MYCOFLORA OF RHIZOMES AND ROOTS OF *ELYTRIGIA REPENS*, A POTENTIAL INOCULUM SOURCE FOR TAKE-ALL IN WHEAT

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ABSTRACT

Elytrigia repens is a host of the wheat take-all pathogen *Gaeumannomyces graminis* var. *tritici* (*Ggt*). While *E. repens* does not suffer substantial damage from infection by *Ggt*, rhizomes and roots of this plant are potential carriers of *Ggt* and the infested residues are likely to provide sources of inoculum for wheat. The mycoflora of rhizomes and roots of *E. repens* collected from three arable cropping sites over six sampling occasions were examined. The possible causes of root and rhizome lesions, and fungi that might provide a level of biological control of *Ggt* in *E. repens* were identified. *Ggt* was not always associated with lesions, and other fungi may also cause lesions on *E. repens*. Most *Ggt* was isolated from *E. repens* collected from an area where severe take-all infection had previously been observed in wheat. *Microdochium bolleyi* co-occurred most frequently with *Ggt*, and the potential of *M. bolleyi* as a bio-control agent for take-all is discussed.

Keywords: *Elytrigia repens*, mycoflora, take-all, *Gaeumannomyces graminis* var. *tritici*.

INTRODUCTION

Take-all, caused by the fungus *Gaeumannomyces graminis* (Sacc.) von Arx and Olivier var. *tritici* Walker (*Ggt*), is an important disease of wheat, causing serious economic losses worldwide. This disease affects autumn-seeded wheat, and damage is related to the extent and time of colonisation of roots and culm bases by *Ggt* (Wiese 1987). In New Zealand, take-all decreased grain yield in wheat by 18% in a field trial (M.G. Crome, unpubl. data). Severe infection has resulted in complete loss of some commercial crops. Resistant wheat cultivars are not available, and fungicides provide only limited control of the disease.

Ggt is a root-inhabiting fungus with little growth and competitive saprophytic ability in soil in the absence of host-plant roots (Skou 1981). Other than infected stubble residues from previous crops, rhizomes and roots of perennial grass weeds are the other potential hosts for the fungus (Nilsson et al. 1981). When roots of wheat seedlings come into contact with *Ggt* associated with perennial grasses, the fungus colonises the wheat roots by dark 'runner hyphae'. The runner hyphae then penetrate root cortices, enter the vascular system and cause phloem breakdown and blockage of the xylem tissues. As a result, plants may die prematurely, hence decreasing grain yield from affected crops (Deacon 1998).

Elytrigia repens is a common grass weed found on cropping land, and is a host of the soil-borne take-all fungus. This plant does not seem to be greatly affected by *Ggt*, except for some fleck-like lesions on the rhizomes (Harvey & Braithwaite 1986). Although *E. repens* can be effectively controlled by the herbicide glyphosate, *Ggt* can remain viable and further colonise dead or dying rhizomes, and can act as a potential source of infection for subsequent wheat crops (Harvey & Braithwaite 1986). The effects of decaying *E. repens* rhizomes on cereal growth have been extensively studied (Lynch & Penn 1980; Lynch et al. 1980; Penn & Lynch 1981), but the fungi associated with *E. repens* have not been considered in detail. The objectives of the present study were to

identify the mycoflora, including *Ggt*, associated with *E. repens*, to assess whether the lesions on the rhizomes and roots of this grass were caused by *Ggt*, and to examine the coincidence of *Ggt* and other fungi isolated from *E. repens*.

MATERIALS AND METHODS

Sampling

Three to 10 tillers of *Elytrigia repens* with rhizomes and roots attached, were sampled over six occasions (22 Oct, 12 Nov, and 4 Dec 2002, 8 Jan, 10 Feb and 7 Mar 2003) from three field research sites, giving a total of 18 samples. Wheat crops are commonly grown on these sites but wheat plants were not always present at the specific location where *E. repens* was visible upon sampling. These sites were located at the Crop & Food Research Lincoln Central Block (Site I); Agronomy Block (Site II) off Boundary Road; and Millennium Block (Site III) off Springs Road, Mid Canterbury, New Zealand. Samples were collected from the areas where *E. repens* patches were visible outside the borders of existing field trials but not from within any trials in progress at each site.

Material preparation

Soil was shaken and washed off the rhizomes. Any fibrous sheaths covering the rhizomes were removed to expose the rhizome internodes. All rhizomes and roots were inspected and categorised into apparently healthy tissues with no disease symptoms (H), tissues showing slight or spot lesions (SL) and tissues with dark lesions (DL). SL and DL were not found on both rhizomes and roots for all of the samples, so isolation for these could not be done.

Fungal isolation

Segments (2 cm long) of rhizomes and of roots (one segment each of DL, SL and H where lesioned tissues were found) were surface sterilised with 1% sodium hypochloride solution (with 0.04% available chlorine) for 3 min and 1 min, respectively, and rinsed twice with sterile reverse osmosis water to remove residual chlorine. Each segment was then cut aseptically into 4 or 5 pieces and plated into Petri plates (one tissue segment per plate) containing potato dextrose agar (PDA) amended with antibiotics (120 mg/litre streptomycin sulfate, 50 mg/litre aureomycin and 50 mg/litre chloramphenicol). The isolation plates were prepared for each site at each sampling occasion. There were some samples for which no DL or SL were found; these were treated as missing plates (Table 1). After three to five days of incubation at 23°C in the dark, the leading edges from developing fungal colonies were subcultured and maintained on PDA or low nutrient agars (such as potato carrot or water agar) in the dark. They were also kept on PDA or carnation leaf agar under 12 h alternate light and dark regimes at 25°C.

TABLE 1: Number of samples for which no lesions were found out of 18 *Elytrigia repens* samples.

Lesion types	Rhizomes	Roots
DL	8	10
SL	1	7

Fungal identification

Fungal isolates were identified to genus and, where possible, to species using culture morphology and light microscopy. Non-sporulating isolates were grouped into morphotypes, based on colony characteristics.

Data analysis

Patterns of presence and absence (incidence) of the fungal species between sites and sampling occasions were examined using a generalised linear model (GLM, McCullagh & Nelder 1989) with Bernouli error structure and a logit link. This analysis is similar to the standard X² analysis of contingency tables. Severity was examined by analysing numbers of isolations with a Poisson GLM with a logarithmic link. Incidence and severity were examined for all segments, and for rhizomes, roots and the three lesion types

separately. Detailed results of these analyses, and individual site and sampling occasion data have not been presented, for simplicity. Other patterns were explored via data tabulation. All analyses were carried out with GenStat (GenStat committee 2003).

RESULTS

The *E. repens* samples were collected from visible grass patches from each site. Lesions of all three types were not found for all samples. Thus, the amount of available material sampled for each of the lesion types varied, and the sites, tissue types and lesions were not equally represented (Table 1). The numbers of samples with presence of a fungal species within a sample from the three sites, and the number of isolations of these fungi from the two tissue types and each of the three lesion types (SL, DL and H) are presented (Table 2).

Fungal isolates

A total of 38 fungal species or morphotypes were recovered from the *E. repens* tissues from the 18 samples (Table 2). Of these, sporulating fungi belonging to 20 genera were identified. There were significant differences ($P < 0.001$) between the fungal species in overall incidence, varying between presence in only one sample (19 fungal species) to presence in 12 (*Fusarium oxysporum*) of the 18 samples. *Fusarium* was the genus most commonly isolated (8 of 38 fungal species). At the species level, *Fusarium oxysporum* (isolated from 12 of 18 samples), *Fusarium culmorum* (10), *Microdochium bolleyi* (nine) and *Ggt* (eight) were the most common. Of the 38 species isolated, 15 have been recorded as pathogenic on wheat or grasses in New Zealand (Pennycook 1989). Incidence of the fungi isolated did not vary significantly with sampling occasion ($P > 0.3$) and only *F. oxysporum* was found on all the six sampling occasions at a site (Site III). There were significant differences ($P < 0.001$) between the fungal species in the overall numbers of isolations, varying between only one isolation made for 19 of the fungal species to 28 for *F. oxysporum*.

Fungi isolated from lesions on *Elytrigia repens* rhizomes and roots

Similar patterns of incidence to those found overall were found on the rhizomes of *E. repens*, with incidence varying between fungal species ($P < 0.01$), and the presence of species varying between the sites ($P < 0.001$ for the site and species interaction). There was no difference in incidence between the sampling dates ($P > 0.8$). Most species were obtained from rhizomes (29 of 38 fungal species) and from tissues showing lesions (31) (Table 2). Numbers of isolations on the rhizomes varied strongly between fungal species ($P < 0.001$). The predominant species isolated from rhizomes were *F. oxysporum* (28 isolations), followed by *F. culmorum* (16), *Ggt* (15), *M. bolleyi* (13) and *Microdochium nivale* (eight). *Microdochium bolleyi* was also the most commonly isolated fungus from the healthy tissues (five of 18 samples).

There was a smaller range in overall incidence between fungal species found in the roots but the number of isolations for these species varied strongly ($P < 0.001$). Of the 38 fungal species, 22 were found on the roots. *Ggt* and *M. bolleyi* both were found in four roots of the samples. There were no significant differences between the number of isolations from the roots with either sampling occasion or sites ($P > 0.15$).

Incidence and numbers of fungal species within DL and SL lesions varied significantly ($P < 0.001$). *Fusarium oxysporum*, U1D5 and *Ggt* were more strongly associated with SL, while *F. oxysporum* and *F. culmorum* were more prevalent in DL samples (isolated from 5 and 7 of 18 samples respectively). Numbers of isolations made from H tissue also varied substantially between fungal species ($P < 0.001$), but did not vary significantly between dates or sites ($P > 0.1$). *Rhizopus oryzae* (isolated from 3 of 18 samples) and *M. bolleyi* (5) were the two only fungal species associated strongly with H tissues of the 18 samples.

Ggt was isolated from all the three sites (Table 3) but most commonly from Site III (10 isolations) ($P < 0.001$), where severe take-all in wheat had been previously recorded (M.G. Cromey, unpubl. data). Most isolates were from rhizomes with slight lesions (10) and none were isolated from healthy rhizomes. *Ggt* was isolated at low frequencies on roots both from lesioned (three counts from DL, two from SL) and healthy tissues (three counts). Most *Ggt* was isolated in samples collected on 12 Nov 2002 from all three sites (Site I 4, II 5 and III 3).

TABLE 2: Number of samples where each fungal species was found from 18 samples of *Elytorgia repens*, and the number of isolations made for each species from rhizomes (Rhi), roots (R), and tissues showing dark lesions (DL), slight lesions (SL) or no lesions (H).

Fungal species	No. of samples where present	No. of isolations					Total
		Rhi	R	DL	SL	H	
<i>Achaetomium</i> spp.	2	2	0	0	0	2	2
<i>Acremonium</i> spp. ¹	1	0	1	0	1	0	1
<i>Alternaria</i> spp.	2	2	0	1	1	0	2
<i>Chaetomium</i> spp. ¹	2	0	2	1	1	0	2
<i>Cladosporium</i> spp. ¹	1	1	0	0	0	1	1
<i>Codinea</i> spp.	1	0	1	0	1	0	1
<i>Fusarium anthophilum</i>	1	1	0	0	1	0	1
<i>Fusarium avenaceum</i> ¹	1	1	0	0	1	0	1
<i>Fusarium culmorum</i> ¹	10	16	1	10	5	2	17
<i>Fusarium equiseti</i> ¹	1	1	0	0	1	0	1
<i>Fusarium oxysporum</i> ¹	12	27	1	7	19	2	28
<i>Fusarium pseudograminearum</i> ¹	1	0	1	1	0	0	1
<i>Fusarium sambucinum</i> ¹	1	0	1	0	1	0	1
<i>Fusarium</i> spp.	1	1	0	0	1	0	1
<i>Gaeumannomyces graminis</i> var. <i>tritici</i> ¹	8	15	8	8	12	3	23
<i>Giocladium</i> spp. ¹	3	6	1	6	0	1	7
<i>Macrophomina petrak</i>	1	0	1	0	1	0	1
<i>Massarina</i> spp.	1	1	0	0	1	0	1
<i>Microdochium bolleyi</i>	9	13	5	5	4	9	18
<i>Microdochium nivale</i> ¹	6	8	2	4	5	1	10
<i>Periconia byssoides</i>	1	0	1	0	0	1	1
<i>Periconia macrospinos</i>	1	0	1	0	0	1	1
<i>Phialophora</i> spp. ¹	3	3	1	0	1	3	4
<i>Phoma</i> spp. ¹	1	1	0	0	1	0	1
<i>Pithomyces</i> spp.	1	1	0	0	0	1	1
<i>Rhizopus oryzae</i>	3	3	1	0	1	3	4
<i>Rhizoctonia</i> spp. ¹	4	2	3	1	2	2	5
<i>Staphylotrichum</i> spp.	1	1	0	0	1	0	1
<i>Trichoderma</i> spp.	2	2	0	0	2	0	2
U1D1 ²	1	0	1	0	0	1	1
U1D2 ²	2	2	0	1	0	1	2
U1D3 ²	5	2	3	2	3	0	5
U1D4 ²	3	4	0	0	3	1	4
U1D5 ²	6	6	3	3	6	0	9
U1D6 ²	2	1	1	1	0	1	2
U1D7 ²	2	3	2	2	1	2	5
U1D8 ²	1	1	0	0	0	1	1
U1D9 ²	1	1	0	0	1	0	1

¹Recorded as pathogenic on wheat or grasses in New Zealand (Pennycook 1989).

²U1D1 to U1D9 are culture morphotypes, which were non-sporulating and were unidentified.

Co-occurrence of *Gaeumannomyces graminis* and other fungi

Thirteen fungal species were isolated along with *Ggt* from individual segments of *E. repens* tissues (Table 4). Most of these were isolated from rhizomes (14 counts) and from tissues with slight lesions (11 counts). Of these species, six have been recorded as

pathogenic on wheat or grasses in New Zealand (Pennycook 1989). Numbers of co-occurrences with *Ggt* were similar for the three sites. *Microdochium nivale* and *M. bolleyi* co-occurred with *Ggt* most frequently (three counts each) (Table 4).

TABLE 3: Isolation frequency of *Gaeumannomyces graminis* var. *tritici* from *Elytrigia repens* tissues (rhizomes and roots) showing dark lesions (DL), slight lesions (SL) and no lesion (H), collected from three field sites (Sites I, II and III).

Tissue type	Lesion type	Site I	Site II	Site III	Total Counts
Rhizome	DL	2	1	2	5
	SL	0	5	5	10
	H	0	0	0	0
Root	DL	2	1	0	3
	SL	1	1	0	2
	H	0	0	3	3
Total counts		5	8	10	23

TABLE 4: Number of co-occurrences of *Gaeumannomyces graminis* var. *tritici* with other fungi isolated from the same piece of *Elytrigia repens* rhizome (Rhi) or root (R) showing similar lesion symptoms. Data are summarised for three field sites (Sites I, II and III) and six sampling occasions.

Fungus	Counts	Lesion	Tissue	Site	Sampling ³
<i>Acremonium</i> spp. ¹	1	SL	R	I	S5
<i>Alternaria</i> spp.	1	DL	Rhi	I	S3
<i>Fusarium culmorum</i> ¹	2	DL	Rhi	II	S3
		DL	Rhi	III	S4
<i>Fusarium oxysporum</i> ¹	2	DL	Rhi	III	S4
		SL	Rhi	III	S6
<i>Microdochium nivale</i> ¹	3	DL	Rhi	II	S3
		DL	Rhi	III	S4
		SL	Rhi	II	S4
<i>Macrophomina petrae</i>	1	SL	R	I	S5
<i>Microdochium bolleyi</i>	3	SL	Rhi	II	S2
		DL	Rhi	I	S3
		SL	R	I	S5
<i>Phialophora</i> spp. ¹	1	SL	Rhi	II	S2
<i>Phoma</i> spp. ¹	1	SL	Rhi	III	S6
<i>Rhizopus oryzae</i>	1	H	R	III	S3
U1D3 ²	2	SL	R	II	S3
		DL	Rhi	III	S4
U1D4 ²	1	SL	Rhi	II	S2
U1D5 ²	1	SL	R	I	S5
Total Counts		DL=8	Rhi=14	I=6	S2=3
		SL=11	R=6	II=7	S3=6
		H=1		III=7	S4=5
					S5=4
					S6=2

¹Recorded as pathogenic on either wheat or grasses in New Zealand (Pennycook 1989).

²U1D3, U1D4 and U1D5 are culture morphotypes, which were non-sporulating and were unidentified.

³Sampling occasions S1 to S3 refer to sampling made on 22 Oct, 12 Nov, and 4 Dec 2002 respectively; S4 to S6 refer to sampling made on 8 Jan, 10 Feb, and 7 Mar 2003 respectively.

DISCUSSION

The diverse group of fungi isolated from rhizomes and roots of *E. repens* suggests that *Ggt* is not the only fungus associated with this grassy weed. Other soil-borne fungi recorded as pathogenic to wheat and grasses in New Zealand could also be associated with this host. The grass persists in the cereal break and rotation better than most other grasses and may act as a bridging species for both pathogen and competitors (Deacon 1974). Decaying *E. repens* rhizomes could also become available to other pathogens, such as *Fusarium culmorum*.

The predominance of *F. oxysporum* and *F. culmorum* in *E. repens* indicates that this host supports these fungi. *Fusarium oxysporum* is a common member of the root zone mycoflora of a number of plants and has the ability to exist as a saprophyte, degrading lignin and complex carbohydrates associated with soil organic debris (Thornton 1965). This fungus is also a pervasive plant endophyte that could colonise plant roots (Kistler 2001). On the other hand, *F. culmorum* is a known dominant coloniser of dead *E. repens* (Penn & Lynch 1981). This could be why these two fungi were isolated in abundance from *E. repens*.

Microdochium bolleyi (Kirk & Deacon 1987; Lascaris & Deacon 1991), *Phialophora* spp., *F. oxysporum* (Wong 1981) and *Trichoderma* spp. (Simon 1989) have been shown to be potential biocontrol agents for *Ggt*, and these fungi were all isolated from the *E. repens* samples collected in the present study. *Microdochium bolleyi* was the only known non-pathogenic fungal species isolated in abundance (9 of 18 samples) (Table 2).

The high isolation numbers of *Ggt* from *E. repens* (23 isolations) indicated the potential role of this grass in perpetuating take-all, due not so much to its susceptibility to infection as to its perennial and vigorous growth habit. The hyphae of *Ggt* might also exist in a more active pathogenic form as inoculum when living in and on rhizomatous *E. repens* than when living saprophytically on decaying residues of other host plants (Nilsson 1981).

The large isolation frequency of fungi (29 species) from the *E. repens* rhizomes and from tissues showing slight or dark lesions (Table 2), and the strong associations of some fungal species with lesion types (*F. oxysporum* and UID5 with SL, and *F. oxysporum* and *F. culmorum* with DL), show that *Ggt* might not be the only fungus causing lesions on the plant tissues investigated. Skipp & Christensen (1981) found that *F. culmorum*, *F. oxysporum*, *Acremonium* spp., *Gliocladium* spp. and *Phoma* spp. were among the fungi capable of causing lesions on the roots of white clover. The observations in the present study correspond with the dominating fungal species isolated from the *E. repens* rhizomes with lesions and those of the total isolation frequency counts with the exception of *M. bolleyi*. The browning of cortical cell walls in the roots, which is caused by the thickening and lignification associated with resistance of plant tissues to invasion by pathogens (Penrose 1987), might also have caused lesions. Penn & Lynch (1981) noted that decaying *E. repens* releases phytotoxins such as ethylene, steam-volatile fatty acids and acetic acid. The mobilisation of nitrogen by other decomposer micro-organisms could contribute to the adverse effects of the pathogenic fungus *F. culmorum* on cereal growth.

Runner hyphae of *Ggt* colonise root surfaces and penetrate into root cortices, so the chances of isolating *Ggt* from both lesioned and healthy root tissues would be similar. Any initial or early infection on the healthy roots might not be severe enough or too early to cause formation of lesion as the browning of tissues could come from both the mycelium (consists of brown, thick-walled macrohyphae) and a response to the presence of competing micro-organisms (Skou, 1981; Penrose 1987). The results of the present study suggest that rhizomes are more resistant to *Ggt* than roots, with hyphae in rhizomes restricted to lesions. However, further colonisation of *E. repens* rhizomes may occur following the application of glyphosate or during natural senescence. If glyphosate is applied to *E. repens*, the roots would break down first, but the slower-decaying rhizomes would remain as a source of *Ggt* inoculum. The relatively high isolation incidence of *Ggt* from Site III (10 counts) (Table 3) suggests that this site would have the greatest risk of take-all in a wheat crop grown at the site.

The effects of take-all on wheat yields depend on the growth stages at which severe disease occurs. Severe infection at early growth stages can affect plant survival, tillering and grain numbers, while severe infection at anthesis will affect grain weights (Hornby 1998). The greatest frequency of *Ggt* isolation (12 incidences) on the third sampling occasion coincided with the estimated time of anthesis for some autumn-sown wheat cultivars in New Zealand. It is likely, that *Ggt* inoculum from living *E. repens* within wheat crops would develop too late to make a major contribution to a take-all epidemic. However, when these infected *E. repens* start to decay or die naturally or following glyphosate application, they could act as a source of inoculum for subsequent wheat crops and contribute to a take-all epidemic.

The fungal species most frequent co-occurring with *Ggt* were *Microdochium nivale* and *M. bolleyi* (Table 4). As *M. bolleyi* has never been recorded as pathogenic to wheat or grasses in New Zealand, it is worth investigating as a potential take-all biocontrol agent. *Microdochium bolleyi* was one of the two fungal species (the other being *Rhizopus oryzae*) associated strongly with H tissues from the 18 samples in our study, and has been considered one of the potential biocontrol agents for take-all (Kirk & Deacon 1987; Lascaris & Deacon 1991). The small number of samples (18) in this study means that any correlation between *Ggt* and *M. bolleyi* cannot be established with any confidence, and so the contribution of *M. bolleyi* to the dynamics of *Ggt* inoculum levels is not conclusive. There is a need to look at the interactions between these two fungi in larger studies in the future. The presence of other wheat pathogens such as *F. culmorum* and *M. nivale* (Pennycook 1989) may also affect *Ggt* inoculum levels, either directly or by competing with *M. bolleyi*. The interactions between these species have yet to be adequately described.

Although the results of this study must be interpreted with caution due to the small number of samples, and the lack of lesions on tissues found in some of these, useful conclusions can still be drawn. *Ggt* was not the only fungus associated with *E. repens* and not all the lesions on the tissues were caused by this fungus. As *M. bolleyi* was the only known non-pathogenic fungus occurring along with *Ggt* (Table 4) it could be a potential biocontrol agent. *Elytrigia repens* could be an inoculum source for take-all in wheat since *Ggt* survives well in the rhizomes, and may further colonise dying rhizomes. Future studies could consider *E. repens* within wheat crops to better relate the effect of *M. bolleyi* on *Ggt* inoculum levels, and the direct effects of glyphosate on *Ggt* survival in decaying *E. repens*.

ACKNOWLEDGMENTS

Dr. Nick Waipara assisted with fungal identification. This project was funded by the New Zealand Foundation for Research, Science and Technology.

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