Summary

Dothistroma needle blight (DNB) is one of the most important diseases of pine. Although its notoriety stems from Southern Hemisphere epidemics in *Pinus radiata* plantations, the disease has increased in prevalence and severity in areas of the Northern Hemisphere, including Europe, during the last two decades. This increase has largely been attributed to expanded planting of susceptible hosts, anthropogenic dispersal of the causative pathogens and changes in climate conducive to disease development. The last comprehensive review of DNB was published in 2004, with updates on geographic distribution and host species in 2009. Importantly, the recognition that two species, *Dothistroma septosporum* and *D. pini*, cause DNB emerged only relatively recently in 2004. These two species are morphologically very similar, and DNA-based techniques are needed to distinguish between them. Consequently, many records of host species affected or geographic location of DNB prior to 2004 are inconclusive or even misleading. The objectives of this review were (i) to provide a new database in which detailed records of DNB from 62 countries are collated; (ii) to chart the current global distribution of *D. septosporum* and *D. pini*; (iii) to list all known host species and to consider their susceptibility globally; (iv) to collate the published results of provenance trials; and (v) to consider the effects of site factors on disease incidence and severity. The review shows that DNB occurs in 76 countries, with *D. septosporum* confirmed to occur in 44 and *D. pini* in 13. There are now 109 documented Pinaceae host taxa for *Dothistroma* species, spanning six genera (*Abies, Cedrus, Larix, Picea, Pinus* and *Pseudotsuga*), with *Pinus* being the dominant host genus, accounting for 95 host taxa. The relative susceptibilities of these hosts to *Dothistroma* species are reported, providing a resource to inform species choice in forest planting. Country records show that most DNB outbreaks in Europe occur on *Pinus nigra* and its subspecies. It is anticipated that the collaborative work described in this review will both underpin a broader global research strategy to manage DNB in the future and provide a model for the study of other forest pathogens.