## Scotland's Plant Health Centre: a multi-sectoral response to challenges from globalisation and climate change

## Chris Quine<sup>1</sup>, Ian Toth<sup>2</sup>, Sonia Humphris<sup>2</sup>, Fiona Burnett<sup>3</sup>, Peter Hollingsworth<sup>4</sup>

<sup>1</sup>Forest Research, Edinburgh, United Kingdom; <sup>2</sup>James Hutton Institute, Dundee, United Kingdom; <sup>3</sup>SRUC - Scotland's Rural College, Edinburgh, United Kingdom; <sup>4</sup>Royal Botanic gardens Edinburgh, Edinburgh, United Kingdom (chris.quine@forestresearch.gov.uk; ian.toth@hutton.ac.uk; sonia.humphris@hutton.ac.uk; fiona.burnett@sruc.ac.uk; phollingsworth@rbge.org.uk)

Plants underpin many ecosystem services. However, these contributions can be disrupted by pests and diseases and disruption is increasing as a result of changing climates and introductions through trade; some of these problem species have wide host ranges or complex life-cycles impacting vegetation across many environments. We describe the development of a novel co-ordinated approach taken by the Scottish Government to tackle these challenges through a Centre of Expertise for Plant Health. The Centre brings together expertise from natural environment and horticulture, forestry and woodlands, agriculture, drawing on a range of skills from social sciences to mathematical modelling to focus on those risks most pertinent to Scotland, and the plants of most importance to its natural heritage, economy and social wellbeing. We will summarise recent studies initiated by the Centre including assessments of the threats of the bacterial pathogen *Xylella fastidiosa* which has over 500 host plant species worldwide and is currently causing major economic losses in Europe. For this and other threats, the Centre's activities will include a focus on understanding possible routes of entry into Scotland, the ability to spread to and infect our major plant species under our climatic conditions, as well as the best methods for control and when to implement them, and how to involve stakeholders to minimise the risk. We will conclude with a summary of the benefits of a cross-sectoral approach for forestry, and lessons learnt in the operation of the Centre.

### Improving the international regulatory framework for managing alien invasive species in trade

#### Michael Ormsby1

## <sup>1</sup>NZMPI, Wellington, New Zealand (michael.ormsby@mpi.govt.nz)

With the international trade of forest products comes the risk of the movement of pests that can be extremely damaging to forest ecosystems and forest economies. Although impacts of biological invasions may be local, at least at first, the causes of introduction are mostly international. International phytosanitary guidelines have been created to help countries that import wood products develop import requirements to minimize pest movement. There are numerous international and regional instruments, binding and nonbinding, which have been developed to deal with the problem of the movement of alien invasive species, however there are gaps in the current international framework. In particular there is a need for regional and global support for countries that lack sufficient resources to implement effective phytosanitary systems. This presentation discusses various initiatives that could reduce the resource burden of regulatory frameworks to improve implementation and therefore reduce global impacts of biological invasions in forests.

## Collaborative strategies to reduce the introduction of exotic Eucalyptus pests in Brazil

Luis Renato Junqueira<sup>1</sup>, Leonardo Rodrigues Barbosa<sup>2</sup>, Patrícia Machado<sup>3</sup>, Jose Cola Zanuncio<sup>4</sup>, Luiz Alexandre Nogueira de Sá<sup>5</sup>, Carlos Frederico Wilcken<sup>6</sup> <sup>1</sup>Instituto de Pesquisas e Estudos Florestais, Piracicaba, Brasil; <sup>2</sup>Embrapa Florestas, Colombo, Brasil; <sup>3</sup>Indústria Brasileira de Árvores, São Paulo, Brasil; <sup>4</sup>Universidade Federal de Viçosa, Departamento de Entomologia/BIOAGRO,, Viçosa, Brasil; <sup>5</sup>Laboratório de Quarentena "Costa Lima", Embrapa Meio Ambiente, Jaguariúna, Brasil; <sup>6</sup>Universidade Estadual Paulista "Júlio de Mesquita Filho", Faculdade de Ciências Agronômicas, Departamento de Proteção Vegetal, Campus Botucatu, Botucatu, Brazil (renato@ipef.br; leonardo.r.barbosa@embrapa.br; patricia.machado@iba.org; zanuncio@ufv.br; luiz.sa@embrapa.br; carlos.wilcken@unesp.br)

The introduction of exotic pests has increased over time due to the growing traffic of people and goods. Just in the last decade, three new eucalypt pests were introduced in Brazil. Responsibility for biosecurity must be shared between government and productive sector, seeking for prevention or contingency of these invaders, avoiding their dispersion to main productive zones in the country. In this regard, the planted forests sector in Brazil has developed a collaborative work, involving research institutions, productive sector and government. Once well consolidated, cooperative research between academy and forest companies has brought besides productivity gains, new tools for pest management, especially biological control programs development. In addition, the BiCEP (Biological Control for Eucalyptus Pests) project was launched in 2013 as an alliance among research institutes from Australia, Brazil, South Africa and Portugal to share information about management of exotic pests and research about new pests and their natural enemies, providing essential knowledge to prevent new introductions or enable their early detection. The access and relevance understanding of this information by government is essential to improve national biosecurity, role played by sectoral associations. Finally, the establishment of partnerships and approximation among different institutions has generated positive signs for reduction of exotic pest introductions in the long-term.

# Genome sequencing uncovers mitotic recombination and rapid evolution in the sudden oak death and sudden larch death pathogen, *Phytophthora ramorum*

Angela Dale<sup>1,2</sup>, Nicolas Feau<sup>2</sup>, Sydney Everhart<sup>3,4</sup>, Guillaume Bilodeau<sup>5</sup>, Javier Tabima<sup>4</sup>, Renate Heinzelmann<sup>2</sup>, Clive Brasier<sup>6</sup>, Brett Tyler<sup>4</sup>, Niklaus Grünwald<sup>4</sup>, Richard Hamelin<sup>2,7</sup>

<sup>1</sup>FPInnovations, Vancouver, Canada; <sup>2</sup>University of British Columbia, Vancouver, Canada; <sup>3</sup>University of Nebraska, Lincoln, USA; <sup>4</sup>Oregon State University, Corvallis, USA; <sup>5</sup>Canadian Food Inspection Agency, Ottawa, Canada; <sup>6</sup>Forest Research, Farnham, United Kingdom; <sup>7</sup>Université Laval, Quebec, Canada (angela.dale@fpinnovations.ca; feaunico@mail.ubc.ca; everhart@unl.edu; guillaume.bilodeau@canada.ca; caifaz01@gmail.com;

renate.heinzelmann@ubc.ca; live.brasier@forestry.gsi.gov.uk; brett.tyler@oregonstate.edu; grunwaln@science.oregonstate.edu; richard.hamelin@ubc.ca)

Genome sequencing is an important tool to monitor outbreaks of invasive species and to understand how evolution and adaptation may occur. Many invasive alien species rapidly adapt to new environments, overcoming small population numbers and reduced genetic diversity. *Phytophthora ramorum*, an Oomycete forest pathogen causing sudden oak and sudden larch death is one such invader. It is limited to asexual reproduction within four lineages, and presumed clonal. We sequenced 107 genomes to monitor pathogen spread and to determine how this pathogen might be able to adapt to new environments with such limitations. Two mechanisms acting at the genomic level may contribute to adaptability and invasiveness in this pathogen. Within lineages, mitotic recombination (MR) associated with transposons and low gene density has generated runs of homozygosity (ROH), resulting in novel genotypic diversity. One ROH enriched in putative pathogenicity genes was fixed in lineage NA1. An independent ROH affected the same scaffold in lineage EU1 suggesting an MR hotspot and selection target. Between the lineages, non-core regions (not shared by all lineages) may undergo rapid evolution. These regions were enriched in putative pathogenicity genes as a striking pattern of gene loss, including all effectors, in the non-core genome of lineage EU2. Furthermore, effectors were under positive selection. *P. ramorum* lineages are diverging via a rapidly evolving non-core genome and the invasive asexual lineages are not clonal, but display genotypic diversity caused by MR. This provides important insights into evolution and potential for adaptation in invasive pathogens.