

INVITED REVIEW

Annual *Medicago*: From a Model Crop Challenged by a Spectrum of Necrotrophic Pathogens to a Model Plant to Explore the Nature of Disease Resistance

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- **Background** Annual *Medicago* spp., including *M. truncatula*, play an important agronomic role in dryland farming regions of the world where they are often an integral component of cropping systems, particularly in regions with a Mediterranean or Mediterranean-type climate where they grow as winter annuals that provide both nitrogen and disease breaks for rotational crops. Necrotrophic foliar and soil-borne pathogens dominate these regions and challenge the productivity of annual *Medicago* and crop legume species.
- **Scope** This review outlines some of the major and/or widespread diseases these necrotrophic pathogens cause on *Medicago* spp. It then explores the potential for using the spectrum of necrotrophic pathogen–host interactions, with annual *Medicago* as the host plant, to better understand and model pathosystems within the diseases caused by necrotrophic pathogens across forage and grain legume crops.
- **Conclusions** Host resistance clearly offers the best strategy for cost-effective, long-term control of necrotrophic foliar and soil-borne pathogens, particularly as useful resistance to a number of these diseases has been identified. Recently and initially, the annual *M. truncatula* has emerged as a more appropriate and agronomically relevant substitute to *Arabidopsis thaliana* as a model plant for legumes, and is proving an excellent model to understand the mechanisms of resistance both to individual pathogens and more generally to most forage and grain legume necrotrophic pathogens.

Key words: Fungal pathogens, medics, annual *Medicago* species, *Medicago truncatula*, *Phoma medicaginis*, *Aphanomyces euteiches*, *Colletotrichum trifolii*, *Mycosphaerella pinodes*, grain legumes.

INTRODUCTION

Annual *Medicago* spp. play an important agronomic role in dryland farming regions of the world (Walsh *et al.*, 2001) where they are often an integral component of cropping systems, particularly in regions with a Mediterranean-type climate (Piano and Francis, 1992) where they grow as winter annuals (Sheaffer and Lake, 1997). Some annual *Medicago* spp. have distinct advantages, such as high levels of hard seededness, that make them attractive over other annual forage legume species such as *Trifolium subterraneum* in many areas.

Annual *Medicago* spp. provide nitrogen for rotational crops (Zhu *et al.*, 1998; Sheaffer *et al.*, 2001; Walsh *et al.*, 2001), are used as forage legumes (Puckridge and French, 1983; Anon., 1988; Prosperi *et al.*, 1989; Chatterton and Chatterton, 1996), have potential as summer annual forages (Zhu *et al.*, 1996; Shrestha *et al.*, 1998; de Haan *et al.*, 2002), and/or can be used as intercrops with grains (de Haan *et al.*, 1997), can be used as smother crops (de Haan *et al.*, 1997; Sheaffer *et al.*, 2002), are useful as over-winter cover crops (Fisk *et al.*, 2001), or can be used as a ‘disease break’ for rotational crops (Walsh *et al.*, 2001).

Annual *Medicago* spp. originated in the Mediterranean region, in which the greatest species diversity occurs (Piano and Francis, 1992). Some 33 species of annual *Medicago* are recognized (Lesins and Lesins, 1979). Of these, *M. polymorpha* is considered to be ubiquitous; *M. truncatula*, *M. orbicularis* and *M. littoralis* are distributed throughout areas with Mediterranean-type climates; while some species have close associations with specific regions, such as *M. murex* with central and western Mediterranean regions, *M. rigidula* with the Irano-Turanian region, *M. tornata* and *M. aculeata* with the western Mediterranean, and *M. blancheana*, *M. constricta*, *M. noeana*, *M. radiata* and *M. rotata* with the eastern Mediterranean region (Piano and Francis, 1992).

The distribution of annual *Medicago* spp. is influenced by edaphic factors including: soil type, levels of soil Ca, P, S and NO₃, and soil salinity (Andrew, 1977; Robson, 1983; Abdelguerfi *et al.*, 1988; Prosperi *et al.*, 1989; Ehrman and Cocks, 1990; Ewing and Robson, 1990; Piano *et al.*, 1991; Bounjemate *et al.*, 1992); climatic factors such as altitude and annual rainfall (Gintzburger and Blesing, 1979; Francis, 1980, 1987; Cocks and Ehrman, 1987; Abdelguerfi *et al.*, 1988; Ehrman and Cocks, 1990; Piano *et al.*, 1991); biotic factors such as regeneration capacity and levels of hardseededness (Francis, 1987; Thomson *et al.*, 1990); and possibly also by available

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rhizobial components (Robson and Loneragan, 1970; Robson, 1983; Vincent, 1988). The effects of these factors on the distribution of annual *Medicago* spp. have previously been reviewed, for example by Piano *et al.* (1991) and by Piano and Francis (1992).

There are numerous pathogens of forage plants, with some 400 fungal, bacterial, viral, mycoplasma and nematode diseases known to affect forage species on a worldwide basis (Haggar *et al.*, 1984). Although some aspects of forage diseases have been extensively reviewed (e.g. Graham *et al.*, 1979; Haggar *et al.*, 1984; Barnett and Diachun, 1985; Braverman *et al.*, 1986; Edwardson and Christie, 1986; Johnstone and Barbetti, 1987; Raynal *et al.*, 1989; Cook and Yeates, 1993; Lenné, 1994a, b; Barbetti *et al.*, 1996), such reviews cover superficially, if at all, necrotrophic fungal diseases of annual *Medicago* spp.

This review outlines the major diseases caused by foliar and soil-borne necrotrophic pathogens and explores the potential for using the spectrum of necrotrophic pathogen–host interactions, with annual *Medicago* as the host plant, to better understand and model pathosystems within the diseases caused by necrotrophic pathogens across forage and grain legumes. The links between annual and perennial *Medicago* spp., the model plant *M. truncatula*, and with grain legume species, in relation to their interactions with one or more related or unrelated necrotrophic pathogens are considered. For this review, we based our definition of ‘necrotrophs’ on that of Agrios (2004), to mean organisms which can have one part of their life cycle on dead host/tissue and which can grow on artificial nutrient media. As much of the existing literature covers one or more annual *Medicago* spp. in addition to *M. truncatula*, discussions in this review relate to annual *Medicago* spp. in general.

NECROTROPHIC PATHOGENS

There are many foliar and soil-borne necrotrophic pathogens of annual *Medicago* spp., and an outline of some of the most important and/or frequently occurring diseases in different regions that are caused by necrotrophic fungal pathogens are listed in Table 1. As indicated, some necrotrophic fungal pathogens (e.g. *Phoma medicaginis*) on annual *Medicago* spp. are also known to stimulate production of high levels of phyto-oestrogenic compounds, such as coumestrol. These compounds can adversely affect ovulation rates in sheep (Smith *et al.*, 1979; Croker *et al.*, 1994a, b, 1999, 2005). It is noteworthy that production of phyto-oestrogen compounds in response to disease varies between genotypes of annual *Medicago* spp. (Barbetti and Fang, 1991; Barbetti and Nichols, 1991).

As also indicated in Table 1, a number of *Fusarium* spp. on annual *Medicago* spp. have been shown to be responsible for the production of deleterious mycotoxins on animal feed material in Australia (Barbetti and Allen, 2005, 2006) and particularly in South Africa, where there is concern about the ability of *Fusarium* spp. on annual *Medicago* spp. to produce mycotoxins on animal feed material (Lamprecht *et al.*, 1986).

HOST RESISTANCE TO NECROTROPHIC PATHOGENS

A range of cultural and chemical strategies have been used to varying degrees for control of diseases in annual *Medicago* spp. (e.g. Barbetti, 1989a; You *et al.*, 1999; Walsh *et al.*, 2001). However, it is the use of resistant cultivars that offers the most effective long-term control measure for annual forage and grain legume diseases. This approach has been spectacularly successful as the main and most reliable avenue for the successful management of the most important pathogens of annual forage legumes such as *Kabatiella* on *Trifolium* spp. (Barbetti, 1996). These same opportunities exist for at least some diseases, such as Phoma blackstem disease, in annual *Medicago* spp. (Barbetti, 1993) providing large-scale screening of germplasm for resistance is undertaken as has been done for many years against *Kabatiella* in Australia (Nichols *et al.*, 1996).

A degree of resistance to many diseases is already available in some annual *Medicago* spp. For example, variation in resistance to stem and leaf disease caused by *Phoma medicaginis* (Renfro and Sprague, 1959; Barbetti, 1987, 1989a, 1990; O’Neill *et al.*, 2003), by *Leptosphaerulina trifolii* (Renfro and Sprague, 1959; Martinez and Hanson, 1963; Barbetti and Nichols, 1991), by *Colletotrichum trifolii* (Parmelee, 1962; Raynal, 1977; Elgin and Ostazeski, 1982; Lamprecht and Knox-Davies, 1984a, b; Lamprecht, 1986b; Troeung and Gosset, 1990; O’Neill and Bauchan, 2000), by *Cercospora medicaginis* (Berger and Hanson, 1963; Barbetti, 1985), by *Pseudopeziza medicaginis* (Schmiedeknecht, 1959), by *Phytophthora medicaginis* (de Haan *et al.*, 2002) and by *Leptotrochila medicaginis* (Semeniuk and Rumbaugh, 1976) has been reported in annual *Medicago* spp. Andrew (1962) demonstrated that *M. denticulata* had much greater resistance to post-emergence by *Pythium* spp. than did *M. minima*.

Methods of identifying host resistance: foliar necrotrophic pathogens

Various types of tests have been used to identify host resistance in annual *Medicago* spp. to necrotrophic foliar pathogens, ranging from laboratory to glasshouse screening tests to evaluations of swards under field conditions as illustrated in Fig. 7. For example, Troeung and Gosset (1990) used laboratory tests to locate resistance to *Colletotrichum trifolii* in annual *Medicago* spp. such as *M. rigidula* and *M. truncatula*. Lamprecht and Knox-Davies (1984b) tested the reactions of 3- and 6-week-old plants of annual *Medicago* accessions using *C. trifolii* spore suspensions at 15–25 °C under glasshouse conditions and assessed disease using the five-point scale of Ostazeski *et al.* (1969) (immune, resistant, intermediate, susceptible, dead) after 14 d to highlight different accession responses to crown rot. Lamprecht (1986b) used five different *C. trifolii* spore suspension application techniques and a sand-bran culture application technique on 4- to 6-week-old injured and uninjured *M. littoralis*,

TABLE 1. Foliar and soil-borne disorders of annual Medicago spp., the causal pathogens, the regions of their occurrence and key references

Disease	Pathogen	Region	Reference
Foliar			
Phoma black stem	<i>Phoma medicaginis</i>	Europe USA South Africa Australia	Sampson and Western (1941) Graham <i>et al.</i> (1979), O'Neill <i>et al.</i> (2003) Lamprecht and Knox-Davies (1984a) Barbetti (1983), Johnstone and Barbetti (1987), Barbetti and Fang (1991), Barbetti and Nichols (1991), Barbetti (1992, 1993) (see Figs 1 and 2 for typical disease symptoms)
Anthracnose	<i>Colletotrichum trifolii</i>	South Africa Canada USA Europe Australia	Lamprecht and Knox-Davies (1984a, b), Lamprecht (1986b) Parmelee (1962) O'Neill and Bauchan (2000) Raynal (1977), Troeung and Gosset (1990) Mackie <i>et al.</i> (1999)
Leptosphaerulina leaf and stem spot	<i>Leptosphaerulina trifolii</i> (syn. <i>L. briostiana</i>)	South Africa USA	Lamprecht and Knox-Davies (1984a) Renfro and Sprague (1959), Martinez and Hanson (1963), Graham <i>et al.</i> (1979)
Pseudopeziza leaf spot	<i>Pseudopeziza medicaginis</i>	Australia South Africa Australia	Barbetti (1989b) Lamprecht and Knox-Davies (1984a) Barbetti (1989b); Mackie <i>et al.</i> (1999) (see Fig. 3 for typical disease symptoms)
Stemphylium leaf spot	<i>Stemphylium botryosum</i> and <i>S. vesicarium</i>	USA	Chilton <i>et al.</i> (1943), Renfro and Sprague (1959)
Stagonospora leaf spot	<i>Stagonospora meliloti</i>	South Africa Australia Western Australia	Lamprecht <i>et al.</i> (1984) Barbetti (1989b), Mackie <i>et al.</i> (1999) Barbetti (1983, 1989b) (see Fig. 4 for typical disease symptoms)
Cercospora leaf spot	<i>Cercospora medicaginis</i>	USA Australia	Berger and Hanson (1963) Barbetti (1985)
Yellow leaf blotch	<i>Leptotrochila medicaginis</i>	North America	Semeniuk and Rumbaugh (1976)
High levels of phyto-oestrogenic compounds, such as coumestrol	<i>Phoma medicaginis</i>	Australia	Francis and Millington (1971), Collins and Cox (1984), Barbetti and Fang (1991), Barbetti and Nichols (1991), Barbetti (1993, 1995a)
Soil-borne			
Decline	Various	South Africa USA Australia	Lamprecht <i>et al.</i> (1988) Thies and Barnes (1991), de Haan <i>et al.</i> (2002) Andrew (1962), Kollmorgen (1974), Kellock <i>et al.</i> (1978), Bretag (1985), Bretag and Kollmorgen (1986), Mebalds (1987), Barbetti (1989c), Neal <i>et al.</i> (1997) (see Figs 5 and 6 for typical root disease symptoms on seedlings and adult plants, respectively)
	<i>Fusarium avenaceum</i>	Australia	Kollmorgen (1974), Bretag (1985), Bretag and Kollmorgen (1986), Mebalds (1987), Barbetti (1989c)
	<i>F. acuminatum</i> , <i>F. avenaceum</i> <i>Phoma medicaginis</i> , <i>Pythium irregulare</i> , <i>Rhizoctonia solani</i> , <i>Pythium</i> spp.	Australia Australia	Kollmorgen (1974) Andrew (1962)
	Species of <i>Pythium</i> , <i>Fusarium</i> and <i>Phoma</i>	Australia	You <i>et al.</i> (2000)
Root rot	<i>Phytophthora clandestina</i> <i>Fusarium avenaceum</i> , <i>F. culmorum</i> , <i>F. graminearum</i> and <i>F. lateritium</i> <i>Pythium irregulare</i> , <i>P. ultimum</i> and <i>P. spinosum</i> <i>Cylindrocladium scoparium</i> <i>Phytophthora medicaginis</i>	Australia South Africa South Africa USA	Clarke and Greenhalgh (1986), Barbetti (1989c) Lamprecht <i>et al.</i> (1988) Lamprecht <i>et al.</i> (1988) Lamprecht (1986a)
Mycotoxin	<i>Fusarium</i> spp.	Australia South Africa	Thies and Barnes (1991), de Haan <i>et al.</i> (1996, 2002) Barbetti and Allen (2005), Barbetti and Allen (2006) Lamprecht <i>et al.</i> (1986)

M. tornata, *M. truncatula* and *M. scutellata* plants held at 15–28 °C under glasshouse conditions and assessed disease on a 0–4 pointscale, where 4 indicated crown completely rotted, to successfully highlight resistance in

M. truncatula. O'Neill and Bauchan (2000) and O'Neill *et al.* (2003) used standardized environmental conditions in growth chambers to screen separately 201 accessions across 36 annual *Medicago* spp. for resistance to *C. trifolii*



FIG. 1. Phoma blackstem on *Medicago truncatula* 'Jemalong'.



FIG. 2. Phoma blackstem on *Medicago polymorpha* 'Serena'.



FIG. 3. *Pseudopeziza* leaf spot on *Medicago polymorpha* 'Circle Valley'.



FIG. 4. *Stagonospora* leaf spot on *Medicago polymorpha* 'Serena'.



FIG. 5. Severe rotting of roots of *Medicago polymorpha* seedlings.

and *Phoma medicaginis*. Semeniuk and Rumbaugh (1976) screened 25 annual *Medicago* spp. for resistance to *Leptotrochila medicaginis* under glasshouse conditions, identifying a high level of resistance in 22 of the species tested.

Frequently, germplasm responses to various diseases are a consequence of opportunistic occurrences of diseases in germplasm trials established for other purposes. A good example of this was the assessment by Lamprecht and Knox-Davies (1984a) of annual *Medicago* spp. varietal reactions (using a 0–4 disease severity index where 4 represents maximum disease) to a range of necrotrophic pathogens (*Phoma medicaginis*, *Leptosphaerulina trifolii*, *Colletotrichum trifolii* and *C. destructivum*, *Cercospora medicaginis*, *Pseudopeziza medicaginis* and *Stemphylium*



FIG. 6. Root disease on established *Medicago polymorpha* plants.



FIG. 7. Field swards of species of annual *Medicago* for identification of varietal resistances or susceptibilities to *Phoma* blackstem disease. Note yellowing and poor growth of the most susceptible varieties.

vesicarium) in experimental field plots at 12 locations in South Africa. In Western Australia, a 0–10 point disease assessment scale is frequently used (Barbetti, 1990), and for leaf pathogens such as *Phoma*, *Leptosphaerulina*, *Pseudopeziza*, plots are rated 0, where there was no disease; 1, where there was >0–9%; 2, \geq 10–19%; 3, \geq 20–29%; 4, \geq 30–39%; 5, \geq 40–49%; 6, \geq 50–59%; 7, \geq 60–69%; 8, \geq 70–79%; 9, \geq 80–89%; and 10, \geq 90% of leaves with lesions. However, depending upon the disease symptoms, especially if multiple diseases are occurring in the same plots, diseases can also be rated using a simplified system where 0 = no disease, 1 = there were >0–10% of stems with mostly small (<3 mm diameter or length) lesions; 2 = there were >10–20% of stems with small lesions; 3 = there were >20–30% of stems with lesions and then ratings 4–10 reflecting an increasing incidence and severity of damage and, ultimately, complete collapse of the sward.

Methods of identifying host resistance: soil-borne necrotrophic pathogens

Various types of tests have been used to identify host resistance in annual *Medicago* spp. to necrotrophic soil-borne pathogens, ranging from glasshouse screening

tests to evaluations under field conditions. For example, de Haan *et al.* (2002) used field assays on single rows of annual *Medicago* spp. at a site that had been artificially prior-inoculated using infested soil. They applied irrigation to maximize disease severity and assessed the level of root rot on plants using the 1–6 point disease scoring system described by Thies and Barnes (1991), which defined resistant germplasm as those with disease scores of only 1–2.

It is important that resistance to seedling death, damping-off and root disease all be determined in the search for annual *Medicago* spp. genotypes with improved field performance against soil-borne pathogens in disease-prone areas. This is because studies with annual *Trifolium* spp. have clearly indicated that resistance to seedling damping-off is frequently specific and under different genetic control to resistance to root rot (e.g. You *et al.*, 2005), and it is likely that the same will apply for annual *Medicago* spp.

Sources of host resistance

Identification of host resistance to many necrotrophic pathogens has frequently been a key aim of cultivar

development programmes, especially as there is large variability in annual *Medicago* spp. in relation to disease resistance, for example Phoma blackstem disease (Barbetti, 1989a, 1990, 1993; O'Neill *et al.*, 2003). However, such resistance has rarely been defined (e.g. as complete or partial, under a monogenic or polygenic control, respectively).

In the United States, de Haan *et al.* (2002) identified three accessions of *M. polymorpha* that had resistance to *Phytophthora medicaginis*. O'Neill *et al.* (2003) identified accessions within *M. constricta*, *M. doliata*, *M. heyniana*, *M. laciniata*, *M. lesinsii*, *M. murex*, *M. orbicularis*, *M. praecox*, *M. soleirolii* and *M. tenoreana* that exhibited a high level of resistance to *Phytophthora medicaginis*. O'Neill and Bauchan (2000) identified 14 accessions of the 201 tested that had resistance to *Colletotrichum trifolii*, including accessions in *M. murex*, *M. muricoliptis*, *M. polymorpha* var. *brevispina*, *M. polymorpha* var. *polymorpha*, *M. radiata*, *M. soleirolii*, *M. truncatula* and *M. turbinata*.

In South Africa, Lamprecht (1986b) identified *M. truncatula* cultivars 'Borong' and 'Cyfield' as the most resistant of nine cultivars tested from across four annual *Medicago* spp. (*M. littoralis*, *M. tornata*, *M. truncatula* and *M. scutellata*).

In Australia, a high degree of resistance, particularly to Phoma black stem, has been identified in screening programmes, useful both as parental materials in breeding and in providing resistant cultivars (Barbetti, 1995b). The incorporation of this resistance in commercial cultivars offers a promising long-term control measure for foliar disease in annual *Medicago* spp. (Barbetti and Nicholas, 1997).

Variation in resistance to stem and leaf disease caused by *Pseudopeziza medicaginis* (Renfro and Sprague, 1959; Barbetti, 1987, 1989a, 1990) and *L. trifolii* (Renfro and Sprague, 1959; Barbetti and Nichols, 1991) has been reported in annual *Medicago* spp.

It is noteworthy that the Mediterranean region has proved to be a productive source for collecting host germplasm with excellent resistance to one or more foliar and soil-borne necrotrophic pathogens. The value of this region as a source of resistance is highlighted by the example of the four introductions of *Trifolium subterraneum* germplasm from Sardinia that were directly released as new cultivars in Australia in the early 1990s, namely cultivars 'Denmark', 'Goulburn', 'Leura' and 'York'. Against important diseases on *T. subterraneum* in Australia, two of these cultivars had good resistance to both Race 1 and Race 2 of *K. caulivora*, two had good resistance to *Uromyces trifolii-repentis*, three had resistance to *Cercospora zebrina* and all four had outstanding resistance to the original race of *Phytophthora clandestina*. This is despite the fact that these diseases occurred infrequently (e.g. *C. zebrina* and *U. trifolii-repentis*) or have never occurred (e.g. *K. caulivora* and *P. clandestina*) in Sardinia, highlighting the value of looking for annual *Medicago* spp. sources of resistance to necrotrophic pathogens from the Mediterranean centre of origin, even if the particular diseases of interest do not occur there

(Barbetti, 1996; Nichols *et al.*, 1996; M. J. Barbetti, unpubl. data). It is interesting that nearly all the major diseases of annual *Medicago* spp., especially in Australia, are caused by necrotrophic pathogens that are common to other pasture legumes and across several continents, including the centre of origin of these host taxa. Presumably, such wide distribution of many of these pathogens is due to their wide host range and/or to their seed-borne nature. However, some annual *Medicago* and *Trifolium* species in Australia can be challenged by a pathogen such as *Phytophthora clandestina* that is only recorded in Australia and is yet to be recorded in the centre of origin of the host taxa. This can be described as a 'new encounter disease' (Buddenhagen, 1977; Allen *et al.*, 1998) for both these legumes. With *Phytophthora clandestina*, there is clear indication of the existence of allopatric resistance (Allen *et al.*, 1998) in Sardinia. It is also interesting that secondary centres of genetic diversity for annual *Medicago* and *Trifolium* spp. in Australia have provided successful sources of naturalized strains with increased resistance to disease for pasture legumes (Barbetti, 1996).

MEDICAGO TRUNCATULA: THE FIRST MODEL MEDICAGO SP.

M. truncatula: why it is an ideal model for necrotrophic pathogens

Although *Medicago* spp. are subject to a very large range of foliar as well as soil-borne necrotrophic pathogens, our knowledge of resistance sources, resistance expression, genetic determination and resistance mechanisms is still inadequate. However, annual *Medicago* spp. are now emerging as appropriate and agronomically relevant plants to study necrotrophic pathogens. Among the annual *Medicago* spp., *M. truncatula* is already proving to be an ideal model plant for both functional and structural genomic studies for identifying agronomically important genes and studying pathogen relationships in legumes. *Arabidopsis*, which to date has been the most valuable model plant to work on genetics and physiology of various aspects of plant biology, is a host of a very restricted range of species of necrotrophic pathogens, and is a less relevant model plant as a result.

Medicago truncatula is being used as a model plant for use in both molecular and classical genetic studies because of its ideal characteristics, such as its small, diploid genome, rapid generation time, self-fertility and ease of seed production (Cook, 1999). *M. truncatula* has proven to be an easily transformed species, ensuring its role as an ideal model system for investigating and elucidating gene function in legume species (Trieu *et al.*, 2000). There are now several large-scale international projects that have been initiated in relation to *M. truncatula* genomics, including the complete sequence description through an international consortium. Databases considering whole genome sequencing and annotation, expressed sequence tags (ESTs), structural genomics and comparative mapping, bacterial artificial chromosome

(BAC) libraries and physical maps, gene expression, metabolic profiling and bioinformatic tools are accessible through the <http://www.medicago.org/> website, which offers adequate links to other sites dealing with *M. truncatula* genomic resources, and legume phylogeny, protocols and publications. There is no resource specifically dedicated to disease resistance in *M. truncatula* as yet, apart from some reported EST libraries constructed while submitting plants to various biotic stresses (Torregrossa *et al.*, 2006).

The close phylogenetic relationship of *M. truncatula* to perennial cultivated *Medicago* spp. such as alfalfa, and other legumes such as pea (*Pisum sativum*), lentil (*Lens culinaris*), chickpea (*Cicer arietinum*) and faba bean (*Vicia faba*) increases the attractiveness of utilizing *M. truncatula* to improve our understanding of important agronomic traits in related grain and forage legume species (Dénarié, 2002). Large crop losses in these grain legumes are due to various necrotrophic pathogens (Tivoli *et al.*, 2006). Use of *M. truncatula* as a model system offers the first real opportunity for understanding the complex genetic and physiological basis of host–pathogen interactions, including secondary metabolite signalling, as has been done earlier for *Arabidopsis thaliana* (Bouwmeester *et al.*, 2003). It can also be used for transferring these insights to other annual *Medicago* spp., to grain legumes and to perennial cultivated *Medicago* spp. In addition, being a field crop species (unlike *Arabidopsis*) it could be readily used directly in the field where appropriate.

M. truncatula: a host of most necrotrophic pathogens affecting *Medicago* spp.

Large-scale screening was recently undertaken of *M. truncatula*, using the significant natural variation in the Australian *Medicago* spp. collection, to assess differential responses to over 25 necrotrophic pathogens including those causing foliar diseases such as Ascochyta blight, Botrytis grey mould, Colletotrichum anthracnose and Phoma black stem, and root diseases including those caused by *Fusarium* and *Rhizoctonia* (Ellwood *et al.*, 2001, 2004, 2005a, b). This clearly shows that *M. truncatula* is suitable as a host for a very large range of necrotrophic pathogens and that variation for resistance can be identified for some of these pathogens within the Australian *Medicago* spp. germplasm resources. The United States Department of Agriculture houses a *Medicago* spp. core collection. Within this, of 201 accessions of annual *Medicago* species, studied by O'Neill and Bauchan (2000) and O'Neill *et al.* (2003), most were observed to be susceptible to Phoma black stem and leaf spot caused by *P. medicaginis* and also to anthracnose caused by *C. trifolii*. No source with a high level of resistance could be found against *P. medicaginis*, but accessions with a high level of resistance to *C. trifolii* were identified (O'Neill and Bauchan, 2000). The screening of four *M. truncatula* lines by Torregrossa *et al.* (2004) identified cultivar 'Jemalong' and line DZA315.16 as resistant to *C. trifolii* Race 1. Therefore,

M. truncatula can be used as a model for most necrotrophic pathogens affecting annual and perennial *Medicago* spp. Disease screening studies involving diseases currently associated with losses in other grain and forage legume species and/or genera have also been undertaken. For example, screenings within *Medicago* spp. have provided key leads in relation to resistance to the fungus *Mycosphaerella pinodes*, which is responsible for ascochyta blight (black spot) on pea (Moussart *et al.*, 2006). From a core collection of 131 natural populations (Prosperi *et al.*, 2002), 34 *M. truncatula* ecotypes and nine ecotypes belonging to other *Medicago* spp. were screened for *My. pinodes* resistance either on plantlets or on detached leaves. High levels of resistance to *My. pinodes* with reduced variability between *M. truncatula* accessions have now been identified (Tivoli *et al.*, 2005; Moussart *et al.*, 2006), where although some flecks were observed on leaves on all the screened accessions, most accessions showed significant restriction of lesion development. Slowly progressing lesions with fructifications were observed on only a few accessions. Three different resistance reactions were noted, including absence of lesions, restricted fungal development to the site of inoculum application and cessation of progressive lesion development (Moussart *et al.*, 2006). These resistance reactions have also been confirmed in another set of *M. truncatula* accessions (D. Rubiales, pers. comm.).

The availability of germplasm showing various resistance levels towards necrotrophic pathogens within the *M. truncatula* collections opens the way to (1) isolate the genes controlling resistance to legume necrotrophic pathogens, and (2) study host–pathogen interactions at the histological, biochemical and physiological levels.

M. truncatula: provides for the isolation of genes controlling resistance in *Medicago* and grain legume species

A cross between cultivar 'Jemalong' and the line F83005.5 allowed genetic analysis of resistance in an F₂ population, indicating that resistance to *C. trifolii* was dominant and controlled either by a major resistance gene showing a distorted segregation or by more than one gene (Torregrossa *et al.*, 2004). Ellwood *et al.* (2005b) have developed and genetically mapped 80 polymorphic markers in a different F₂ population from a cross segregating for resistance to *P. medicaginis* and showed that resistance is under the control of a major gene. Therefore, a rather simple genetic control has been shown in *M. truncatula* for resistance to two major necrotrophic pathogens of *Medicago* spp., namely *C. trifolii* and *P. medicaginis*. This opens up the way not only for gene isolation based on genomic resources developed in *M. truncatula* but also for comparative analysis of resistance expression, genetic control and resistance mechanisms between *M. truncatula* and other *Medicago* spp. and grain legumes.

The model plant *M. truncatula* can constitute an efficient bridge between grain and forage legumes. Synteny between *Medicago* spp. as well as between *Medicago* and grain legumes such as pea (Gualtieri *et al.*,

2002; Kalo *et al.*, 2004) should allow a comparative analysis of genes or quantitative trait loci involved in resistance to necrotrophic pathogens in these species, including the number of genes involved, genomic localization, contribution to variation, etc. This same perspective could easily be applied where pathogens are common to certain other species (such as *C. trifolii* and *P. medicaginis* between different *Medicago* spp., and probably also *P. medicaginis* var. *pinodella* and *My. pinodes* and between *M. truncatula* and *P. sativum*). The suitability of such an approach is illustrated by a study by Kamphuis *et al.* (2005) in which they were able to conduct disease screening and genetic analyses in *M. truncatula* for resistance to different *Phoma* species taken from different legume crops.

M. truncatula: boosts understanding of host–pathogen interactions in both *Medicago* spp. and grain legumes

During pathogenic interactions between annual *Medicago* spp. and *C. trifolii*, O'Neill and Bauchan (2000) observed resistant reactions that were similar to those found in incompatible interactions between this pathogen and alfalfa, with fungal development severely restricted to host tissues at the point of inoculation. They suggested a hypersensitive response, possibly involving phytoalexins, as in the *M. sativa*–*C. trifolii* pathosystem (O'Neill, 1996). Cytological observations by Torregrossa *et al.* (2004, 2006) also showed that resistance was linked to a hypersensitive reaction. Subsequent microarray analysis showed that a strong correlation existed between the number of up-regulated genes and the resistance phenotype. Large differences appeared at 48 h post-inoculation and a large number of defence genes were involved.

Toyoda *et al.* (2004) described the *M. truncatula*–*My. pinodes* interaction and suggested it as a new pathosystem for genetic dissection of susceptibility to fungal pathogens. They observed that as on peas, attenuation or suppression of host defences contributes to establishment of susceptibility. In the case of ascochyta blight resistance on chickpea, Muehlbauer *et al.* (2005) compared the sequences from selected chickpea BAC clones with *M. truncatula* genome sequences. They successfully identified several orthologous contigs. The same approach, based on comparative genomics and synteny analyses, was developed by Ford *et al.* (2005) for ascochyta blight resistance on lentils.

An instructive view of the relevance of *M. truncatula* as a model species for *Medicago* spp. as well as for grain legume pathogens is presented by the example of *Aphanomyces euteiches*, a pathogen causing severe root rot and important yield losses on grain legumes (pea, lentil, vetch, etc.) as well as on alfalfa. The screening of the French core collection (Prosperi *et al.*, 2002) showed that there is a large variation within *M. truncatula* ecotypes for resistance to a pea *A. euteiches* isolate, and that the *M. truncatula* resistant ecotypes present a much higher level of resistance than that observed on pea (Pilet-Nayel *et al.*, 2005; Tivoli *et al.*, 2005; Moussart

et al., 2006). Such variation was previously reported in the US by Vandemark and Grunwald (2004) for *M. truncatula* accessions evaluated for resistance to *A. euteiches* Race 2, which is pathogenic to alfalfa. Genetic studies (Jacquet *et al.*, 2005a, b; Pilet-Nayel *et al.*, 2005), as well as cytological and transcriptomic studies (Jacquet *et al.*, 2005a, b), have been developed using susceptible and resistant lines of *M. truncatula*. In order to gain insight into molecular and physiological changes in diseased legume roots, a transcriptomic approach of *M. truncatula* during infection by *A. euteiches* was developed by Nyamsuren *et al.* (2003), which demonstrated that classical mechanisms of pathogenesis as well as new specific gene regulations are involved in root rot disease development caused by *A. euteiches*. Recently, Colditz *et al.* (2005) conducted a comparative proteomic analysis of the interaction formed between three lines of *M. truncatula* and a single *A. euteiches* strain. Several proteins were identified to be differentially induced after infection of the susceptible or resistant lines. This example shows that through complementary genetic and genomic-based strategies, such a pathosystem can be dissected within *M. truncatula* and comparative analysis subsequently carried out between this model species and other *Medicago* spp. and grain legumes to provide a better understanding of the nature of both resistance and susceptibility to necrotrophic fungal pathogens.

CONCLUSIONS

Host resistance clearly offers the best strategy for cost-effective, long-term control of necrotrophic foliar and soil-borne pathogens, particularly as useful resistance to a number of these diseases has been identified in annual *Medicago* germplasm collections. Previously, *Arabidopsis* had been the most valuable model plant to work on genetics and physiology of various aspects of plant biology, including host–pathogen relationships. However, recently and initially, the annual plant *Medicago truncatula* has emerged as a more appropriate and agronomically relevant substitute as a model plant for legumes. Because it is both a host of foliar and soil-borne fungal necrotrophic pathogens of numerous *Medicago* spp. in addition to several necrotrophic fungal pathogens of other grain legumes, *M. truncatula* is proving an excellent model upon which to dissect and to understand the mechanisms of resistance to necrotrophic pathogens of legumes in general. For example, the genetic and genomic resources now available in relation to *M. truncatula* will boost genetic analyses in grain legume species and therefore contribute to improved understanding of the structure and function of host resistance genes in relation to necrotrophic fungal pathogens across forage and grain legumes.

Important reasons for annual *Medicago* spp. proving to be ideal model crops include the following. First, these species are at the 'meeting point' between the model plant *M. truncatula*, other annual *Medicago* spp., perennial *M. sativa* and various grain legumes species, with several

necrotrophic fungal pathogens able to attack more than one of annual or perennial *Medicago* and grain legume species (e.g. *A. euteiches*, *C. trifolii* and *P. medicaginis*). Secondly, genetic studies undertaken in relation to identification of resistance genes to fungal necrotrophic pathogens can be easily transferred to *M. truncatula* not only from other annual or perennial *Medicago* spp., but also from grain legumes. Parallel approaches can now be undertaken across both annual and perennial *Medicago* species and grain legumes to provide better understanding of the nature of resistance, particularly for related necrotrophic fungal pathogens such as *P. medicaginis* and *My. pinodes*, the former a pathogen on annual and perennial *Medicago* spp. and pea, the latter a pathogen only on pea. In future, closer consideration of the common links between *M. truncatula*, other annual and perennial *Medicago* spp., and other grain legumes will not only enable wider application of genetic and genomic approaches to be undertaken on legumes, but also hasten transfer of relevant knowledge on necrotrophic pathogens between *Medicago* as the model genus, *M. truncatula* as the model plant and grain legumes. For example, improved understanding of key plant–pathogen interactions has already been demonstrated in relation to resistance against *A. euteiches* and *C. trifolii*. Clearly, modelling of host–pathogen interactions in annual *Medicago* spp., including *M. truncatula*, will greatly improve our understanding of the nature of both resistance and susceptibility to necrotrophic fungal pathogens across forage and grain legumes. This will undoubtedly help in the development of new forms of resistance in legumes to a variety of necrotrophic pathogens.

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