

**DIAROD COST Action: Minutes from Working Group 1 -The pathogen - defining the current disease situation**

**Leader - Jan Stenlid (SE)**

**Deputy - Irene Barnes (SA)**

**Task 1: Distribution and severity of Dothistroma needle blight (DNB) in Europe - an integrated approach to defining the current disease situation**

***Milestone 1: Produce and provide a standardised format for a disease distribution database.***

All 27 countries responded to the questionnaire. Lots of information provided on 1<sup>st</sup> records, current distribution, and host species. Older records thought to be less reliable. Where possible we be relying more on records based on molecular identification.

Anna Brown advises EFSA is also reviewing some of the early data. JS should review and compare with our information

Action Point - JS to compile and organise information and refer queries back to member countries. Ultimate aim to draft a paper maybe?

Action Point JS to look at generating maps (also see milestone 3)

***Milestone 2: Produce and provide standardised molecular identification methodology.***

Irene Barnes - MS2 basically completed. Most researchers using the same robust techniques e.g. Ios primers, also sequencing.

***Milestone 3: Produce disease distribution maps for DNB, including information on species, disease severity and historical records where data are available.***

Not possible to compile a complete map at present, but more detail should be available at the country level

Anna Brown – great project to offer to a GIS-literate individual as a SSSM?

**Task 2: Genetic Diversity of DNB in Europe - using pathogen population genetic diversity to infer origins and movement**

**Milestone 1:** Produce and provide standardised molecular methodologies for assessing genetic diversity

Irene Barnes - Microsatellite markers now available for both species

**Milestone 2:** Document the genetic diversity of different populations of *D. septosporum* and *D. pini* within Europe and use this to infer origins.

Jan Stenlid - We need a common methodology. Any suggestions?

*Discussion:*

Irene Barnes – she and Martin Mullett are trying to find out how to combine datasets given the use of diff platforms, machines etc. Can only guarantee the same alleles if the work is carried out in the same laboratory, same machine.

Jan Stenlid – recommends researchers at least use the same marker. Irene Barnes can then compare the statistics, even if not exact same alleles. Emphasise establish species before doing anything further. Use the Doth A marker or the MT primers (also useful as species identification – see Ios)

### ***Milestone 3: Inform regulatory authorities of risk of new genotypes***

Irene Barnes – maybe information on species present and virulence more relevant.

Additional comments on naming – 1 species, 1 fungus name. Teleomorph not to be used for Dothistroma in published work anymore - *D. Septosporum* or *D. pini*. (recommended reading: 'DNA barcoding of Mycosphaerella species of quarantine importance to Europe' Quaedvlieg et al. 2012 Persoonia 29, 101-115)