production and trade of lychee (*Litchi chinensis*): implications for Florida growers. Proc. Fla. State Hort. Soc. 118:247-249.

Huang, C. W., J. R. Tsai, P.-J. Ann, H. F. Ni, and H. R. Yang. 2013. Evaluation of recommended fungicides for the control of *Peronophythora* fruit downy blight of lychee. Plant Pathol. Bull. 22(4):339-352.

Ko, W. H., H. S. Chang, H. J. Su, C. C. Chen, and L. S. Leu. 1978. Peronophythoraceae, a new family of Peronosporales. Mycologia 70:380-384.

Kobayashi, Y., E. Kimishima, T. Nishio, and N. Nagao. 1986. *Peronophythora litchii* isolated from fruit imported from Taiwan. Res. Bull. Plant Protect. Serv. Japan 22:55-60.

Kraturisha, C., M. Tospol, V. Rukvidhyasatra, and K. Bhavakul. 1995. *Peronophythora litchii* associated with root rot of litchi. 2nd National Plant Protection Conference, Chiang Mai, Thailand.

Li, B.-J., P.-Q. Liu, X.-L. Liu, H.-Z. Huang, Q.-Y. Weng, and Q.-H. Chen. 2016. Establishment of nested-PCR and LAMP assays for detection of *Peronophythora litchii* (In Chinese). J. Agric. Biotech. 24(6):919-927.

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Wang, H., H. Sun, G. Stammler, J. Ma, and M. Zhou. 2010. Generation and characterization of isolates of *Peronophythora litchii* resistant to carboxylic acid amide fungicides. Phytopathology 100:522-527.

Ye, W., Y. Wang, D. Shen, D. Li, T. Pu, Z. Jiang, Z. Zhang, X. Zheng, B. M. Tyler, and Y. Wang. 2016. Sequencing of the litchi downy blight pathogen reveals it is a *Phytophthora* species with downy mildew-like characteristics. Mol. Plant Microbe Interact. 29(7):573-583.

Plants for Planting Quarantine Pest Evaluation Data Sheet
April 28, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Phakopsora phyllanthi*** Dietel

Hosts: ***Phyllanthus***

Taxonomy and description of the pest:

Phakopsora phyllanthi is a fungal plant pathogen in the Pucciniomycetes class and *Phakopsoraceae* family, and a causal agent of rust in Indian gooseberry (*Phyllanthus emblica*) Tahitian gooseberry (*Phyllanthus acidus*) (Dietrich and Ko, 2015; Hansen et al., 2016; Jarial et al., 2011).

Known distribution:

Brazil (Beenken, 2014; Berndt et al., 2007), China (Zhuang, 2001), Ecuador (Berndt et al., 2007), French Guyana (Berndt, 2013), India (Mundkur, 1943), Indonesia (Boedijn, 1959), Malaysia (Williams and Liu, 1976), Myanmar (Herbarium IMI, 1971), Philippines (Arthur and Cummins, 1936), Thailand (Lorsuwan et al., 1984), and Venezuela (Berndt et al., 2007).

In the United States, *Phakopsora phyllanthi* has been reported in Florida (Hansen et al., 2016) and Hawaii (Dietrich and Ko, 2015).

Biology of the pest:

On Indian gooseberry (*Phyllanthus emblica*) (local name, "aonla"), *P. phyllanthi* telia, which form in pustules, are sub-epidermal bearing teliospores that are unicellular, papillate, and sessile. The teliospores are borne singly. The uredial stage is not observable on the diseased Indian gooseberry plants (Jarial et al., 2011).

Tahitian gooseberry trees (*Phyllanthus acidus*) infected with *P. phyllanthi* appear unhealthy with thinning canopy and branches that appear barren due to leaf drop, which occurs during heavy infection (Dietrich and Ko, 2015). Leaves show necrotic yellow leaf spots on upper and lower surfaces. Leaves have uredinial pustules on the lower surfaces appearing as white-brownish raised spots with powdery urediniospores spreading from the center of the pustules. In addition, pustules and lesions form on infected fruit. (Dietrich and Ko, 2015).

Primary transmission of *P. phyllanthi* is by urediniospores, which are spread by wind or splashing rain to other plants. Dietrich and Ko (2015) observed that *P. phyllanthi* is a challenging disease to control, especially under cool conditions with long periods of wetness. This is partly because there are no specific fungicides effective against *P. phyllanthi* and because splashing rain promotes transmission. It is possible that *P. phyllanthi* is autoecious (i.e., completes its life cycle on one host) (Hansen et al., 2016).

Movement and transmission:

The primary mode of *P. phyllanthi* transmission is by urediniospores, which are spread by wind or splashing rain to other plants (Dietrich and Ko, 2015). No information about possible seed transmission of *P. phyllanthi* is available.

Damage potential of pest:

Few details about *P. phyllanthi* rust damage are available. In 2011, Jarial et al. reported a *P. phyllanthi* rust outbreak on Indian gooseberry (*Phyllanthus emblica*) in Himachal Pradesh, India. On mature plants, the severity of the disease was only 2–5%, but in nursery plants, disease severity ranged from 10–78%.

The leaves and pale yellow to white, sour fruits of Tahitian gooseberry (*Phyllanthus acidus*) are used in Asian cultures to make candies, pickles, chutneys, relish and preserves (Hansen et al., 2016). In the United States, *P. acidus* is found in Hawaii and, occasionally, in southern parts of Texas and Florida. The number of Tahitian gooseberry plants currently grown in Florida is small, but future increase in dooryard plantings is anticipated, as well as a growth of the Tahitian gooseberry industry (Hansen et al., 2016). In Hawaii, *P. emblica* and *P. acidus* are grown in backyards, especially those of families from Asia or Pacific Regions. Seedlings and fruit are available for purchase at nurseries

and farmers markets around Hawaii (Dietrich and Ko, 2015).

Interest in the commercial cultivation of the ethno-*Phyllanthus* species (Indian and Tahitian gooseberries) is increasing. It is, therefore, important that the distribution of *P. phyllanthi* and its associated damage to host plants, including the endemic Hawaiian species *Phyllanthus distichus*, be determined (Dietrich and Ko, 2015).

Control:

Although there are no specific fungicides to control *P. phyllanthi*, broad-spectrum fungicides can be used cautiously to control this fungus in Tahitian gooseberry farming in Hawaii (Dietrich and Ko, 2015). It is recommended that growers observe good sanitation practices, such as removing and destroying infected plant parts including leaves and fruits as soon as symptoms appear. It is also recommended to sanitize tools before and after use and keep the foliage dry when irrigating, to lower disease incidence and severity (Dietrich and Ko, 2015).

Known host range:

Phyllanthus acidus (syn. *Cicca acida*)(Berndt et al., 2007; Dietrich and Ko, 2015), *Phyllanthus benguetensis* (Arthur and Cummins, 1936), *Phyllanthus distichus* (Mundkur, 1943), *Phyllanthus emblica* (Boedijn, 1959; Jarial et al., 2011), *Phyllanthus nanus* (Herbarium IMI, 1971), *Phyllanthus niruri* (Arthur and Cummins, 1936; Teodoro, 1937), and *Phyllanthus phyllanthi* (Patel et al., 1985).

Current APHIS Regulatory Status of Hosts:

***Phyllanthus* spp.** All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada

***Phyllanthus maderaspatensis*:** All propagules are NAPPRA from all countries

***Phyllanthus saffordii*:** All propagules are protected under the Endangered Species Act (ESA-E)

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, which is a host of ***Phakopsora phyllanthi,*** is not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Phyllanthus

References:

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
January 21, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Phomopsis durionis***

Hosts: ***Durio, Pachira***

Taxonomy and description of the pest:

Phomopsis durionis is a fungal plant pathogen in the phylum Ascomycota, class Sordariomycetes, order Diaporthales, and family Diaporthaceae (Webster and Weber, 2007). The teleomorph of *Phomopsis* is *Diaporthe,* although "*Phomopsis*" is most often applied to disease causing organisms (Udayanga et al., 2011). *P. durionis* is the causal pathogen of durian leaf spot disease (syn: Phomopsis leaf spot) (Tongsri et al., 2016).

Along with the pathogens *Colletotrichum gloeosporioides*, *Lasiodiplodia theobromae*, and *Phytophthora palmivora*, *P. durionis* was found to be a causal agent of durian fruit rot (syn: Phomopsis fruit rot), a post-harvest fruit rot. *P. durionis* is the most prevalent among the fungal agents causing durian fruit rot (Tongsri et al., 2016).

Phomopsis fruit rot is one of the most important post-harvest fruit rots of durian, alongside Phytophthora fruit rot, caused by *Phytophthora palmivora*, Diplodia fruit rot, caused by *Diplodia theobromae*, and Fusarium fruit rot, caused by *Fusarium solani* (Lim and Sangchote, 2003).

P. durionis is also a pathogen of *Pachira macrocarpa* (syn: *Pachira aquatica*) (Xi et al., 2000).

Species limits in the genus *Phomopsis* were previously defined by morphology, culture

characteristics, host association, host pathogenicity and virulence (Uecker, 1988). However, morphology is no longer sufficient to delineate species in the genus *Phomopsis*, and further species revision is needed (Farr et al., 1999). The use of chemotypes in species classification and identification up to this point has been limited and has not been taxonomically conclusive (Rehner and Uecker, 1994).

Molecular techniques are now used to describe species in *Phomopsis.* The internal transcribed spacer (ITS) region in the *Phomopsis* genome has been used to describe taxonomic species limits. ITS, elongation factor 1α (EF1α) partial sequence data, and mating-type phylogenies of *Phomopsis* have been compared without combining the genes in phylogeny to understand correlation relationships between biological and phylogenetic species concepts (Santos et al., 2010). ITS sequence data was shown to be highly variable within a biological species of *Phomopsis*, while partial sequences from the translation EF1α were more reliable indicators of species limits. However, ITS sequence data can be used for identification of phylogenetic relationships if interpreted according to a biological species concept and the morphology of the isolates (Udayanga et al., 2011).

EF1α has been used to identify other species in the genus *Phomopsis* and is informative in many ascomycete fungi for identifying species (Shirahatti et al., 2014). Therefore, sequence data from EF1α would be a reasonable candidate for PCR-based identification of *P. durionis.*

There are no reports of *P. durionis* in the United States.

Known distribution:

China (Xi et al., 2000) and Thailand (Tongsri et al., 2016).

P. durionis is widespread in areas growing *Pachira macrocarpa* (Xi et al., 2000) and *Durio zibethinus* (Lim and Sangchote, 2003).

This pathogen is not known to occur in the United States.

Biology of the pest:

Phomopsis leaf spot affects seedlings and stressed durian trees, especially under warm, humid conditions. Symptoms include necrotic circular leaf spots about one mm in diameter with dark margins and yellow halos. In durian seedlings, affected leaves are aborted, resulting in overall defoliation of the stem. Signs of the *P. durionis* are pycnidia, which occur as black, pin-head sized dots in necrotic leaf spots (Tongsri et al., 2016).

Visually, the causes of post-harvest fruit rots in durian are difficult to distinguish without observation or isolation of the pathogen. Phomopsis fruit rots cause small dark brown to black round to oblong lesions on ripening fruits. As the fruits ripen, these lesions become black, and

grey mycelium of the pathogen can be observed in the lesions. The tips of the fruit spines also become necrotic (Lim and Sangchote, 2003).

The asexual stage of *P. durionis* is most commonly observed. The pathogen produces black, ostiolate pycnidia that contain long, filiform and bent stylospores. *P. durionis* produces alpha-conidia, which are hyaline, fusiform and ellipsoid to oval in shape, aseptate, and typically biguttulate. Conidiophores are hyaline, branched, and usually multiseptate and filiform. Conidia are spread by rain splash and wind (Lim and Sangchote, 2003; Udayanga et al., 2011). Asci are unitunicate and clavate. Ascospres are biseriate to uniseriate, fusioid, ellipsoid to cylindrical, septate, and hyaline (Udayanga et al., 2011).

Phomopsis spp. are hemibiotrophic pathogens. The genus consists of common endophytes in the sapwood of angiosperm plants in both tropical and temperate regions. Members of the genus are also common as saprophytes in decaying material that may have been endophytes in the living plant host (Promputtha et al., 2010; Udayanga et al., 2011). Latent infections of *P. durionis* have also been reported in the flowers, leaves, and stems of affected durian trees (Tongsri et al., 2016).

Movement and transmission:

P. durionis produces conidia in the pycnidia present in infected leaf lesions. Conidia are spread by wind and rain splash. Infected propagative plant material, plant debris, and fruits are therefore also sources of inoculum (Lim and Sangchote, 2003).

Seed transmission has been reported of other species of the genus *Phomopsis*. For example, seed transmission of *P. sojae*, pathogenic to soybeans, has been extensively reported (Hepperly and Sinclair, 1978), as has that of pathogenic *P. azadirachtae* in neem (Girish et al., 2010). As a non-pathogenic endophyte, *P. castanea* has been reported to be transmitted by chestnut tree seeds (Washington et al., 1999).

Durians are propagated clonally for commercial production; therefore, mother plants should be disease free to avoid spreading the pathogen (Brown, 1997).

Damage potential of pest:

Durian is a tropical tree cultivated mostly in Asia. Producing countries include Borneo, southern Burma, Cambodia, southern India, Indonesia, Malaysia, New Guinea, Philippines, Sri Lanka, Thailand, and Vietnam. There is now limited production in Latin American and the Caribbean as well (Paull and Ketsa, 2014). Thailand is known as the world's top producer of durian in both number of tons produced and value of the crop (Brown, 1997), but exact data on the production, import and export of durian has not been assembled by the Food and Agriculture Organization of the United Nations. Thus, available data is somewhat contradictory. Durian is also produced commercially in Malaysia, Indonesia, the Philippines, and Vietnam (Siddiq and Nasir, 2012).

Durian is a popular fruit in Southeast Asia. It is typically eaten with sticky rice or processed in a wide variety of methods, including bakery goods, drinks, and fermentation products. Although international consumers are demanding increasing quantity and diversity of tropical fruits, durian's short shelf life—two to five days—has limited significant expansion into international markets (Ho and Bhat, 2015). In Thailand alone, 137,649 hectares of durian were planted and produced 927,194 tons of fruit in 1999. Ninety-eight percent of this production was consumed domestically; exports were primarily to Hong Kong, Singapore, Taiwan, and China. From 1997-2001, Thai production of durian increased steadily to meet export demand (Krasachat, 2012). In Indonesia, agricultural credit lending collateral has been based on durian production (Dury et al., 1996).

Post-harvest losses from Phomopsis fruit rot are found to be of greater yield concern than Phomopsis leaf spot (Tongsri et al., 2016). *P. durionis* is not listed as a quarantine pest in Thailand, Malaysia, Vietnam, or Indonesia (IPPC, 2016), but is listed as a quarantine pest in the US.

Control:

The fungicide Mancozeb (Dithane M-45) can control *Phomopsis*-related premature defoliation of nursery trees (Lim and Sangchote, 2003). However, in the orchard, management of Phomopsis leaf spot is mostly cultural. When possible, infected plants and infested plant debris should be removed from the nursery or orchard to reduce inoculum for the next growing season. Particularly susceptible cultivars, such as 'Mon Thong', are found among the top commercial cultivars in Thailand (Tongsri et al., 2016), and could be avoided to control problems in nurseries and orchards.

To control Phomopsis fruit rot post-harvest, fruits should not come in contact with soil or plant debris. To aid in this process, pruning out diseased plant material before harvest, followed by spraying fruits with carbendazim is recommended. Within six hours of harvest, fruits are typically treated with 500 µg of carbendazim or thiabendazole for two to three minutes (Sangchote et al., 1996). The fungicide Aliette is also used to combat a variety of post-harvest fungi, including *Phomopsis* spp. (Nanthachai, 2000).

Quarantine decisions on *Phomopsis* spp. are challenging due to unclear species boundaries within the genus. With molecular data, species boundaries and host ranges are currently under revision (Rehner and Uecker, 1994). Complicating matters further, many *Phomopsis* spp. have been observed as endophytes in asymptomatic plants. The differences between pathogenic and non-pathogenic isolates are currently unknown, making decisions on quarantine more complicated (Palm, 2001).

Known host range:

Durio zibethinus (Lim and Sangchote, 2003) and *Pachira macrocarpa* (Xi et al., 2000).

Although there have been no reports to date of *P. durionis* on other hosts, the presence of this pathogen on other hosts should not be ruled out. Members of the genus are common endophytes in asymptomatic angiosperms, and the differences between non-pathogenic and pathogenic isolates in the genus are not well understood. Fledgling understanding of species boundaries within *Phomopsis* complicates determination of host range (Promputtha et al., 2010; Rehner and Uecker, 1994; Udayanga et al., 2011).

Current APHIS Regulatory Status of Hosts:

The importation of the following plants for planting genus that is a host of *Phomopsis durionis* is currently regulated under the following quarantines:

Durio: All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada.

Proposed Action under NAPPRA:

The importation of the following plants for planting genera, excluding seeds and excluding cut flowers and greenery, that are hosts of ***Phomopsis durionis***, are not authorized pending pest risk analysis (NAPPRA) from**:**

Durio	All countries
Pachira	All countries except Canada, China, Costa Rica, Indonesia, Taiwan, Vietnam

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
May 06, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Pseudocercospora ceratoniae*** (Pat. & Trab.)

Hosts: ***Ceratonia***

Taxonomy and description of the pest:

Pseudocercospora ceratoniae is a fungal plant pathogen in the Dothideomycetes class, Canodiales order, and *Mycosphaerellaceae* family and the causal agent of Cercospora leaf spot of carob.

The pathogen was previously known as *Cercospora ceratoniae* (Deighton, 1976). The *P. ceratoniae* teleomorph is thought to be *Mycosphaerella cuprea* (Varo et al., 2010).

Known distribution:

Algeria (Killian, 1925; Patouillard, 1903), China (Hsieh, n.d.; Varo et al., 2010), Croatia (Miličević et al., 2014), Cyprus (Morton, 1987; Varo et al., 2010), Italy (Longo and Tirrò, 2005; Perrotta et al., 1998), Malta (Porta-Puglia and Mifsud, 2006), Portugal (Braun et al., 2013), Spain (Varo et al., 2010), South Africa (Varo et al., 2010), and Taiwan (Hsieh, n.d.; Varo et al., 2010).

In the United States, *P. ceratoniae* is present in Florida (Varo et al., 2010).

Biology of the pest:

Fungal morphology and infection. *P. ceratoniae* is a hyphomycetous fungus (Perrotta et al., 1998) that invades and ramifies densely within the host leaf palisade parenchyma and epidermis (Killian, 1925). Dark brown stroma—termed 'caespitula' by Perrotta et al. (1998)—form on the abaxial leaf surface (Hsieh, n.d.) and bear clusters of light brown, unbranched conidiophores, formed within the leaf, that protrude from the stomata. Light olive-yellow, septate conidia (Varo et al., 2010) are borne singly on the conidiophores as terminal blastospores (Perrotta et al., 1998). Furthermore, pycnidia (surrounded by a shell that is initially thin but later thickens), containing pycniospores, may also form. Rupture of the pycnidial wall releases the spores, which form a slimy pink mass (Killian, 1925).

Mycosphaerella cuprea, a fungus associated with both living and fallen leaves of the carob plant, was suggested to be the sexual (telomorph) stage of the *P. ceratoniae,* but its role in the disease epidemiology is unclear (Varo et al., 2010).

Hot, humid conditions favor spore germination and infection, leading to high disease incidence and severity and extensive defoliation. Overseasoning through dryer times may be facilitated by the formation of dark-colored estrogenica (asexual) or pseudothecia (sexual) (Varo et al., 2010).

Disease symptoms and signs. *P. ceartoniae* causes Cercospora spot, leaf spot of carob. Early spring symptoms include small (1-3 mm) circular to irregular, dark-red, vein-limited necrotic lesions surrounded by a chlorotic halo on leaves, especially along the midribs and on petioles (Hsieh, n.d.; Perrotta et al., 1998; Varo et al., 2010). The lesions subsequently enlarge (10-15 mm), coalesce, and turn dark brown, often with thin gray centers that break away (Perrotta et al., 1998; Varo et al., 2010). Severe defoliation of both, mature field plants or nursery seedlings can result when disease is severe, especially when petioles are invaded. Such trees may not produce fruit, and there may be consequent weakening of the tree that increases susceptibility to other more serious diseases (Perrotta et al., 1998; Varo et al., 2010).

Pathogenicity of *P. ceratoniae* is influenced by its production of the host non-specific perylenequinone toxin, cercosporin, which acts as a photosensitizer after the absorption of light energy triggers its conversion from a non-toxic form to an activated state that reacts with oxygen to generate toxic singlet oxygen and superoxide (Daub and Chung, 2007; Varo et al., 2010; You et al., 2008). These toxins lead to peroxidation of host cell membrane lipids, causing membrane disruption and cell death, presumably facilitating leakage of nutrients into the apoplast where fungal hyphae can utilize them.

Movement and Transmission:

P. ceratonia conidia, produced on the leaf surfaces, are easily dislodged and transported

long distances by wind currents (Varo et al., 2010). Because members of the genus *Pseudocercospora* can persist in plant debris for up to two years (Anonymous, 2019b), defoliated carob leaves likely serve as reservoirs for re-infection via rainsplash, as is the case with *Cercospora* leaf spot of beets (Pethybridge et al., 2017). No information is available on transmission through seed, or by budding or grafting—alternative means of carob propagation (Morton, 1987).

Damage potential of pest:

Carob was brought to the United States and Mexico in the mid-1800s by Spanish missionaries, who introduced seedlings; additional seeds from Israel were received a few years later (Morton, 1987). The trees were planted in Arizona, Texas and Florida. Cercospora spot is among the most common foliar carob diseases (Varo et al., 2010).

Value of crops affected (by plant part):

Pods. Carob (*Ceratonia siliqua* L), a dioecious, warm-climate evergreen tree common to low altitudes of the Mediterranean region, has been cultivated for centuries for its pods, which are valued as a sugar-rich fodder for livestock (cattle, horses, pigs, goats, and rabbits) and is even used for flavoring dog biscuits and uncured tobacco (Morton, 1987). Humans discovered the use of carob as a "healthy" chocolate substitute (Tous et al., 2013) and the pods are also used for commercial production of alcohol (Perrotta et al., 1998; Tous et al., 2013). A targeted effort to identify superior carob cultivars for human consumption began in 1949 (Morton, 1987). Carob is gaining attention as a desirable alternative crop for dryland Mediterranean areas for diversification and revitalization of coastal agriculture (Tous et al., 2013).

Seeds. There is increasing interest in a tragacanth-like gum that can be extracted from the endosperm of carob seeds and is useful as a stabilizer in drugs, cosmetics, detergents, paint, ink, shoe polish, adhesives, insecticides and match heads (Morton, 1987; Tous et al., 2013).

Wood. The hard, densely-grained heartwood of the carob tree is valued for furniture-making and lathe-based woodworking (Morton, 1987).

Control:

No information is available on the specific management of *P. ceratonia* on carob, but recommendations for control of diseases caused by other species of *Pseudocercospora* and *Cercospora* in other plant hosts center on the bi-weekly use of fungicides starting as leaves emerge in the spring (Anonymous, 2019a, 2019b; Ganesha and Jayalakshmi, 2017; Pethybridge et al., 2017). Some fungicides effective against *Cercospora* diseases include myclobutanil, azoxystrobin, propiconazole, thiophanate-methyl, mancozeb and

chlorothalanil, or combinations of these chemicals (Anonymous, 2019a). The emergence of strobilurin-resistant strains of *Cercospora beticola*, causing leaf spot in beets, led to the identification of other effective fungicides and fungicide-bacteria combinations, including benzovindiflupyr + difenoconazole, boscalid, fluxapyroxad + pyraclostrobin, penthiopyrad, and copper octanoate + *Bacillus amyloliquefaciens* strain D747 (Pethybridge et al., 2017).

Cultural control measures include avoidance of overhead irrigation or watering in the early morning; removal and burning of defoliated leaves is also recommended to reduce inoculum (Anonymous, 2019a; Varo et al., 2010).

Recent research on the production, by several *Cercospora* species, of the light-triggered toxin cercosporin has suggested possible new avenues for disease management (Daub and Chung, 2007). For example, fungal penetration of coffee leaves by *C. coffeicola* was reduced in crops planted in shade, and disease symptoms caused by *C. beticola* in sugar beets grown in low light conditions were delayed and less severe.

Known host range:

Ceratonia siliqua L. (carob, St. John's Bread) (Varo et al., 2010).

Current APHIS regulatory status of host:

***Ceratonia* spp.** All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada.

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, that is a host of ***Pseudocercospora ceratoniae***, is not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Ceratonia

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
January 09, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Pseudocercospora pistacina*** (syn. ***Septoria pistacina***)

Hosts: ***Pistacia***

Taxonomy and description of the pest:

Pseudocercospora pistacina is a fungal pathogen in the Ascomycota phylum, Dothideomycetes class, Capnodiales order, and Mycosphaerellaceae family. It is the causal agent of fruit spot in pistachio (Mycobank, 2017). Synonyms for *P. pistacina* include *Septoria pistacina* (the basionym), *Dothidea pistaciae*, and *Mycosphaerella pistacina* (the sexual morph) (Crous et al., 2013).

The first description of *Septoria* spp. causing leaf spot on pistachio (*Pistacia vera*, in France) was published in 1842, and the causal agent was given the name *S. pistaciae* (Desmaziéres, 1842). The same year, a fungus causing leaf spot of *Pistacia* spp. in Crimea was described as *Dothidea pistaciae* (Léveillé, 1842). In 1884, *D. pistaciae* was transferred to *Septoria*—receiving the name *S. pistaciae*, which was already in use (Cooke, 1884). Allescher (1901) proposed the binominal *S. pistacina* to replace *S. pistaciae* (Lév.) Cooke 1884 and to differentiate it from *S. pistaciae* Desm. 1842 (Crous et al., 2013). A third species was discovered on pistachio in Sicily and given the name *S. pistaciarum* (Caracciolo, 1934). The sexual morphs for two of the three species—*Mycosphaerella pistacina* (for *Septoria pistacina*) and *Mycosphaerella pistaciarum* (for *Septoria pistaciarum*) were reported in 1956 (Chitzanidis, 1956; Teviotdale et al., 2001). The naming of these species caused confusion, leading Crous et al. (2013) to elucidate the taxonomy of the species. Their assessment placed *S. pistacina* in the *Pseudocercospora* genus.

Known distribution:

Greece (Chitzanidis, 1956), Iran (Aghajani et al., 2009; Banihashemi, 2015), Syria (Spaulding, 1961), and Turkey (Aghajani et al., 2009; Videira et al., 2016).

P. pistacina is not known to occur in the United States. However both *S. pistaciarum* and *S. pistaciae* have been found in the United States—in Arizona and California, respectively (Michailides, 2005).

Biology of the pest:

On leaves, *P. pistacina* causes numerous brown, amphigenous, angular spots that are confined by leaf veins to 30 mm in length and 3-6 mm in diameter (Crous et al., 2013). The leaf spots appear on both sides of the leaf and contain numerous small, aggregated, immersed pycnidia. On fruits, spots are grey to pale brown, 1–4 mm diameter, coalescing to form larger spots, surrounded by a distinct, reddish margin (Crous et al., 2013). *P. pistacina* pycnidia are subepidermal, globose to depressed, to 300 µm in diameter with a wide central ostiole. Conidiophores are 10-30 × 3-5 µm, subcylindrical, pale brown, and smooth. They are 0–3-septate and may be branched or not. Conidia are pale brown, smooth, guttulate, subcylindrical, curved, medianly septate, constricted at the septum and 31.8-47.0 × 3.6-4.8 µm in size (Crous et al., 2013; Michailides, 2005). *M. pistacina* produces black pseudothecia that are 90-100 × 80-110 µm (Chitzanidis, 1956; Michailides, 2005). Asci are 44.5-54.5 × 13-14.5 µm, and each has eight ascospores that are 26-40 × 3–5 µm (Chitzanidis, 1956; Michailides, 2005).

P. pistacina overwinters in fallen leaves infected while on the tree in previous seasons (Michailides, 2005). Pseudothecial primordia appear on fallen leaves early, and young asci develop through early March. Most ascospores are mature and ready for discharge from late April through May, which happens during or after rain (Michailides, 2005). Secondary infections are caused by *P. pistacina* conidia and may continue until late fall. In mid-September, production of spermogonia—with an unknown role in the *P. pistacina* life cycle—begins and continues on fallen leaves until December (Michailides, 2005).

In early summer, dark pycnidia appear on both sides of *P. pistacina*-infected leaves. The infected area is circular and about 0.5 cm in diameter, expanding to 1.0 cm as the disease progresses. Maturing pycnidia display cirrhi of pycnidiospores extruding from the ostioles. When this happens, the symptoms are quite pronounced. Eventually, infected areas coalesce causing the leaf to become chlorotic and necrotic late in the growing season (Aghajani et al., 2009).

Movement and transmission:

P. pistacina conidia spread through rain or sprinkler water (Michailides, 2005). The disease is found on fallen leaves well into December and can remain viable through the winter. The fungus is apparently not seedborne.

Damage potential of pest:
P. pistacina has been observed to lower plant germination rates and cause leaves to become chlorotic and sometimes necrotic, eventually killing the plant (Michailides, 2005). Severe epidemics of *Septoria* spp. can cause widespread premature defoliation and reduced tree vigor.

In 2016, pistachio production in the United States was valued at $1.5 billion (USDA, 2017).

Control:
Preventative fungicide sprays offer control of *P. pistacina*. Dithiocarbamates (zineb, macozeb) are recommended (Michailides, 2005). After the fruit has matured to 1 cm, chlorothalonil and copper fungicides can be applied, but these fungicides can cause phytotoxic damage to young fruit (Michailides, 2005). Benzimidazole fungicides are also effective. Applications should begin when the first leaves unfold and repeated monthly, if necessary, until early June (Michailides, 2005). None of these fungicides are registered for California pistachios.

Known host range:

Pistacia mutica (Banihashemi, 2015) and *P. vera* (Chitzanidis, 1956).

Current APHIS Regulatory Status of Host:

Pistacia: All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada.

Proposed Action under NAPPRA:

The importation of plants for planting of the following genus, excluding seeds and excluding cut flowers and greenery, that is a host of ***Pseudocercospora pistacina*** *(syn:* ***Septoria pistacina)***, is not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Pistacia

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
May 06, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Sirosporium carissae***

Hosts: ***Carissa, Ziziphyus***

Taxonomy and description of the pest:

Sirosporium carissae is a fungal ascomycete plant pathogen of the Dothidiomycetes class, Mycosphaerellales order and Mycosphaerellaceae family and a causal agent of leaf spot in *Carissa* spp. (Kapoor, 1968) and *Ziziphus jujuba* (Pandey et al., 1986).

According to (Kamal and Rai, 1982), *Pseudocercospora carissae* is a synonym of *S. carissae*, but the *P. carissae* name is not used elsewhere in the literature.

Known distribution:

India (Kamal, 2010; Kapoor, 1968).

Biology of the pest:

Little information is available about the biology of *S. carissae*. The pathogen is known only to occur in India, and most publications referencing *S. carissae* (or *P. carissae*) are simply lists of fungal species present in the country (Ellis, 1976; Kamal, 2010; Mall, 2012).

Kapoor (1968) provided a detailed description of *S. carissae* fungal structures. Colonies are hypophyllous, dark olivaceous to black, effuse, velvety, and cause chlorosis in surrounding tissue. The *S. carissae* mycelium is partly superficial and partly immersed in the substratum and linked by hyphae passing through the stomata. The immersed hyphae are branched, septate, often constricted at the septa, hyaline to sub-hyaline, smooth-walled, and 2–4 µm thick. They form 1-cell thick, more or less spherical, dark brown pseudostromata. The superficial hyphae are branched, pale brown to brown, slightly rough, and 2–4 µm thick. Conidiophores arise from the individual cells of the stromata and are erect, fasciculate, simple, cylindrical to clavate, brown to dark brown, smooth-walled, spetate, 12–16 × 4–6 µm, and each bears1–3 conidial scars. Conidia are formed singly at the apex of the conidiophores and at the tips of the successive growing points, which develop below and to one side of the previous terminal conidium, very variable in shape and size, are cylindrical to narrowly obclavate, flexuous, pale brown, striate, often deeply constricted at the septa, with 1–30 transverse septa. Rarely oblique longitudinal septa are present in the basal cells, 30–200 µm wide near the apex, provided with exserted scar at the base.

Symptoms of most *Sirosporium* diseases manifest on leaf surfaces as reddish brown spots that often lead to premature defoliation (Berbegal et al., 2012; Cacciola, 2007; Dar et al., 2015; Poletto et al., 2016).

Movement and transmission:

No information about movement or transmission of *S. carissae* is available.

Damage potential of pest:

No information is available about damage caused by *S. carissae*.

Carissa L. is a genus with about 36 species of evergreen shrubs or small trees that are native to tropical and subtropical regions of Africa, Asia, and Oceania. Most *Carissa* plants have been utilized in traditional medicine for various ailments, and several have been phytochemically studied (Kaunda and Zhang, 2017). The phytochemical and pharmalogical studies of *Carissa* spp. have led to the identification of 123 compounds including terpenes, flavonoids, lignans, sterols, simple phenolic compounds, fatty acids, and esters and have indicated various bioactive potentials (Kaunda and Zhang, 2017).

Ziziphus jujuba (“jujube”) is distributed widely in the United States, from Pennsylvania and Washington D.C. to Florida, and from Florida and Georgia, westward through Arkansas, Texas, New Mexico, and California (Zhao and Yao, 2016). Commercial production of jujube is limited, but interest is growing, and it is predicted to become an industry in the U.S. by the mid-2030s (Zhao and Yao, 2016).

In the U.S., *C. carandas* ("karanda") has been cultivated in a limited way in Florida and California and in some experimental gardens in Puerto Rico (Morton, 1987).

Other *Carissa* spp. are somewhat popular in parts of the U.S. *C. grandiflora* ("natal plum") is considered one of Florida's and California's best seaside shrubs, where the plant is prized for its fragrant blooms and delicious fruit (Gilman, 2014a; Gragg, 2011). *C. macrocarpa* is planted as a hedge or foundation plant in the coastal landscapes of Florida (Gilman, 2014b). The susceptibility of *C. grandilora* or *C. macrocarpa* to *S. carissae* is unknown.

Control:

No information is available about the control of *S. carissae*.

Known host range:

Carissa sp. (Ellis, 1976), *C. carandas* (Kamal, 2010), *C. spinarum* (Kamal, 2010; Kapoor, 1968; Sarbhoy et al., 1971), and *Ziziphus jujuba* (Pandey et al., 1986).

Current APHIS Regulatory sttaus of hosts:

Carissa: All propagules except seeds must enter Postentry Quarantine from all countries except Canada.

***Ziziphus*:** All propagules except seeds are NAPPRA from all countries except Canada.

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, excluding seeds, and excluding cut flowers and greenery, that is a host of ***Sirosporium carissae***, is not authorized pending pest risk analysis (NAPPRA) **from all countries:**

Carissa

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
April 22, 2018

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: **Tomato Leaf Curl New Delhi Virus (ToLCNDV)**

Hosts: ***Benincasa, Capsicum, Carica, Cucumis, Cucurbita, Datura, Daucus, Eclipta, Hibiscus, Lagenaria, Luffa, Momordica, Solanum*** **(including** ***Lycopersicum)***

Taxonomy and description of the pest:

Tomato leaf curl New Delhi virus (ToLCNDV) is a bipartite species (DNA-A + DNA-B) in the genus *Begomovirus* in the family *Geminiviridae* (Brown et al., 2015). The Begomovirus genus of plant viruses has the largest number of virus species. Particles of this genus and family are twinned (geminate), 18-30 nm, and encapsidate a circular, single-stranded DNA of ~2.7 kb that is easily cloned and sequenced (Brown et al., 2015). Taxonomic identity among begomoviruses is based on pairwise sequence comparisons of DNA-A, regardless of whether viruses are monopartite or bipartitite, using 89% (Fauquet et al., 2008) or the proposed 91% (Brown et al., 2015) identity to separate species, and 94% identity to distinguish isolates.

The type species ToLCNDV [Bangladesh-Jessore-Severe-2005] is formally abbreviated as ToLCNDV-IN [BG-Jes-Svr -05] DNA-A:AJ875157 DNA-B:AJ875158 (Brown et al., 2015). Formal begomovirus names include descriptors in square brackets ("[ ]").

Tomato leaf curl disease is a devastating disease in Asia and Australia and a serious constraint to tomato production throughout the Indian subcontinent. The disease has been known for years, but characterization of a geminivirus as the causal agent did not occur until the early 1990s as

molecular technologies became available. Tomato (*Solanum lycopersicum*) in Australia was the source of the first geminivirus to be sequenced from leaf curl diseased tomato, which was a monopartite virus whose cloned DNA-A, introduced by agroinoculation, reproduced disease symptoms on several hosts (Dry et al., 1993). This virus became known as *Tomato leaf curl virus* (ToLCV), which is now an accepted begomovirus species having 36 isolates from the same geographic region (Brown et al., 2015).

Tomato leaf curl-associated viruses, ITmLCV in India, were known to be whitefly transmitted and have a wide host range (Muniyappa et al., 1991), and referred to also as ITLCV (Srivastava et al., 1995) and ToLCV-India (Padidam et al., 1995b). The first whitefly-transmitted geminiviruses (WTGs) to be sequenced from tomato in India, ToLCV-(In1) and ToLCV-(In2), were collected in bulk from tomato fields near New Delhi, in Northern India (Padidam et al., 1995b). Two DNA-A molecules were recovered that shared 94% sequence identity but only 45-47% identity with begomoviruses for which sequences were known, including those associated with tomato leaf curl disease in Australia (Dry et al., 1993) and Southern India (Hong and Harrison, 1995). DNA-B molecules typical of New World viruses were also detected, but were not required for systemic infection and symptom development. Sequences of DNA-A were sufficiently different from those of other viruses (44-66%) to consider it a distinct virus, provisionally named ToLCV-India, and to suggest it evolved more recently (Padidam et al., 1995a). In all, ToLCV-India more closely resembled *African cassava mosaic virus* than it did ToLCV or the *Tomato yellow leaf curl virus*.

ToLCV-India was renamed ToLCV-ND to distinguish the WTGs in Northern India from those common in Southern India and from ToLCV, having a phylogenetically distinct monopartite genome. The species name accepted was *Tomato leaf curl New Delhi virus*, and the first two isolates became ToLCNDV-[India:New Delhi:Mild:1992] U15016 (DNA-A) and ToLCNDV-[India:New Delhi:Severe:1992] U15015 (DNA-A) and U15017(DNA-B) (Fauquet et al., 2003). The third isolate from Lucknow in India (ITLCV) also had a bipartite genome (Srivastava et al., 1995), and was renamed ToLCNDV-[IN:Luc] Y16421.

The International Committee on Taxonomy of Viruses (ICTV) recognized *Tomato leaf curl virus* as a species along with 28 other species beginning with the name “Tomato leaf curl” and followed by a modifier referring to the geographic location from which isolates of the species have been described (Fauquet et al., 2008). Of these 28 species, ToLCNDV is the largest, having 11 approved isolates from India, eight from Pakistan, one from Bangladesh, and one from Thailand. The number of ToLCNDV isolates compiled by the ICTV study group (Brown et al., 2015) has increased to 87 isolates, not including recent reports of ToLCNDVfrom Spain (Juárez et al., 2014; Ruiz et al., 2015).

Thus ToLCNDV is not a single virus, but a species of begomovirus with nearly 90 recognized isolates, variants, or strains, some of which may be recombinants with other begomoviruses or be associated with DNA-B or β satellites known to be associated with other viruses (Jyothsna et al., 2013; Shafiq et al., 2010). The identity of the strain used in many publications is not always

clear, making it a challenge to assess distribution and host range data and to generalize on biological properties and ecological niches of ToLCNDV.

Known distribution:

Bangladesh (Maruthi et al., 2005b; Singh-Pant et al., 2012), India (Reddy et al., 2005; Srivastava et al., 2015), Indonesia (Mizutani et al., 2011), Pakistan (Tahir and Haider, 2005), Spain (Juárez et al., 2014; Ruiz et al., 2015), Taiwan (Chang et al., 2010), Thailand (Ito et al., 2008), and Tunisia (Mnari-Hattab et al., 2015).

ToLCNDV is not known to occur in the United States.

Biology of the pest:

Members of the ToLCNDV species of the Begomovirus genus infect a wide range of dicotyledonous plants. The genome components are easily isolated and cloned into plasmids, which are infectious. DNA-A alone can replicate and cause symptoms, when agroinoculated into tomato and *Nicotiana benthamiana.* Simultaneous introduction of DNA-B or β satellites, found in some samples positive for ToLCNDV, enhances symptoms (Jyothsna et al., 2013).

Movement and transmission:

A frequent property of begomoviruses is lack of seed transmission and the inability to be sap or mechanicallly transmitted, although many in this group can be mechanically transmitted only to tobacco, *Nicotiana benthamiana* (Chang et al 2010). No reports in the ToLCNDV literature have described testing whether the virus is transmitted through seeds from infected plants to their progeny. However, there are reports of sap/mechanical transmission of a cucurbit strain ToLCNDV-OM (ToLCNDV oriental melon isolate, most closely related to the cucumber isolate ToLCNDV-Cuc, from Thailand) from infected cucurbit species to most, but not all, other cucurbits and test species (Chang et al., 2010; López et al., 2015; Sohrab et al., 2013c). In the Chang et al. study the OM strain was sap transmissible at a rate of over 93%. Interestingly, ToLCNDV-OM did not infect tomato, pepper or muskmelon plants by either mechanical inoculation or agroinfection (Chang et al 2010).

An isolate from sponge gourd (*Luffa cylindrica*) from India was sap transmitted to ridge gourd (*L. acutangula*), sponge gourd, and *N. benthamiana* (Sohrab et al., 2013c). Standardized conditions for inoculation were developed to assist in screening sponge gourd germplasm for resistance to ToLCNDV (Sohrab et al., 2013b). A ToLCNDV isolate from pumpkin showing symptoms of pumpkin yellow mosaic disease in Northern India was also found to be mechanically transmissible (Maruthi et al., 2007).

A tomato isolate of ToLCNDV, collected in Bangladesh, was transmitted in a persistent manner by the whitefly *Bemisia tabaci* (Gennadius) (Hemiptera: Aleyrodidae) (Maruthi et al., 2005a).

Transmission efficiency increased with acquisition time, from 4% after 30 minutes to 85% after 24 hours, and with inoculation access time, from 3% at 15 minutes to 84% at 24 hours. Single *B.tabaci* adults transmitted at 10% efficiency, groups of 5 at 50%, and 10-15 at 90%. The latter result was comparable to the 100% transmission rates achieved with both ToLCNDV-Svr[Jes] and ToLCJV-Mld in the NRI insectary using 10 *B. tabaci* per test plant. Experimental transmissions to test plants or to screen germplasm have used 24 hours for both acquisition and inoculation, with 10 or more whiteflies (Maruthi et al., 2005a). Adults retain the virus for life.

Damage potential of pest:

Tomato leaf curl disease is a major constraint to tomato production in India. Affected plants show vein clearing, mottling, crinkling, puckering and upward or downward curling of leaves. Plants are stunted, bushy in appearance, and have sterility and poor fruit set (Jyothsna et al., 2013). In 137 samples collected from diseased tomato, potato, and cucurbit plants in India (2003-2010), 82% were positive for ToLCNDV, and 44% were associated with β satellites.

ToLCNDV has been primarily reported as the causal agent of leaf curl disease in tomato or other solonaceous crops. In recent years, ToLCNDV has emerged and induces serious (up to 100%) loss in yield from diseases in several other crops. These include yellow mosaic of sponge gourd in India (Sohrab et al., 2003), pumpkin in northern India (Maruthi et al., 2007; Phaneendra et al., 2012), bitter gourd in Pakistan (Tahir et al., 2010), cucumber, bottle gourd and muskmelon in Thailand (Ito et al., 2008), Oriental melon in Taiwan (Chang et al., 2010), and zucchini in Spain (Juárez et al., 2014). ToLCNDV also causes apical leaf curl of potato in northern India (Usharani et al., 2004) and is particularly severe in fields adjacent to sponge gourd, which harbors the virus (Sohrab et al., 2013a).

The damage potential increases in areas where the more aggressive B-biotype of *Bemisia tabaci* has been introduced. Comparison of transmission efficiency by the B-biotype vs. the indigenous biotype, conducted with ToLCNDV associated with pumpkin yellow mosaic disease in northern India, showed the B-biotype require half the time for acquisition and inoculation and also reach much higher populations (Maruthi et al., 2007).

Control:

Resistance to ToLCNDV has been identified in *Luffa cylindrica*, sponge gourd, in which the yellow-mosaic disease causes 100% loss under epidemic conditions (Sohrab et al., 2003). A single dominant gene in a genetic background of resistant parents, based on disease reaction of segregating and backcross generations when inoculated with a purified strain by whiteflies, controls resistance to ToLCNDV in sponge gourd (Islam et al., 2010). Screening of sponge gourd and genetic populations was conducted under natural epiphyotic condidtions, and by whitefly inoculation in insect-proof greenhouses. Several NBS-LRR-type resistance gene candidates have been identified in *L. cylindrica* (Saha et al., 2013). Since cultivation of tomato and sponge gourd in the North Indian plains region overlap in timing, resistance in the cucurbit

may contribute to a decrease in incidence of leaf curl disease in tomato.

In response to the recent emergence of ToLCNDV in Spain, mechanical inoculation was used to determine host range and screen *Cucumis melo* germplasm to detect tolerance in accessions from India (López et al., 2015). This was the first report of a source of tolerance to ToLCNDV infection in melon. Tolerance was detected in four genera and 13 species of cucurbits. Provided the results correlate with whitefly transmission, control in Spain by resistance is promising.

Other approaches to resistance that have been reported include transgenic artificial microRNAs to interfere with symptom production (Vu et al., 2013) and recombinant antibodies to block virus replication (Zakri et al., 2010). Induction of resistance by use of biologicals has achieved some success with whitefly-transmitted viruses (Mishra et al., 2014), but this has not been reported for ToLCNDV.

Known host range:

ToLCNDV hosts include *Benincasa hispida* (Roy et al., 2013), *Capsicum annuum* (Hussain et al., 2004; Khan et al., 2006), *Carica papaya* (Raj et al., 2008), *Cucumis melo* (Ito et al., 2008), *Cucumis sativus* (Ito et al., 2008; Mizutani et al., 2011), *Cucurbita moschata* (Phaneendra et al., 2012), *Cucurbita pepo* (Juárez et al., 2014), *Datura stramonium* (Muniyappa et al., 1991), *Daucus carota* (Sivalingam et al., 2011*)*, *Eclipta prostrata* (Haider et al., 2006), *Hibiscus cannabinus* (Raj et al., 2007), *Lagenaria leucantha* (Ito et al., 2008), *Luffa cylindrica* (Sohrab et al., 2013a), *Momordica charantia* (Tahir and Haider, 2005), *Solanum lycopersicum* (syn. *Lycopersicum esculentum*) (Maruthi et al., 2005a; Reddy et al., 2005), *Solanum melongena* (Pratap et al., 2011), *Solanum nigrum* (Juárez et al., 2014), *Solanum tuberosum* (Usharani et al., 2004).
ToLCNDV hosts identified by artificial inoculation include *Luffa acutangula* (Sohrab et al., 2003) and *Nicotiana benthamiana* (Usharani et al., 2004).

ToLCNDV-OM variant hosts include *Cucumis melo. var. makuwa* Makino (Chang et al., 2010).

ToLCNDV-OM variant hosts identified by artificial inoculation include *Capsicum annuum, Capsicum annuum* var. *grossum, Citrullus lanatus, Cucumis amaranticolor, Cucumis melo* var. *conomon* cv. Silver Charm, *Cucumis melo* var. *reticulatus*, *Cucumis metuliferus*, *Cucumis murale, Cucumis pepo* var. zucchini, *Cucumis quinoa*, *Cucumis sativus*, *Cucurbita moschata*, *Datura stramonium*, *Lagenaria siceraria*, *Luffa cylindrica*, *Nicotiana benthamiana*, *Nicotiana edwardsonii*, *Nicotiana occidentalis*, *Nicotiana tabacum*, *Phaseolus vulgaris*, *Solanum lycopersicum*, *Vigna mungo*, *Vigna radiata*, and *Vigna unguiculata* (Chang et al., 2010).

<u>Current APHIS Regulatory Status of Hosts</u>:

Carica: All propagules except seeds are Postentry Quarantine from all countries except Canada.

Cucurbita okeechobeensis* ssp. *okeechobeensis: All propagules regulated under the Endangered Species Act Plants (ESA-E).

Datura: Per Federal Order effective August 6, 2014 All propagules except seeds prohibited from Albania, Algeria, Argentina, Austria, Bahrain, Belgium, Benin, Bolivia, Brazil, Bulgaria, Burkina Faso, Canary Islands, Cape Verde, Cayman Islands, Chile, Colombia, Costa Rica, Cote D'Ivoire, Cyprus, Czeck Republic, Denmark, Ecuador, Egypt, Estonia, Finland, France, Gambia (The), Germany, Ghana, Greece, Guinea, Guinea-Bissau, Hungary, Iraq, Ireland, Israel, Italy, Jordan, Kenya, Kosovo, Kuwait, Latvia, Liberia, Libya, Lithuania, Luxembourg, Mali, Malta, Morocco, Netherlands, Niger, Nigeria, Palestinian Authority (West Bank), Panama, Paraguay, Peru, Poland, Portugal (including the Azores), Romania, Russia, Saudi Arabia, Senegal, Sierra Leone, Slovakia, Slovenia, South Sudan, Spain, Sweden, Switzerland, Syria, Togo, Tunisia, Turkey, United Kingdom (all regions), Ukraine, Uruguay, Venezuela, Western Sahara.
NAPPRA from India; Postentry Quarantine from all other countries.

<u>Proposed Action under NAPPRA</u>:

The importation of the following plants for planting genera, excluding seeds and cut flowers and greenery, that are hosts of **Tomato leaf curl New Delhi virus**, are not authorized pending pest risk analysis (NAPPRA) **from all countries**:

Benincasa, Carica, Datura, Daucus, Eclipta, Lagenaria, Luffa, Momordica

The importation of the following plants for planting genera, excluding seeds and cut flowers and greenery, that are hosts of **Tomato Leaf Curl New Delhi Virus**, are not authorized pending pest risk analysis (NAPPRA) **from all countries, except those mentioned after the genus**:

Cucumis	All except Canada and Netherlands
Cucurbita	All except Canada

The importation of all propagules except seeds of the following plants for planting genera that are hosts of Tomato Leaf Curl New Delhi Virus are already regulated under NAPPRA and are therefore not listed here again:

Capsicum, Hibiscus, Solanum* (including *Lycopersicum)

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
June 12, 2018

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Uredo artocarpi***

Hosts: ***Artocarpus***

Taxonomy and description of the pest:

Uredo artocarpi is a fungal plant pathogen in the Pucciniomycetes class, Pucciniales order, and *Pucciniaceae* family. *U. artocarpi* causes breadfruit rust.

Known distribution:

American Samoa, Cook Islands, Micronesia, Fiji, French Polynesia, Futuna, India, Marshall Islands, Niue, Palau, Papua New Guinea, Philippines, Rotuma, Samoa, Solomon Islands, Thailand, Tonga, Tuvalu, Vanuatu, West Indies, and northern South America (McKenzie, 2013).

In the United States, *Uredo artocarpi* is found in Hawaii (McKenzie, 2013; Redfern, 2010) and Puerto Rico (Zerega et al., 2004).

Biology of the pest:

Uredo artocarpi produces small (0.1-0.2 mm diameter), raised, round uredinia on the abaxial surfaces of breadfruit leaves that have corresponding brownish areas on the adaxial surface. Urediniospores are light yellow with spiny surfaces (McKenzie, 2013). Symptoms of breadfruit rust, caused by *U. artocarpi,* include tiny brown pustules on the abaxial surface, and brown discoloration on the adaxial surface of older leaves (McKenzie, 2013).

Transmission:
No information is available regarding *U. artocarpi* dissemination or introduction pathways, or whether seed transmission occurs.

Damage potential of pest:

No specific information is available on production losses due to breadfruit rust. However, based on information about the importance of breadfruit to meet nutritional needs of a wide range of tropical human populations as well as its role as a critical component of the natural environment, as described below, the impacts of severe rust outbreaks in certain regions could be significant.

Breadfruit has been an important staple crop and primary component of traditional agroforestry systems in the Pacific for more than 3,000 years (Anonymous, 2017; Meilleur et al., 2004). The species originated in the South Pacific and was spread throughout Oceania by islanders settling other islands. Hundreds of varieties have been cultivated around the tropics, and it is now grown in nearly 90 countries. Breadfruit was a significant element in a wide range of oral traditions and everyday activities and was, historically, produced by large-scale cultivation in groves or plantations (Meilleur et al., 2004). The trees are easy to grow, beneficial to the environment, and produce an abundance of highly nutritious, tasty fruit and edible seeds. The trees begin bearing in three to five years and are productive for many decades (Anonymous, 2017).

Breadfruit has high protein content, many essential vitamins, and substantial amounts of fiber. Like banana and plantain, it is eaten either ripe as a fruit or underripe as a vegetable (Meilleur et al., 2004). In addition to its nutritional qualities, breadfruit is a multipurpose species, and all parts of the tree are used (Anonymous, 2011; Parrotta, 1994; Zerega et al., 2004). It is an essential component of home gardens and traditional agroforestry systems, creating an overstory shelter for many cultivated and native plants and providing mulch, shade and shelter for pollinators and seed dispersing insects and birds. In the Pacific, breadfruit agroforests have protected mountain slopes from erosion for more than two millennia. They also provide construction materials, medicine, fabric, glue, insect repellent, animal feed, and more.

Breadfruit is a very important local cash crop for many Pacific Islanders, but because it is usually produced for local use, commercial production figures are difficult to obtain. However, the international market for breadfruit demand is increasing in countries such as New Zealand, Australia, Canada and the United States that have growing Pacific island communities (Anonymous 2017). Furthermore, this crop has been envisioned as playing a potential role in food security. Its food value equals or exceeds that of taro, making this fruit alone capable of sustaining between 75,000 to several hundred thousand people annually (Meilleur et al., 2004). Thus, the National Tropical Botanical Garden in Kauai, Hawaii noted the potential of this crop, which they called the 'tree of bread,' to play a significant role in alleviating hunger in the tropics (Anonymous, 2017).

Control:
No information on breadfruit rust is available in the literature.

Known host range:

U. artocarpi has been reported only from breadfruit—*Artocarpus altilis* (Parkinson) Fosb. (syn. *A. communis* J.R. and G. Forst.; *A. incisus* L.f.).

Current APHIS Regulatory Status of Hosts:

Artocarpus: All propagules except seeds must enter Postentry Quarantine Program from all countries except Canada

Proposed Action under NAPPRA:

The importation of the following plants for planting genus, (all propagules excluding seeds and excluding cut flowers and greenery) that is a host of ***Uredo artocarpi***, is not authorized pending pest risk analysis (NAPPRA) **from all countries**:

Artocarpus

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United States Department of Agriculture
Animal and Plant Health Inspection Service
Plant Protection and Quarantine

Plants for Planting Quarantine Pest Evaluation Data Sheet
March, 04, 2019

In order to prevent the introduction of quarantine pests into the United States, § 319.37-4 allows the APHIS Administrator to designate the importation of certain taxa of plants for planting as not authorized pending pest risk analysis (NAPPRA). APHIS has determined that the following plant taxa should be added to the NAPPRA category. In accordance with paragraph (b)(1) of that section, this data sheet details the scientific evidence APHIS evaluated in making the determination that the taxa are hosts of a quarantine pest.

Quarantine Pest: ***Ustilago shiraiana***

Hosts: **All taxa of Subfamily Bambusoideae (Family Poaceae): including** *Arundinaria, Bambusa, Indocalamus, Phyllostachys, Pleioblastus, Sasa, Sasaella, Sasamorpha, Semiarundinaria, Sinarundinaria*

Taxonomy and description of the pest:

Ustilago shiraiana is a fungal plant pathogen in the Ustilaginomycotina class, Ustilaginales order, and Ustilaginaceae family and the causal agent of bamboo smut (known as "susu" or "jinengo" in Japan).

The pathogen is also known as *Bambusiomyces shiraianus* (Hennings) (Vánky, 2011); and *Cintractia bambusae* Miyake & Hori may be a synonym, although Hori (1905) reported differences between *C. bambusae* and *U. shiraiana* spore morphology.

The related fungus *Ustilago hypodytes* (syn. *Tranzscheliella hypodytes*) also causes bamboo smut (Vánky, 2011).

Known distribution:

China, India, Japan, Korea (Democratic People's Republic), Korea (Republic), Sri Lanka, Russia, and Taiwan (CABI, 1989; EPPO, 2010; Vánky, 2011).

In the United States, *U. shiraiana* is present in California, Florida, Louisiana, Maryland, Mississippi, and Texas (EPPO, 2010).

Biology of the pest:

***Fungal morphology and infection*.** The sori, first appearing as swellings 1-2 cm long within the culms (Mordue, 1991), contain individual 6-9 x 6-10 micron, brown, powdery spores, spherical to subglubose or elliptical in shape, with oil droplets at the center (Hori, 1905). Mordue (1991) identified these propagules as "ustilospores." Freshly collected spore germination in water, under laboratory conditions, occurs within 10 hours, producing either a spindle-shaped structure called a "promycelium" (Hori, 1905) or a holobasidium, containing flattened, ovoid to ellipsoidal basidiospores (Vánky, 2011). Hori (1905) speculated that spores produced by the promycelium could be carried into the soil by rain or wind in a preceding season or could be windblown into contact with new shoots, where, if humidity is suitably high, they could germinate and send a germ tube into the bamboo plant. However, Mohanan (1997) reported that chlamydospores that lack a resting period are the primary propagules that move from the soil surface to the new bamboo shoots. Patterson and Charles (1916) reported that the fungus may remain dormant in the rhizomes or stems for an indefinite period.

***Disease symptoms and signs*.** Bamboo smut can occur throughout the season whenever environmental conditions are suitable (Hori, 1905); humidity of 98% and temperatures of 20-24°C are optimal for chlamydospore germination (Zhu, 1988). Infections are most common on young internodes and shoot tips but occasionally occur on older stems (Mordue, 1991). Sporogenous mycelium colonizes internal tissues, leading to the formation of fruiting bodies (Hori, 1905; Mohanan, 1997; Mordue, 1991; Tanaka et al., 2009; Young and Haun, 1961). *U. shiraiana* sori occur on the bamboo stem surface, surrounding the shortened internodes of young end-branches (Vánky, 2011). In this location, they may be obscured by the leaf sheaths, which become swollen, until the sheaths and bracts begin to open. At that time, the exposed spores are easily blown away by wind or washed off by rainfall (Hori, 1905). Sori also appear on lower leaf sheaths, initially between the veins but later becoming confluent, and on shoot tips. Shoot elongation is impaired and affected tissues may wrinkle or bend (Hori, 1905). The branches become brittle, reducing or eliminating their value and utility. Witches' brooming (also called "hexenbesen") and other organ distortions are common. New branches, forming after smut establishment, may appear healthy for some time but can become diseased if favorable conditions continue (Hori, 1905; Mohanan, 1997). Smut symptoms generally spread over all branches of an infected plant (Hori, 1905; Zhu, 1988). In some cases, the disease is concentrated at the outer edge of a forest, where plants are more exposed to wind-blown spores. Early reports indicated that the disease could lead to the death of an entire bamboo forest (Hori, 1905), but Mordue (1991) suggested that the disease and its economic impact are usually limited to local areas.

Movement and Transmission:

The primary means of pathogen dissemination is via wind-borne spores—primarily ustilospores and basidiospores (Mordue, 1991), but it is possible that spores are also washed into the soil from which they could later transfer via wind to new plants (Hori, 1905). *U. sharaiana* apparently remains viable within rhizomes and stems for an extended period (Patterson and Charles, 1916), so it is likely that the movement of fresh bamboo tissues, whether for commercial purposes or for planting, could also be a means of dissemination. Seed transmission has not been reported.

Damage potential of pest:

Bamboo is a commercially important crop in many countries, in demand for its use in building materials ("the poor man's timber"), household utensils, paper pulp, weaving materials, and erosion control, as well as for its use as a popular food (bamboo shoots) (Hori, 1905; Rishi et al., 2014; Singh et al., 2013). It was considered a promising industry for the southern United States as early as the 1910s, when the USDA introduced a number of valuable bamboo species (Marlatt et al., 1918). As bamboo smut was considered to be among the worst maladies to affect bamboo, the USDA considered it essential to protect the fledgling crop from this disease (Marlatt et al., 1918). Interestingly, efforts to prevent the entry of such pathogens into the U.S. did not apply to bamboo timber (mature, dried culms and canes) that was imported for the manufacture of fishing rods and furniture, or to edible, canned bamboo shoots (Marlatt et al., 1918). *U. shiraiana* was accidentally introduced in 1909 in bamboo plants imported from Japan to a USDA plant introduction station, but all symptomatic plants in the field were destroyed (Turner, 2008; Young and Haun, 1961). The disease reappeared in the field about six years later but again was eradicated by burning. However, tly bamboo smut has been reported in several U.S. states (CABI, 1989).

Control:

The most effective management approach for most smuts is prophylactic (Patterson and Charles, 1916). Unfortunately, fungicide treatment of seeds, a common practice to control cereal smuts, is not practicable for bamboo because of its perennial habit and because propagation is commonly vegetative.

Once infection occurs, early diagnosis is key to disease management, but *U. shiraiana* sori remain covered by the leaf sheaths of bamboo for some time before emerging. Thus, careful scrutiny of young shoot growth, including opening of the glumes and feeling of the internode surfaces for sori, is recommended (Patterson and Charles, 1916). Growers should also be vigilant for signs of witches' brooming.

Common cultural control consists of eradication by removing and burning smutted branches of bamboo and related species (including wild relatives) before sori open to release the spores

(Hori, 1905; Patterson and Charles, 1916). Bamboo is generally propagated through seeds, daughter plants that emerge from shoots, and vegetative culms (Singh et al., 2013). Young and Haun (1961) advised that destruction of the culms was insufficient, however, noting that all rhizomes should be dug up and burned as well.

The use of chemicals, either by spraying Bordeaux mixture onto plants or sprinkling lime onto bamboo forest floors (after they are cleared of defoliated leaves) may be somewhat effective (Hori, 1905) but is not considered a robust control measure (Patterson and Charles, 1916).

Bamboo cultivars having resistance to smut have not been reported. Hori (1905) noted, though, that smut had not yet been reported to occur on Moso-bamboo (*Phyllostachys mitis*) despite being grown in proximity to other bamboos that did become infected. Hori did not suggest this species as a potential source of resistance, fearing that it would ultimately succumb to the disease. Breeding for disease resistance in bamboo is extremely challenging because seed propagation is limited by a flowering cycle of as long as 120 years, and there are high rates of seed sterility and short viability (Singh et al., 2013). Furthermore, flowering is monocarpic, with culms dying after flowering, and genome polyploidy is common (Singh et al., 2013). Attempts to breed for virus disease resistance in bamboo using traditional methods have been disappointing. However, in recent years, there have been promising advances in bamboo propagation using *in vitro* approaches, molecular markers useful in characterizing genetic diversity have been identified, a few key genes have been cloned, and plant transformation and transgenic approaches are being explored (Singh et al., 2013).

USDA import regulations generally prohibit import of bamboo and bamboo products that are not thoroughly dried; bamboo stakes, canes or poles must be fumigated on arrival (USDA, 2011; USDA-APHIS, 2015).

Known host range:

Known hosts are restricted to members of the subfamily Bambusoideae (tribes Bambuseae, Arundinarieae, and Olyreae), family Poaceae. They include *Arundinaria* spp. (Vánky, 2011), *Arundinaria chino* (Mordue, 1991), *A. debilis* (Mordue, 1991), *A. simoni* (Hori, 1905; Mordue, 1991), *A. wightiana* (Ramakrishnan and Ramakrishnan, 1948), *Bambusa* spp. (Vánky, 2011), *Bambusa veitchii* (Mycobank, n. d.), *B. vulgaris* (EPPO, 2010), *Indocalamus debilis* (Vánky, 2011), *I. tessellatus* (Vánky, 2011), *Phyllostachys* spp. (NARO, n. d.), *P. aurea* (Vánky, 2011), *P. bambusoides* (Hori, 1905; Vánky, 2011), *P. congesta* (Vánky, 2011), *P. edulis* (Mordue, 1991), *P. henonis* (Mordue, 1991; Patterson and Charles, 1916), *P. heterocycla* (Vánky, 2011), *P. makinoi* (Mordue, 1991; Vánky, 2011), *P. nigra* (Mordue, 1991; Vánky, 2011), *P. puberula* (Hori, 1905), *P. quilioi* (Mordue, 1991; Patterson and Charles, 1916), *P. stauntonii* (Vánky, 2011), *Pleioblastus chino* (Vánky, 2011), *P. maximowiczii* (Vánky, 2011), *P. vaginatus* (Vánky, 2011), *P. simonii* (Vánky, 2011), *Sasa* spp. (CABI, 1989), *S. albomarginata* (Mordue, 1991), *S. kurilensis* (Vánky, 2011), *S. nana* (Mordue, 1991; Vánky, 2011), *S. nipponica* (Vánky, 2011), *S. paniculata* (Vánky, 2011), *S. senanensis* (Mordue, 1991; Vánky, 2011), *Sasaella ramosa*

(Mordue, 1991; Vánky, 2011), *Sasa tessellata* (Vánky, 2011), *Sasamorpha borealis* (Vánky, 2011), *Semiarundinaria yashadake* (Vánky, 2011), and *Sinarundinaria wightiana* (Vánky, 2011).

In the United States, *U. shiraiana* has been reported on *Phyllostachys henonis* and *P. quilioi* (Patterson and Charles, 1916).

Proposed Action under NAPPRA:

The importation of the following plants for planting genera, excluding seeds, and excluding cut flowers and greenery, that are hosts of ***Ustilago shiraiana*,** are not authorized pending pest risk analysis (NAPPRA) **from all countries:**

All taxa of subfamily Bambusoideae (Poaceae)

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