

PLANT SCIENCE SCAN

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BACKGROUND: The Plant Health Science Directorate of the Canadian Food Inspection Agency routinely scans external sources to identify information that might be of possible regulatory significance or interest to Canada's national plant health. This Plant Science Scan report was prepared by the Canadian Food Inspection Agency's staff as a mechanism to highlight potential items of interest, raise awareness and share significant new information related to plant health.

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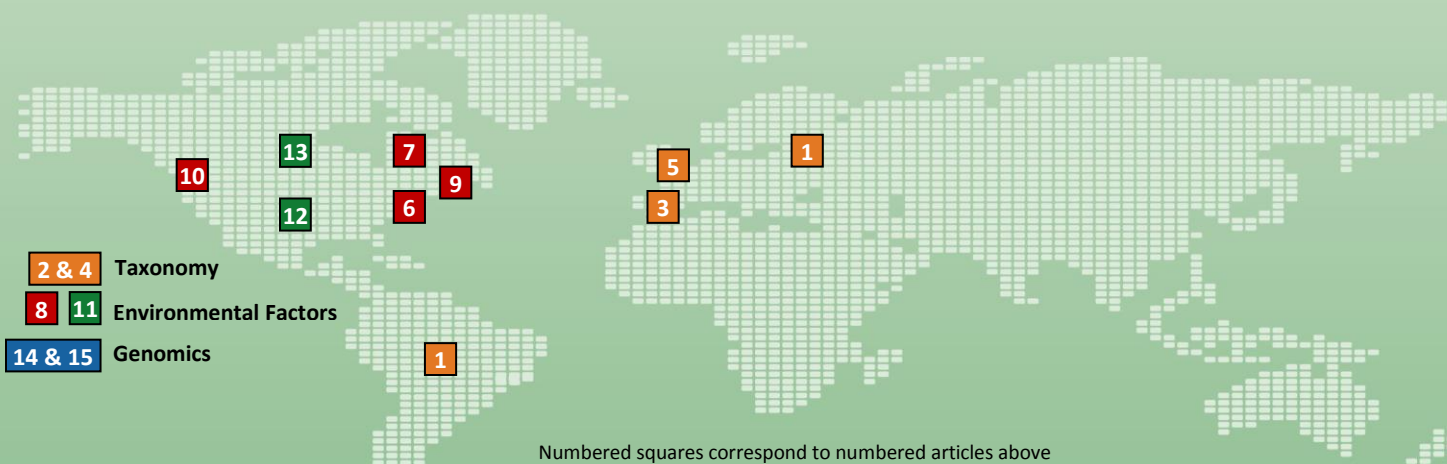
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Pathology

1. A new root-knot nematode, *Meloidogyne luci*, infects multiple hosts in Europe and South America

Meloidogyne ethiopica is a tropical root knot nematode which was initially described in Tanzania in 1968 (Whitehead 1968). Since 2004, this nematode has been reported from Slovenia, Italy, Greece, Portugal and Turkey on several crops (cucumber, kiwifruit, corn, tomato) (Aydınlı *et al.* 2013; Conceição *et al.* 2012; Maleita *et al.* 2017; Širca *et al.* 2004). In 2014, a new, morphologically similar species, *Meloidogyne luci*, was reported in vegetables, flowers and fruits in Brazil, Iran and Chile (Carneiro *et al.* 2014). Interestingly, recent molecular studies on populations of *Meloidogyne spp.* from Slovenia, Greece, Turkey, Brazil and South Africa showed that populations originally identified as *M. ethiopica* in Europe and Turkey corresponded in fact to *M. luci* (Gerič Stare *et al.* 2017; Janssen *et al.* 2016).

Since its first description in 2014, *M. luci* has been found to naturally infect okra, kiwifruit, snapdragon, broccoli, cucumber, carrot, soybean, stonecrop, lettuce, lavender, common bean, yacón, rose, tomato, potato, and grapevine. Additionally, the experimental host range of *M. luci* (as '*M. ethiopica*') includes cultivated plants of economic importance such as barley, corn, and potato (EPPO 2017). Symptoms of decline and stunting, as well as root galling have been reported on a number of species such as bean, tomato, and soybean, but data is generally lacking on the extent of damage and the

economic impact this nematode may cause on its different hosts.

Meloidogyne luci has a probable tropical origin, however it may have the potential to survive outdoors under a continental climate (hot summers and cold winters), even in areas where soil temperatures fall below zero during winter (Strajnar *et al.* 2011). More studies are needed to estimate the establishment potential of this nematode under Canadian climatic conditions.

As a root-knot nematode species, the most probable pathways for the introduction and spread of *M. luci* include infested soil and growing media, plants for planting, and bulbs and tubers from countries where the nematode occurs. Soil attached to machinery, tools, footwear or plant products is also another possible pathway.

Meloidogyne luci is a recently described new species and, to our knowledge, is not regulated by any country.

SOURCES: Aydınlı, G., Mennan, S., Devran, Z., Širca, S. and Urek, G. 2013. First report of the root-knot nematode *Meloidogyne ethiopica* on tomato and cucumber in Turkey. *Plant Disease* 97(9):1262-1262.

Carneiro, R. M., Correa, V. R., Almeida, M. R. A., Gomes, A. C. M., Deimi, A. M., Castagnone-Sereno, P. and Karssen, G. 2014. *Meloidogyne luci* n. sp. (Nematoda: Meloidogynidae), a root-knot nematode parasitising different crops in Brazil, Chile and Iran. *Nematology* 16(3):289-301.

Conceição, I. L., Tzortzakakis, E. A., Gomes, P., Abrantes, I. and Da Cunha, M. J. 2012. Detection of the root-knot nematode *Meloidogyne ethiopica* in Greece. *European journal of plant pathology* 134(3):451-457.

EPPO. 2017. EPPO Alert List: addition of *Meloidogyne luci* together with *M. ethiopica*, 2017/218, EPPO Reporting Service no. 11.

Gerič Stare, B., Strajnar, P., Susič, N., Urek, G. and Širca, S. 2017. Reported populations of *Meloidogyne ethiopica* in Europe identified as *Meloidogyne luci*. *Plant Disease* 101(9):1627-1632.



Janssen, T., Karssen, G., Verhaeven, M., Coyne, D. and Bert, W. 2016. Mitochondrial coding genome analysis of tropical root-knot nematodes (Meloidogyne) supports haplotype based diagnostics and reveals evidence of recent reticulate evolution. *Scientific Reports* 6:22591.

Maleita, C., Esteves, I., Cardoso, J., Cunha, M., Carneiro, R. and Abrantes, I. 2017. Meloidogyne luci, a new root-knot nematode parasitising potato in Portugal. *Plant Pathology*. Širca, S., Urek, G. and Karssen, G. 2004. First report of the root-knot nematode Meloidogyne ethiopica on tomato in Slovenia. *Plant disease* 88(6):680-680.

Strajnar, P., Širca, S., Knapič, M. and Urek, G. 2011. Effect of Slovenian climatic conditions on the development and survival of the root-knot nematode Meloidogyne ethiopica. *European Journal of Plant Pathology* 129(1):81-88.

Whitehead, A. G. 1968. Taxonomy of Meloidogyne (Nematodea: Heteroderidae) with descriptions of four new species. *Journal of Zoology* 31(3):263-401.

2 Re-classification of *Clavibacter michiganensis* subspecies on the basis of whole-genome and multi-locus sequence analyses

Since the turn of the twenty first century, the bacterial genus *Clavibacter* has consisted of only one single species, *Clavibacter michiganensis*. This species has multiple subspecies that are highly host-specific plant pathogens, namely, *C. michiganensis* subsp. *michiganensis* (bacterial canker and wilt of tomato), *C. m. sepedonicus* (bacterial ring rot of potato), *C. m. insidiosus* (wilting and stunting in alfalfa), *C. m. nebraskensis* (wilt and blight of maize), and *C. m. tessellarius* (leaf freckles and leaf spots in wheat), and etc.

In a recent research publication led by scientists from the Canadian Food Inspection Agency (CFIA), whole genome sequence analysis based on average nucleotide identity (ANI) and digital DNA-DNA hybridization (dDDH) as well as multi-locus sequence analysis (MLSA) of seven housekeeping genes were employed to better define the taxonomic positions of the subspecies of *C. michiganensis*; the results of these analyses clearly differentiated the *Clavibacter* subspecies into distinct clades at the

genomospecies level. Therefore, the authors proposed the establishment of all plant pathogenic subspecies as new species with the exception of the type subspecies as *C. m. michiganensis*. The new species include *Clavibacter capsici* sp. nov., comb. nov., *C. tessellarius* sp. nov., comb. nov., *C. insidiosus* comb. nov., *C. nebraskensis* comb. nov. and *C. sepedonicus* comb. nov. In the new classification, the species descriptions remain the same as for the former descriptions of corresponding subspecies.

This new taxonomic system, as pointed out by the authors, not only resolves the long-standing problem of having only a single species within the well-established genus, *Clavibacter*, but it also provides a practical solution for plant pathologists and policy makers dealing with quarantine and regulated plant pathogens. At present, *C. michiganensis*, *C. sepedonicus* and *C. insidiosus* are quarantine or regulated pathogens of important agricultural crops in many countries, while *C. capsici* is a newly described plant pathogen for which the range of distribution and risk to agriculture need to be assessed. In Canada, *C. sepedonicus*, the causal agent of bacterial ring rot of potato, is regulated by the CFIA under the Seed Potato Certification Program with a zero tolerance. There are stringent testing requirements for this pathogen on seed potatoes every year. The revised classification, and accordingly a simpler nomenclature, simplifies regulatory documents and more accurately reflects biological reality.

SOURCES: Li, X., Tambong, J., Yuan, K. X., Chen, W., Xu, H., Lévesque, C. A. and De Boer, S. H. 2018. Re-classification of *Clavibacter michiganensis* subspecies on the basis of whole-genome and multi-locus sequence analyses. *International Journal of Systematic and Evolutionary Microbiology*.



3 First report of *Xylella fastidiosa* infecting cherry (*Prunus avium*) and *Polygala myrtifolia* plants in Spain

During official surveys in late autumn 2016 in Mallorca Island, Spain, some cherry and *Polygala myrtifolia* plants located in a garden center near the locality of Manacor showed symptoms of marginal leaf scorch, leaf chlorosis, defoliation and general decay. Molecular analyses confirmed the presence of *X. fastidiosa* in the plants. In addition, multilocus sequence typing (MLST) of seven housekeeping genes further identified *X. fastidiosa* subsp. *fastidiosa* on one cherry tree and three *P. myrtifolia* plants and *X. fastidiosa* subsp. *multiplex* on one *P. myrtifolia* plant. This is the first detection of *X. fastidiosa* in Spain and of the subsp. *fastidiosa* on cherry and *P. myrtifolia* in Europe; thus expanding on the known distribution of this bacterium.

Xylella fastidiosa is a regulated pest for Canada and phytosanitary import requirements are currently in place to mitigate the risk of introduction of this species on grapevine propagative material. This bacterial pathogen causes diseases in a wide variety of plants such as almond, cherry, grape, citrus elm, olive and coffee trees and many ornamental plants. In Canada, it has been very rarely reported from elm (*Ulmus* spp.) as elm leaf scorch and from bigleaf maple (*Acer macrophyllum*). This bacterium has not been reported from any other hosts in Canada. It is believed that colder climatic conditions in Canada may limit the pathogen's natural distribution.

SOURCE: Olmo, D., Nieto, A., Adrover, F., Urbano, A., Beidas, O., Juan, A., Marco-Noales, E., López, M. M., Navarro, I. and Monterde, A. 2017. First detection of *Xylella fastidiosa* on cherry (*Prunus avium*) and *Polygala myrtifolia* plants, in Mallorca Island, Spain. Plant Disease(ja).

4 Taxonomic revision of the bacterial wilt pathogen *Ralstonia solanacearum*

Ralstonia solanacearum is a bacterial plant pathogen that has a very wide host range, including over 200 plant species, in over 50 families. Strains of this species are differentiated into five races, according to host range, and into five biovars, according to the utilization of various carbohydrates, and into four phylotypes, based on ITS sequence analysis. The different classifications of *R. solanacearum* have caused a considerable amount of confusion in the literature. Most races/biovars of *R. solanacearum* have a high temperature optimum (35 °C) and are not expect to overwinter in large areas in Canada. However, race 3/biovar2, which attacks mainly potato, tomato, and geranium without serious impact on other solanaceous crops, has lower temperature optimum (27°C) and is considered a threat to the Canadian potato industry. Currently, Canada regulates race 3/biovar 2 of *R. solanacearum*.

The large host range, pathogenic specialization, cultural and physiological properties, as well as the phylogeny of *R. solanacearum* support the fact that this species would probably be better described by a species complex. In a recent study, the taxonomy of the *R. solanacearum* species complex was revised using a combination of genomic and proteomic methods, and it was proposed to separate this complex into three distinct species: *Ralstonia pseudosolanacearum*, *Ralstonia solanacearum* and *Ralstonia syzygii*. This new species delimitation was found to be congruent with the previous phylotype classification: *R. pseudosolanacearum* (phylotypes I and III), *R. solanacearum* (phylotype II) and *R. syzygii* (phylotype IV). In addition, it was suggested that *R. syzygii* was composed of three subspecies. In summary, the following taxonomic revision of the *R. solanacearum* complex was proposed:



- *Ralstonia pseudosolanacearum* sp. nov.
- *Ralstonia solanacearum* (with a revised description)
- *Ralstonia syzygii* (with a revised description)
- *Ralstonia syzygii* subsp. *syzygii* subsp. nov.
- *Ralstonia syzygii* subsp. *indonesiensis* subsp. nov.
- *Ralstonia syzygii* subsp. *celebesensis*

It is worth noting that the race 3/biovar 2 strains of the previous *R. solanacearum* species complex, which mainly attack potato, tomato, and geranium, belong to the new *R. solanacearum* species in this revised classification. This new taxonomy more accurately reflects biological reality, and provides a practical solution for plant pathologists and policy makers dealing with quarantine and regulated plant pathogens. *R. solanacearum* (Race 3/Biovar 2) is a quarantine or regulated pathogen of potato in many countries.

SOURCES: EPPO. 2017. Taxonomic revision of *Ralstonia solanacearum*. EPPO Reporting Service 2017 no 10 (pages 11-12) <http://archiveseppoint/EPPOReporting/2017/Rse-1710pdf>.

Safni, I., Cleenwerck, I., De Vos, P., Fegan, M., Sly, L. and Kappler, U. 2014. Polyphasic taxonomic revision of the *Ralstonia solanacearum* species complex: proposal to emend the descriptions of *Ralstonia solanacearum* and *Ralstonia syzygii* and reclassify current *R. syzygii* strains as *Ralstonia syzygii* subsp. *syzygii* subsp. nov., *R. solanacearum* phylotype IV strains as *Ralstonia syzygii* subsp. *indonesiensis* subsp. nov., banana blood disease bacterium strains as *Ralstonia syzygii* subsp. *celebesensis* subsp. nov. and *R. solanacearum* phylotype I and III strains as *Ralstonia pseudosolanacearum* sp. nov. International journal of systematic and evolutionary microbiology 64(9):3087-3103.

5 First report of *Phytophthora ramorum* on Japanese larch (*Larix kaempferi*) in France

In May 2017, *Phytophthora ramorum* was identified for the first time on Japanese larch in Brittany in the forest of Saint-Cadou in Finistère in France. The affected stand is about fifty years old and the symptoms observed are wilting, yellowing and reddening of needles.

This is the first report of this pathogen affecting Japanese larch in mainland Europe.

Phytophthora ramorum causes “sudden oak death” in the United States, and since 2009, the pathogen has spread from rhododendrons to plantation-grown Japanese larch and caused extensive dieback and mortality in south-west United Kingdom (UK) and resulted in the felling of millions of larch trees. Apart from the UK, the Republic of Ireland has been the only other country where larch has suffered the impacts of *P. ramorum* infection.

At the infested site in France, there were no rhododendrons near the infected larch. Vaccinium plants, which support sporulation of *P. ramorum*, were found near the outbreak site but they were symptom free. Research is underway to learn more about this outbreak in France and how extensive it is as well as to identify the mating type and genetic lineage of the pathogen at the affected location. Of note, the climate of Brittany and its neighboring regions of Normandy and Pays de la Loire is conducive to infection by *P. ramorum*.

SOURCES: COMTF. 2017. Japanese larch (*Larix kaempferi*) was found *P. ramorum* positive for the first time in France. California Oak Mortality Task Force Report. July 2017. <http://www.suddenoakdeath.org/wp-content/uploads/2017/07/COMTF-Report-July-2017-1.pdf>

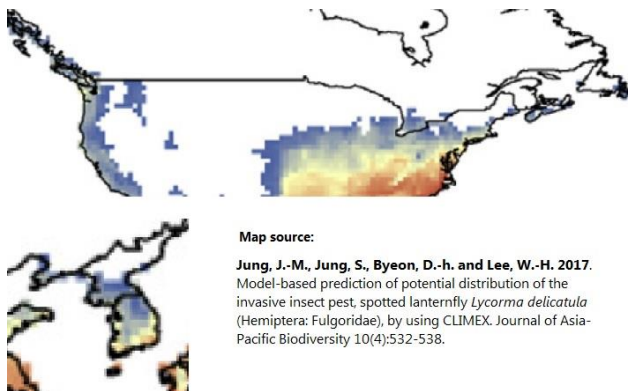
PONTE. 2017. Discovery of *Phytophthora ramorum* on Japanese larch in Brittany (France). Pest Organisms Threatening Europe (PONTE). <https://www.ponteproject.eu/news/discovery-phytophthora-ramorum-japanese-larch-brittany-france/>



Entomology

6 Spotted lanternfly in Delaware

The current distribution of this pest (to end of 2017) covers some 780,000 hectares (7,800 square kilometres) in Pennsylvania's southeast corner, and has spread into Delaware, to one county which neighbours on two infested counties in Pennsylvania. It is not yet certain that this bug will survive in eastern Canada (most likely it would in coastal B.C.), but certainly with climate change, the risk is high that it could survive. It remains to be seen whether it can reproduce successfully without its primary host present, and whether it would be able to establish based on only the presence of grapevines or alternate hosts; the main host of the adult is tree-of-heaven (*Ailanthus*), but it has also been seen on willows. Nymphs can feed on many plants, and seem to do quite well on grapevines. A recent predictive map of the potential range of *Lycorma delicatula* was recently published, which suggests survival in British Columbia is probable and likely in Ontario; the Niagara region has a close climate match to much of South Korea, which is infested by the pest:



SOURCE: <https://dda.delaware.gov/plantind/spotted-lanternfly.shtml>

7 Future winter mortality of hemlock woolly adelgid

The hemlock woolly adelgid (*Adelges tsugae*) is a tree-killing pest, newly found as widely established in southern Nova Scotia. Two small incursions in Ontario have also been found, and it also exists in an established invasive population in much of the eastern United States. Its effect on the landscape is expected to be profound, but certainty regarding its cold-hardiness, and how far north its harm will extend, is not great. This research is the first multi-year transect study that correlates local temperature to HWA survival, and allows for a rigorous projection of HWA survival in Canada. Based on the HWA mortality threshold of 91% being the limit at which permanent populations can sustain themselves, HWA is projected to expand to all of Nova Scotia, central and northeastern Maine, all of New Hampshire, Vermont, New York (excluding the highest elevations), just north and south of the Saint Lawrence River in Quebec, southern Ontario, all of the lower Michigan peninsula and all but the central upper peninsula, by the period 2071–2100. This information can be used to inform the design of regulations: for example, based on this research and the extrapolations it makes, it seems unlikely that natural spread will carry this insect from Nova Scotia into eastern Ontario or Quebec, because (barring adaptation of the pest) most of New Brunswick will remain long-term free of the pest. Therefore, regulations could focus on preventing or minimising spread northwards from southern Ontario, and in roughly 10-15 years we should concern ourselves also with spread coming around the eastern end of the Great Lakes, at Kingston. This is based on a reasonable climate change estimate, which



supposes a greater than 2 degree Celsius change by the end of the century.

SOURCE: McAvoy, T., Régnière, J., St-Amant, R., Schneeberger, N. and Salom, S. 2017. Mortality and recovery of hemlock woolly adelgid (*Adelges tsugae*) in response to winter temperatures and predictions for the future. *Forests* 8:doi:10.3390/f8120497

8 The development of gypsy moth (*Lymantria dispar* L.) under different temperatures

Lymantria dispar (gypsy moth) is one the most destructive insect pests of deciduous forests, causing heavy defoliation to a wide range of economically important tree species such as species of *Quercus* (main host), *Alnus*, *Malus*, *Acer*, *Populus*, *Salix*, *Crataegus*, and *Prunus*. Previous studies have shown that certain climatic conditions (e.g., low precipitation or uneven rainfall) can affect the development of *L. dispar*, which in turn can influence the outbreaks and damage caused by this pest. The authors of this study investigated the effect of temperature on the development of the gypsy moth. For this study, egg masses of *L. dispar* were collected in Hungary from three different host tree species: *Quercus robur*, *Quercus cerris*, and *Fraxinus ornus*. Larvae were reared in the laboratory and tested under three different temperatures (20°C, 25°C, 30°C). The authors measured the developmental time, weight, number of larval stages, mortality and fecundity of each developing larva. It was found that most of the larvae developed successfully under each temperature, although at 25°C there was no larval mortality and it appeared to produce the most favourable growth overall. There was a significant difference among the developmental times of the larvae under the three different temperatures; at 30°C larvae developed in the shortest amount of time. Larval weight was also influenced by the different temperatures as differences in weight were found beginning at the 6th larval instar of males and for the entire larval development of females. The results from this study indicate that

temperature, along with other climatic conditions, has an effect on the development of this pest.

Lymantria dispar is a regulated quarantine pest of Canada and poses a significant threat to Canada's forests, biodiversity and economy. The European gypsy moth is present so far in Ontario, Quebec, New Brunswick, Nova Scotia and Prince Edward Island, while the Asian gypsy moth is not known to occur in North America, although introductions of this pest have been detected but were successfully eradicated. Further knowledge of the gypsy moth's biology, including factors affecting its development, will help the CFIA continue to mitigate the risk of this pest, especially preventing it from entering British Columbia.

SOURCE: Hillebrand, R., Tuba, K. and Lakatos, F. 2015. The development of gypsy moth (*Lymantria dispar* L.) under different temperatures. Pages 243-246 in D. Marčić, M. Glavendekić, P. Nicot, eds. *Proceedings of the 7th Congress on Plant Protection*. Plant Protection Society of Serbia (PPSS), Belgrade, Serbia.

9 Description of an establishment event by the invasive Asian longhorned beetle (*Anoplophora glabripennis*) in a suburban landscape in the northeastern United States

Arrival, establishment, and dispersal are three ecological phases that are commonly used to describe the establishment of non-native species in a new area. Both arrival and dispersal phases have been well described for the Asian longhorned beetle (ALHB) (*Anoplophora glabripennis* Motschulsky), in multiple locations in North America and Europe. The transitional phase, establishment, is however not well understood for this species. The establishment phase serves as the decisive interval during which expanding populations stabilize and increase their distribution to ensure that the decline of such populations and their dissolution become



unlikely. In the current study conducted in Worcester, Massachusetts, the authors reported that ALHB seemed to move rapidly from the natal tree (the tree that was first attacked), to infest numerous trees within the stand, and perhaps also some trees well beyond the stand, long before the population in the originally infested tree grew to sizes reported from previous studies. The latter studies conducted in Toronto, Canada (Turgeon et al., 2015), and in Paddock Wood, Southern England (Straw et al., 2016), arrived at a different conclusion - adults ALHB tended to remain on their natal tree and there was a relatively slow spread of infestation to new trees. Results from the Worcester study also showed that ALHB population initially infested one or two *Acer rubrum* trees before moving through the stand to infest additional *A. rubrum*, based, not on distance or direction, but on tree size, with infestation biased towards trees with larger trunk diameters (mean diameter at breast height approximately between 17.0 and about 21.8 cm). The strong preference shown for *A. rubrum* agrees with the report by Dodds et al. (2014) which found that beetles in mixed stands of *A. rubrum*, *Acer saccharum*, and *Acer platanoides*, tended to infest only *A. rubrum* trees.

It is the opinion of the authors of this paper that studies on how ALHB populations behave when establishing in novel environments may have practical applications for management and eradication efforts. The effective use of surveys depends on a sound understanding of the probabilities associated with the directions, distances, and frequencies of propagule movement, and survey efforts may find new efficiencies from increased focus on tree size and in identifying the boundaries of infestations.

The Asian longhorned beetle is a regulated pest in Canada. Native to Asia, this beetle attacks and kills healthy deciduous trees, especially maple. Its larvae feed within the

trunk and branches of trees eventually causing the trees to die.

SOURCE: Hull-Sanders, H., Pepper, E., Davis, K., Trotter III, R. T. 2017. Description of an establishment event by the invasive Asian longhorned beetle (*Anoplophora glabripennis*) in a suburban landscape in the northeastern United States. PLoS ONE 12(7): e0181655

10 Performance of the tree-killing bark beetles *Ips typographus* and *Pityogenes chalcographus* in non-indigenous lodgepole pine and their historical host Norway spruce

The European spruce bark beetle, *Ips typographus*, is a highly destructive pest of spruce trees throughout Europe and can kill millions of Norway spruce (*Picea abies*) during outbreaks. This beetle is not present in North America and information on potential host tree species that are native to North America is sparse. The study investigated if the North American lodgepole pine (*Pinus contorta*), native to north-western USA and western Canada, could serve as a host to *I. typographus*, as well as to the bark beetle species *Pityogenes chalcographus*, in Europe. The authors tested if proportions of storm-felled trees colonized by *I. typographus* and *P. chalcographus* differed between lodgepole pine and Norway spruce. It was found that both bark beetles species could colonize and reproduce in the non-indigenous lodgepole pines, although these trees were colonized much less frequently than Norway spruces – 38% of the Norway spruces were attacked by these beetles, while only 4% of lodgepole pines were attacked. Specifically, *I. typographus* attacked only 0.2% of lodgepole pines in the first summer of field research and 1.6% in the second summer. It was also found that the reproductive success of this beetle was five-fold higher in Norway spruce than in lodgepole pine. The results from this study indicate that the risk of *I. typographus* colonizing lodgepole pines after an introduction is low. For this species, establishment in North American



spruce species is much more probable. Information on potential host species of *I. typographus*, especially those that are native to North America, is relevant to the CFIA as this species is a regulated pest of Canada.

SOURCE: Schroeder, M. and Cokoş, D. 2017.

Performance of the tree-killing bark beetles *Ips typographus* and *Pityogenes chalcographus* in non-indigenous lodgepole pine and their historical host Norway spruce. *Agricultural and Forest Entomology*.



Botany

11 Climatic niche shifts are common in introduced plants

Whether or not introduced species' climatic niches are conserved across continents has remained a long-standing question in ecology and conservation. A recent study in *Nature Ecology & Evolution* investigated how often introduced plant species experienced climatic niche shifts, and whether or not these niche shifts can be predicted.

Atwater *et al.* (2017) evaluated niche dynamics in 815 introduced terrestrial plant species from every continent. Occurrence data was downloaded from the Global Biodiversity Information Facility (GBIF), with occurrences in the United States supplemented with data from the Early Detection and Distribution Mapping System (EDDMapS). Using a series of models, the authors compared the native range of each species with their introduced ranges across the globe.

Evidence of climatic niche shifts was found in 65-100% of the 815 species, depending on which model was used. Individual species responses varied, but in general niche shifts corresponded with changes in climate availability at the continent scale, and were largest in long-lived and cultivated species. It

was also determined that species introduced to warmer continents tended to shift towards occupying warmer climatic niches. The authors proposed that shifts in the climatic niche of introduced species are an expected consequence of intercontinental range expansion, and that species' future distributions may be predicted based on species' traits and differences in climates between continents.

Understanding how climate influences species distributions is necessary for our ability to predict the future distribution of introduced species in response to climate change, as well as our understanding of how biogeography influences the ecology and evolution of species. The results of this study are important to keep in mind when applying environmental niche models to assess the risk and establishment potential of introduced species as well as mitigate the potential damage caused by invasive species, and may benefit risks assessors as they conduct risk assessments.

SOURCE: Atwater, D.Z., Ervine, C. and Barney, J.N. 2017. Climatic niche shifts are common in introduced plants. *Nature Ecology and Evolution*. <https://doi.org/10.1038/s41559-017-0396-z>

12 Mislabelling of invasive plants may contribute to their spread

Native plants are increasingly being promoted as alternatives to invasive ornamental plants in the horticultural industry. However, a recent U.S. study by Zaya *et al.* (2017) revealed that gardeners intending to plant native plants may actually be planting mislabelled invasive plants and contributing to their spread. Through analysis of nuclear microsatellite loci, the authors tested the identity of 34 plants labelled as *Celastrus scandens* (American bittersweet), a native species in North America, by



comparing them with reference plants of *C. scandens* and *C. orbiculatus* (oriental bittersweet), the latter a similar but highly invasive woody vine introduced in eastern Canada and the U.S. from Asia. Results showed that 18 of the 34 plants (53%) purchased as native *C. scandens* were actually *C. orbiculatus*. The mislabelled plants were more likely to be purchased online or by phone and were less expensive than accurately labeled plants, suggesting that *C. orbiculatus* may be easier to obtain and/or propagate than its native congener. To reduce the problem of mislabelling, the authors proposed instituting penalties on suppliers, encouraging self-policing, and disseminating useful information to consumers and producers.

This study highlights the potential role of mislabelling in the spread of invasive plants as well as the importance of having good genetic reference material for proper species identification. Considering the growing popularity of regional campaigns to grow native plants instead of non-native, invasive plants, additional studies with a larger number of species would be beneficial to better understand the scope of the problem. The CFIA recently dealt with a similar situation when notified of a plant at a Quebec nursery labelled as a regulated pest plant (*Dioscorea polystachya*), which was determined through morphological and molecular identification to be *Dioscorea nipponica*, a non-invasive plant and fortunately of no concern.

SOURCE: Zaya, D. N., Leicht-Young, S. A., Pavlovic, N.B., Hetrea, C. S. and Ashley, M. V. 2017. Mislabeling of an invasive vine (*Celastrus orbiculatus*) as a native congener (*C. scandens*) in horticulture. *Invasive Plant Science and Management* 10(4): 313-321.

13 Generation of a DNA barcode reference library for the vascular plants of Canada

A significant challenge to using a barcoding approach for plant species identification is often the limitation of a sufficiently comprehensive reference DNA barcode library to query for species-level assignment. Recently, such a library was created for Canada's vascular plants through a collaborative effort between plant taxonomists and research scientists from across Canada. The logistical challenge of collecting geographically representative specimens was addressed by utilizing the vast collections of well-annotated and expertly identified voucher specimens found in herbaria across the country. The use of herbarium specimens also provided an opportunity to integrate a molecular data set with the annotated voucher specimens and in some cases, led to corrections in the distribution data for some species.

The CFIA's molecular identification research laboratory has developed a DNA barcoding method which is used by the Agency's genotyping and botany laboratory as a complementary tool for the identification of Canada's regulated plant pests. Similar to the approach used for the study mentioned above, these DNA barcodes were developed for all regulated pest plants as well as for a subset of related species, from voucher specimens accessed from herbaria. Ultimately, this comprehensive DNA barcode library for Canada's vascular plants will increase the accuracy of the Agency's molecular diagnostic capabilities for identification of unknown plant samples and also serve as a complementary method for studying changes in the distribution of vascular plants in Canada.

SOURCES: Kuzmina *et al.*, 2017. Using herbarium-derived DNAs to assemble a large-scale DNA barcode library for the vascular plants of Canada. *Applications in Plant Sciences* 5(12): 1700079



Biotechnology

14 Everything in its place – mitigating the risk of gene flow from plants with novel traits

When the Canadian Food Inspection Agency (CFIA) evaluates the environmental safety of a plant with a novel trait (PNT) a key consideration is whether genes from the PNT will spread to sexually compatible plants. In crops with sexually compatible plants in Canada, the potential effect of the trait in other plants must be carefully evaluated. Novel traits in weed populations may lead to changes in weed control tactics. In natural environments, novel traits might impact plant fitness and lead to changes in genetic diversity. Gene flow may be managed by growing the crop only in areas where sexually compatible plants are not present. Another way to reduce gene flow is to change the PNT, for example by preventing or delaying flowering. However, when sexually compatible plants are present, it is very difficult to eliminate gene flow and further mitigation of potential adverse effects may be required. Reducing the fitness of crop-wild hybrids is a way to mitigate gene flow. The idea is to introduce a gene that is bad for wild relative-crop hybrids but beneficial to crops and is tightly-linked with the target genes novel to the crop. This will reduce the chance that crop-wild hybrids will be competitive and spread. A group of researchers in China applied this concept to rice. Yan et al. (2017) silenced a rice gene in cultivated rice that reduced seed shattering using artificial microRNA and antisense RNA techniques. This also reduced seed shattering in crop-weed hybrids by partially silencing expression of a seed shattering gene. As a result, fewer seeds were in the soil of the field plots where the cultivated rice with the shattering gene silenced was grown. The silencing of the shattering gene did not reduce

yield, an important factor when considering whether this mitigation technique is likely to be used commercially.

This rice example demonstrates the potential for mitigating the risk of gene flow from a PNT to sexually compatible plants. In particular, it may be applied to crops with weeds of the same species such as canola and weedy *Brassica* taxa. However, the level of mitigation achieved will vary depending on the crop type and its dispersal and seed germination characteristics. In the future, trait developers may choose to use this or other methods to mitigate gene flow in future PNTs. Before a PNT can be grown outside, its environmental safety must be assessed by CFIA's Plant and Biotechnology Risk Assessment Unit. This assessment would include evaluation of the intended novel trait as well as any changes made to mitigate gene flow.

SOURCES: Yan, Huanxin, et al. 2017. "Reduced weed seed shattering by silencing a cultivated rice gene: strategic mitigation for escaped transgenes." *Transgenic research* 26.4: 465-475.

15 Uncovering New Genes through Genome-Wide Association Study: Breeding Perspectives

The identification and characterization of genes associated with physiological, developmental, and morphological traits in cultivated plants is paramount for the quality, safety, and sustainability of food production systems. It also helps bridge the ubiquitous knowledge-gap regarding the genetic basis of phenotypic variation while contributing to the enhancement of crop improvement. This explains why, over time, from Gregor Mendel to the modern and sophisticated genetic engineer, scientists have strived to unravel the mysteries of the genome. To assist in this endeavour, the scientific community has developed a wealth of genomic and plant breeding resources as well as breakthrough technologies and techniques such as high-quality genome sequences,



dense SNP maps, extension germplasm collections, public databases of genomic information, and genome-wide association studies.

Genes that underlie agronomic traits are traditionally identified through quantitative trait locus (QTL) linkage mapping using bi-parental populations such as F₂ and recombinant inbred lines. While providing valuable insights, the QTL approach has shown some limitations such as low mapping resolution and limited genetic diversity between the mapping population parents. To illustrate, only two allelic variations are analyzed in biparental population during a QTL study. Consequently, all the other alleles that naturally occur in the plant landscape are missed. A genome-wide association study (GWAS) analyzes associations between nucleotide polymorphisms and phenotypic variance using a diverse population. Because the technique allows the detection of many natural allelic variations simultaneously in a single study and has benefited from recent advances in high-throughput sequencing technologies, GWAS has become a powerful tool for the identification of genes associated with important agronomic and ecological traits. Thus, Yano *et al.* (2016) used the technique to uncover on the chromosome 1 of rice (*Oryza sativa*) the gene *LOC_Os01g62780* responsible for the flowering date. Five years earlier, Zhao *et al.* (2011) elucidated the molecular basis of the interaction between genotypes and the environment (GxE) in the rice crop. They uncovered on chromosome 7 of rice the gene that regulates the circadian rhythm and light sensing. It is one of the genes that would determine regional adaptation of plants. Molecular advances in the field of plant nutrient acquisition (Raghotham and Karthikeyan, 2005) have demonstrated the interaction between nitrate and phosphates transporters with the N and P status of the soil. The discovery of genes that regulate photosensitivity and/or nutrient acquisition efficiency may provide new opportunities for

crop improvement, that is, the development of cultivars with: i) varying degrees of photosensitivity (long-day, short-day, day-neutral) that would adapt to specific or a wider range of latitudes or to changing climate; and/or ii) specific nutrient management requirements (e.g., low-input, high-input production systems).

SOURCES: Raghothama, K.G., Karthikeyan, A.S. 2005. Phosphate acquisition. *Plant Soil* 274:37–49

Yano, K., Yamamoto, E., Aya, K., *et al.* 2016. Genome-wide association study using whole-genome sequencing rapidly identifies new genes influencing agronomic traits in rice. *Nat. Genet.*, 48(8):927-34. doi: 10.1038/ng.3596.

Zhao, K., Tung, C-W, Eizenga, G. C., *et al.* 2011. Genome-wide association mapping reveals a rich genetic architecture of complex traits in *Oryza sativa*. *Nat. Commun.*, 2:467. doi: 10.1038/ncomms1467

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