SHORT COMMUNICATION

Control of pathogenic PAC strains by non-pathogenic PAC strains *in planta* does not correlate with higher competitiveness of non-pathogenic PAC strains *ex planta*

Ivo Hugentobler • Vanessa Reininger • Thomas N. Sieber

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Abstract Ascomycetes of the Phialocephala fortinii s.l.-Acephala applanata species complex (PAC) are frequent root endophytes of forest trees. Roots are colonized by multiple PAC genotypes that interact, and recent findings indicate that adverse effects on plant performance caused by pathogenic PAC strains are attenuated by non-pathogenic PAC strains. However, it was not known if this "self-control" works only in planta, or also ex planta, i.e., prior to infection during saprotrophic life of the PAC. Interactions between PAC strains were therefore studied in a plant-free system on malt extract agar. The mycelia of two pathogenic (A and T1) and two nonpathogenic (B and C) PAC strains were mixed pairwise 5:1, 1:1 and 1:5 (fresh weight ratios) and incubated at 15 and 25 °C. Mycelial biomass of each strain was measured after 2 and 8 weeks. The combination of strains and the mixture ratio had a significant effect on strain biomass, whereas temperature influenced only the biomass of pathogenic strain T1. Biomass production of strain T1 was inhibited by all other strains, whereas biomass production of the other pathogenic strain A was significantly stimulated by the two nonpathogenic strains. This contrasts strongly with results from a previous experiment in planta using strains A, B and C, because the two non-pathogenic PAC strains successfully inhibited the pathogenic strain, probably by space occupation or the induction of host resistance. Therefore, it is impossible

I. Hugentobler Naturkonzept AG, 8266 Steckborn, Switzerland

V. Reininger Plant and Soil Ecology Lab, Algoma University, Sault Ste. Marie, ON P6A 2G4, Canada

T. N. Sieber (⊠) Institute of Integrative Biology (IBZ), ETH Zurich, 8092 Zurich, Switzerland e-mail: thomas.sieber@env.ethz.ch to predict the outcome of PAC-PAC interactions *in planta* based on the results gained from interactions *ex planta*.

Keywords Microsatellite-based quantification · Mycelial biomass · Competition · Root endophytes · Dark septate endophytes (DSE)

Introduction

Ascomycetes of the Phialocephala fortinii s.l.-Acephala applanata species complex (PAC) are ubiquitous tree-root endophytes and dominate the endophytic assemblages in roots of conifers and members of the Ericaceae in the Northern hemisphere (Addy et al. 2000; Queloz et al. 2011; Grünig et al. 2007, 2008a, b; Sieber 2002; Ahlich and Sieber 1996; Holdenrieder and Sieber 1992). PAC form multicellular sclerotia and chlamydospores in phellem cells of roots exhibiting secondary growth and in cortex cells of primary roots (Tellenbach et al. 2010; Sieber and Grünig 2013). PAC can behave as commensals, mutualists or opportunistic pathogens, depending on genetic traits and environment, and may affect plant performance (Grünig et al. 2008b). However, mutualistic behaviour in terms of plant growth stimulation was not exhibited by any of more than 30 PAC strains (Tellenbach et al. 2011). All strains reduced the host's growth increment, but some strains provided control of soil-borne pathogens and significantly reduced plant mortality (Tellenbach et al. 2011; Tellenbach and Sieber 2012).

PAC species and genotypes live spatially closely together in root cells, making competition for space and nutrients highly probable (Sieber and Grünig 2006; Grünig et al. 2008b; Queloz 2008; Queloz et al. 2005; Reininger et al. 2012). The mechanisms of competition may include the production of allopathic metabolites and toxins (antibiotics) inhibitory to other PAC species or genotypes, mycoparasitism, occupation of infection sites and the induction of systemic resistance (Harman et al. 2004; Pareja-Jaime et al. 2010). However, mycoparasitism or formation of barrier or inhibition zones between different PAC genotypes interacting on cellophane overlaid on water agar could never be observed (Sieber, unpublished). Colonies of different genotypes merge and hyphal growth is mutually limited only physically by the presence of hyphae, or biochemically by nutrient depletion. Thus, PAC species probably compete directly for space and nutrients on a first-come, first-served basis. Nevertheless, there seems to be a kind of "self control" among PAC genotypes, i.e., pathogenic strains are controlled by non-pathogenic strains as demonstrated recently by Reininger et al. (2012). The growth increment of plants singly inoculated with a pathogenic PAC strain was strongly reduced compared to that of plants dually inoculated with the same pathogenic strain and a nonpathogenic strain of PAC, indicating that non-pathogenic PAC strains successfully compete with pathogenic strains, probably by space occupation or the induction of systemic resistance. PAC "self control" in planta seems to work independently of temperature (Reininger et al. 2011a, 2012), an important finding particularly with regard to global warming. However, the contribution of the interaction between the PAC strains during the saprotrophic phase outside the host (ex planta) prior to the infection of the roots to this "self control" system could not be differentiated from the contribution of the interaction between the PAC strains during the biotrophic phase inside the host (in planta). Therefore, a plant-free experiment was designed to measure the pure effect of interactions between PAC strains ex planta on mycelial biomass production of PAC.

Materials and methods

Strain information and setup of experiment to test mycelial interactions

Four PAC strains originating from roots collected at the same location (Bödmerenwald, Switzerland, $46^{\circ}58'57.13''$ N/8°49' 23.90" E) but differing in pathogenicity were used in this experiment (Table 1). The strains were incubated on 2 % (*w*/*v*) malt extract agar (MEA; 20 g l⁻¹ malt extract (Hefe Schweiz AG, Stettfurt, Switzerland), 15 g l⁻¹ agar) at 20 °C in the dark. After 2 weeks, one colonized plug of agar (diameter 4 mm) from the margin of the growing colony was transferred to 50 ml of 2 % malt broth (20 g l⁻¹ malt extract) in a 100-ml Erlenmeyer flask per strain and incubated at 20 °C in the dark on a rotary shaker at 90 r.p.m. After 20 days, the mycelium was harvested under sterile conditions by pouring the content of the Erlenmeyer flask into a sieve. The retained mycelium was washed twice with sterile water and blotted dry. Mycelia of two strains were mixed at ratios of 5:1, 1:1 and

1:5 (w/w) for each of the six possible combinations of the four strains. The total mycelial fresh weight of each mixture amounted to 0.6 g. Correspondingly, 0.6 g mycelium of a pure culture of each of the four strains served as controls. The mycelia were suspended in 10 ml sterile water and homogenized with a blender for 10 s. Then, another 30 ml of sterile water was added to obtain a final mycelium concentration of 15 g l^{-1} , and 1.4 ml of this suspension was distributed homogenously on the surface of 20 ml MEA in each of four Petri dishes per strain, strain combination and mixture ratio. Two of the four Petri dishes were incubated at 15 °C and the other two at 25 °C. Mycelium was harvested after 2 and 8 weeks of incubation as follows. Per Petri dish, three rectangular colonized pieces of MEA measuring 10×20 mm in surface view were cut with a scalpel and served as replicates. The uppermost colonized 1 mm was then removed from the rectangular MEA pieces, frozen at -80 °C, freeze-dried and DNA extracted as described previously (Grünig et al. 2003). Amplification of microsatellites and microsatellite fragment analysis occurred according to Queloz et al. (2010), and mycelial weight estimation according to Reininger et al. (2011b) and Reininger and Sieber (2012, 2013) (see below).

Calibration of the microsatellite-based quantification method

Multiplex and singleplex PCR for the amplification of microsatellites of PAC has been developed recently, and allele data are available for more than 5,000 PAC strains (Queloz et al. 2010). The suitability of four microsatellite loci (mPF 043, mPF 049, mPF 142B, and mPF 860B) for DNA quantification was tested by Reininger et al. (2011b), and locus mPF 142B showed to be most suitable because this locus produced fewest stutter bands. The same locus was also used in this study and calibration of DNA amounts followed the protocol of Reininger et al. (2011b). The four strains were cultivated in malt broth as described above. The mycelium was harvested and lyophilized. The freeze-dried mycelia of the strain to quantify (target strain 1) and the admixed strain (additional strain 2) were mixed according to the weight ratios (m_1/m_2) 1:14, 3:12, 5:10, 7:8, 9:6, 11:4, 13:2, and 14:1 amounting to a total weight of 15 mg, and a constant amount of 15 mg mycelium (mr) of a third strain (reference strain) was added. Mycelial mixtures were homogenized, DNA extracted as described previously (Grünig et al. 2003), locus mPF 142B amplified by PCR, fragment lengths and peak areas determined (see below). The coefficients (slopes) (β_1 and β_2) of the calibration curves were determined by linear regression exploiting the proportionality of the peak and mycelial ratio according to Reininger et al. (2011b): $(p_r/p_1) \sim (m_r/m_1)$, $(p_r/p_1) \sim (m_r/m_1)$ p_2)~(m_r/m₂), respectively (p_r =peak area of the reference strain; p₁, p₂ peak areas of the target strain 1 and the additional strain 2). The resulting equations were used to estimate the mycelial weight of m1 and m2 in the colonized pieces of MEA.

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Table

Strain label	Culture coll accession m	lection umbers	PAC species	Pathogenicity ^c	Driginal host	Allele length of locus mPF_142B	Mycelial I mycelium	oiomass [m per g subs	g trate] of]	Stimulation living sprue	/inhibition c ce roots at 18	f endophytic myce 3 °C and 23 °C du	elial growth ally nocula	t of the strain in the ted with strain ^f	first column in
						[40]	su and in the su and in the su and success of the subscription of	of incubation is (1:1) at 2 is with stra	n in peat: 0 °C in in ^e	18 °C			23 °C		
	ETH ^a (CBS^{b}					A	в	0	A	в	0	A	B	0
A	6_2_7v	134503	Phialocephala subalmina	pathogenic	Vaccinium myrtillus	174	I	6.2	- 1.9		inhibition	slight inhibition	1	slight inhibition	slight inhibition
В	6_37_6v	134504	Phialocephala	not pathogenic	Vaccinium	162	1.1	Ι	2.8	no effect	I	inhibition	no effect	I	nhibition
С	7_45_5	119281	suoaipna Phialocephala	not pathogenic	myruuus Picea abies	154	0.7	1.2	-	no effect	no effect		no effect	no effect	l
T1	T1_52_2	134898	Jorunu 5.5. Acephala applanata	pathogenic	Picea abies	141	n.a. ^g	n.a.	n.a.	n.a. ^g	n.a.	n.a.	n.a. ^g	n.a.	ı.a.
^a ETH Zui	rich, Zurich	, Switze	rland												
° CBS-KN	JAW Funga	d Biodiv	versity Centre, Utrec.	ht. The Netherl	ands										

^c Pathogenicity on spruce seedlings according to Tellenbach et al. (2011)

^d according to Queloz et al. (2010)

^e according to Reininger (unpublished)

^f according to Reininger et al. (2012)

^g not available

Amplification of microsatellites by competitive PCR

Locus mPF_142B was amplified by PCR according to Queloz et al. (2010) in 15 μ l volumes containing 2 μ l 1:50 or 1:500 diluted DNA, 50 mM KCl, 10 mM Tris–HCl, 1.5 mM MgCl₂, 200 μ M dNTPs (Amersham Pharmacia Biotech), 0.4 μ M of each primer (F, GCTTTCACATCACCATCCAG; R, GGTG AGTTGGTTGCGAGTTT) and 0.3 U Taq polymerase (Amersham Pharmacia Biotech). The running conditions were 2 min at 94 °C followed by 36 cycles of denaturation for 30 s at 94 °C, annealing for 30 s at 53 °C, and extension for 30 s at 72 °C (followed by a final extension step of 10 min at 72 °C).

Microsatellite fragment analysis

Fifteen-fold diluted triplicates were prepared from each PCR reaction: 4 μ l of the dilutions were mixed with 9.05 μ l Hi-DiTM formamide and 0.25 μ l GeneScanTM 500 LIZTM (Applied Biosystems). Fragment lengths and the peak area, i.e., the amount of PCR product, of each fragment, were measured using an ABI 3730x1 DNA analyser (Applied Biosystems) and analysed using the GeneMapper v. 4.0 software (Applied Biosystems) (Queloz et al. 2010).

Statistical analyses

The effects of strain combination, mixture ratio, temperature and duration of incubation on mycelial dry weight [used synonymously: 'mycelial density', 'mycelial biomass'; mg freeze-dried mycelium per 200 mm³ ($10 \times 20 \times 1$ mm) of MEA] of each strain was determined using ANOVA:

$$y_{ijklm} = \mu + \alpha_i + \beta_j + \gamma_k + \delta_l + e_{ijklm} \tag{1}$$

- *i* 1, 2, 3, 4 (strain combination, e.g. A, A & B, A & C, A & D)
- *j* 1, 2, 3 (mixture ratio: 1:5, 1:1, 5:1)
- k 1, 2 (temperature: 15 °C, 25 °C)

- *m* 1, 2, 3, 4, 5, 6 (six replicates)
- y_{ijklm} mycelial dry weight of the m^{th} replicate of the i^{th} combination of strains mixed at the j^{th} ratio incubated for the l^{th} duration at the k^{th} temperature
- μ overall mean mycelial dry weight
- α_i effect of the strain combination
- β_j effect of the mixture ratio
- γ_k effect of temperature
- δ_l effect of the duration of incubation

 e_{ijklm} random error.

Interactions not shown in formula (1).

Goodness of fit and normal distribution of residuals were tested using residual analyses. If necessary, the response variable 'Mycelial dry weight' (y_{ijklm}) was transformed. The full models were reduced deleting non-significant factors. Full and reduced models were compared using chi-square tests to avoid loss of fit. Tukey's HSD post-hoc test was used for pairwise comparisons. All statistical analyses were performed using R (R Development Core Team 2010).

Results

Macroscopically, all cultures looked uniform, and there was barely a difference between dual and single cultures, indicating that the mycelia had been homogeneously distributed all over the surface of the medium during inoculation. No demarcation lines or barrier zones could be recognized to differentiate genotypically different thalli.

Calibration of the microsatellite-based quantification method was successful for all strain mixtures, since the additional strain (strain 2) did not have a disturbing effect on the estimation of the biomass of the target strain (strain 1) in any of the strain mixtures. None of the β_2 coefficients deviated significantly from zero, i.e., the bivariate regressions could be reduced to univariate regressions. All β_1 coefficients differed significantly from zero and assumed values close to 1. Thus, the resulting calibration curves allowed estimating the mycelial weight of any strain (m₁ and m₂) in any of the colonized pieces of MEA (Reininger et al. 2011b).

The factors 'strain combination', 'mixture ratio' and the interaction between these two factors had a significant effect on the biomass of all strains (Table 2). Biomass was highest if strains were cultured singly, except for strain A, which grew better in combination with strain B or C (Fig. 1a; see below). In addition, 8 weeks compared to 2 weeks of incubation led to greater biomass of strains A, B and T1, but not of strain C. T1 was the only strain exhibiting a significant temperature effect. It accumulated more biomass at 25 °C than at 15 °C. However, although not significant, temperature had to be retained in the models for strains A and B to avoid loss of fit. Strain B was influenced by an intricate network of interactions between all four factors.

Strains significantly differed in competitiveness. Strain A was most competitive and accumulated more biomass per volume of substrate (biomass density) than any other strain independently on the strain combination, mixture ratio, duration of incubation and temperature (Fig. 1). In contrast to single culture, growth of strain A was statistically significantly stimulated in dual culture with strain B or C at a mixture ratio of A:B=A:C=5:1 (Fig. 1a). Even at a mixture ratio of 1:5, biomass of A was always greater than that of the other strain. In contrast, presence of strain T1 did not lead to stimulation of A (Fig. 1a). Strain B was significantly inhibited by A and C if

 Table 2
 Results of the analyses

 of variance showing the best
 fitting, reduced model for the

 mycelial dry weight of each strain
 fitting

Strains and factors	Df	Sum of Squares	Mean Square	F value	р	Significance level ^a
Strain A						
Strain combination (1)	2	7.078	3.5388	12.8257	< 0.00001	***
Mixture ratio (2)	2	19.312	9.6559	34.9961	< 0.00001	***
Duration of incubation (3)	1	6.8	6.7996	24.6439	< 0.00001	***
Temperature (4)	1	0.036	0.0361	0.1307	0.7181	
Interaction $(1) \times (2)$	4	7.402	1.8504	6.7065	0.00005	***
Residuals	188	51.872	0.2759			
Strain B						
Strain combination (1)	2	26.3227	13.1614	290.2111	< 0.00001	***
Mixture ratio (2)	2	18.2748	9.1374	201.4818	< 0.00001	***
Duration of incubation (3)	1	0.2727	0.2727	6.0122	0.01527	*
Temperature (4)	1	0.0222	0.0222	0.4899	0.48499	
Interaction $(1) \times (2) \times (3) \times (4)$	29	10.9865	0.3788	8.3536	< 0.00001	***
Residuals	162	7.3469	0.0454			
Strain C						
Strain combination (1)	2	0.8404	0.4202	5.8547	0.00342	**
Mixture ratio (2)	2	8.101	4.0505	6.4372	< 0.00001	***
Interaction $(1) \times (2)$	4	1.9392	0.4848	6.7549	0.00005	***
Residuals	187	13.421	0.0718			
Strain T1						
Strain combination (1)	2	6.1635	3.08173	71.1574	< 0.00001	***
Mixture ratio (2)	2	4.7556	2.37778	54.903	< 0.00001	***
Duration of incubation (3)	1	0.3276	0.32761	7.5645	0.00655	**
Temperature (4)	1	0.2137	0.21373	4.9351	0.02755	*
Interaction $(1) \times (2)$	4	1.0706	0.26766	6.1803	0.00011	***
Residuals	182	7.8822	0.4331			

^a significance levels: * 0.05≥ p>0.01; ** 0.01≥p>0.001; *** 0.001≥p

mixed at B:A=1:5, B:C=1:5 or B:C=5:1 (Fig. 1b). Strain C was significantly inhibited by all three strains if mixed at C:A=C:B=C:T1=1:5, but not at a mixture ratio of 5:1 (Fig. 1c). T1 was inhibited by all other strains independently on the mixture ratio (Fig. 1d).

Discussion

The microsatellite-based method developed by Reininger et al. (2011b) proved to be reliable to measure fungal biomass of each strain in strain mixtures, because both the correlation coefficients (\mathbb{R}^2) and the slopes (coefficient β_1) of the regression lines were close to 1, indicating excellent fit of measured values and model. Strain A produced denser mycelia on malt extract agar than any other PAC strain, and it was the only strain showing significant growth stimulation in the presence of other strains (Fig. 1). Similarly, growth of strain A was stimulated on 1:1 (ν/ν) peat:vermiculite by the presence of strain B or C in another study (Table 1) (Reininger, unpublished). Under saprotrophic conditions, growth of A seems to

be stimulated by the presence of other PAC strains. This contrasts with the performance of A under biotrophic conditions in roots. Growth of the endophytic mycelium of A is inhibited if the roots are simultaneously colonized by other PAC strains (Table 1) (Reininger et al. 2012).

In single culture, formation of denser mycelia was positively correlated with pathogenicity, i.e., the two pathogenic strains A and T1 produced denser mycelia than the nonpathogenic strains B or C (Fig. 1). However, in dual culture there was no such correlation since growth of A was stimulated, whereas growth of T1 was inhibited by the presence of any other PAC strain (Fig. 1a and d).

Predictability of the endophytic biomass accumulating in dually inoculated plants by the mycelial density developing in plant-free dual culture is strain-dependent. Prediction was possible for dual cultures of strains B and C, but not for those including strain A. For example, presence of non-pathogenic strain B stimulated growth of pathogenic strain A on malt extract agar in the current experiment and in peat:vermiculite, but inhibited growth in living spruce roots (Fig. 1a, Table 1) (Reininger et al. 2012), indicating that strain A is a strong



Fig. 1 Bar charts depicting the effects of the factors '*Strain combination*' and '*Mycelial mixture ratio*' on the *mycelial dry weight* [*mg*] of the target (*hatched areas*) and the additional (*blank areas*) strain after 2 weeks of incubation on MEA at 25 °C. (**a**) *target strain A*, (**b**) *target strain B*, (**c**)

target strain C, (d) *target strain T1*. Different letters above the bars indicate significantly different effects of the treatments on mycelial dry weight of the target strain (Tukey's HSD)

competitor on dead organic matter but not in living plant tissues. This is probably the reason why this strain behaves as a necrotrophic organism, i.e., it must kill the plant tissue to exploit it. However, strain A is only able to kill if no other PAC strain is present (Reininger et al. 2012; Tellenbach et al. 2011). In planta, non-pathogenic PAC strains B and C successfully compete with pathogenic strain A, probably by space occupation or the induction of host resistance, thereby keeping endophytic biomass of pathogenic strains below the threshold above which plant growth is inhibited significantly (Sieber 2007). In contrast to strain A, mycelial densities resulting from interactions between the non-pathogenic strains B and C on malt extract agar were mostly congruent with interactions between the two strains in planta. Growth of B was significantly inhibited by the presence of C, both on malt extract agar in the current experiment and in planta (Fig. 1b) (Reininger et al. 2012). Pathogenic strain T1 behaved rather like nonpathogenic strains B and C on malt extract agar, i.e., completely different than pathogenic strain A. Biomass accumulation of T1 was strongly reduced by the presence of any of the other three strains (Fig. 1). Performance of T1 in plants dually inoculated with T1 and another PAC strain has never been tested, and thus, a comparison *ex planta* and *in planta* is not possible for this strain.

In summary, predictability of the mycelial densities resulting from a tripartite PAC-PAC-plant interaction by the outcome of a dipartite interaction between two PAC strains in a plant-free system depends on the strains involved. Consequently, the outcomes of interactions in dual PAC-PAC systems are not always additive, i.e., the results of a tripartite interaction is not simply the sum of the results of all dual interactions. Interacting PAC genotypes do not show any signs of inhibition (barrier zone formation, antibiosis), stimulation or mycoparasitism when grown on artificial media *ex planta*. Growth seems only to be limited by nutrient depletion of the medium, and exploitation of the substrate occurs on a firstcome, first-served basis. Hyphae intermingle in the contact zone and grow as far into the others' "territory" as nutrients support growth. Thus, the mechanisms responsible for the attenuation of adverse effects on plant growth caused by pathogenic PAC by non-pathogenic ones remain enigmatic and require further studies.

References

- Addy HD, Hambleton S, Currah RS (2000) Distribution and molecular characterization of the root endophyte *Phialocephala fortinii* along an environmental gradient in the boreal forest of Alberta. Mycol Res 104(10):1213–1221
- Ahlich K, Sieber TN (1996) The profusion of dark septate endophytic fungi in non-ectomycorrhizal fine roots of forest trees and shrubs. New Phytol 132:259–270
- Grünig CR, Linde CC, Sieber TN, Rogers SO (2003) Development of single-copy RFLP markers for population genetic studies of *Phialocephala fortinii* and closely related taxa. Mycol Res 107(11):1332–1341
- Grünig CR, Brunner PC, Duò A, Sieber TN (2007) Suitability of methods for species recognition in the *Phialocephala fortinii–Acephala applanata* species complex using DNA analysis. Fungal Genet Biol 44:773–788
- Grünig CR, Duò A, Sieber TN, Holdenrieder O (2008a) Assignment of species rank to six reproductively isolated cryptic species of the *Phialocephala fortinii* s. 1.-*Acephala applanata* species complex. Mycologia 100(1):47–67
- Grünig CR, Queloz V, Sieber TN, Holdenrieder O (2008b) Dark septate endophytes (DSE) of the *Phialocephala fortinii* s.l.—*Acephala applanata* species complex in tree roots: classification, population biology, and ecology. Botany 86(12):1355–1369. doi:10.1139/b08-108
- Harman GE, Howell CR, Viterbo A, Chet I, Lorito M (2004) *Trichoderma* species—opportunistic, avirulent plant symbionts. Nat Rev Microbiol 2(1):43–56
- Holdenrieder O, Sieber TN (1992) Fungal associations of serially washed healthy non-mycorrhizal roots of *Picea abies*. Mycol Res 96(2): 151–156
- Pareja-Jaime Y, Martin-Urdiroz M, Roncero MIG, Gonzalez-Reyes JA, Roldan MDR (2010) Chitin synthase-deficient mutant of *Fusarium* oxysporum elicits tomato plant defense response and protects against wild-type infection. Mol Plant Pathol 11(4):479–493
- Queloz V (2008) La face cachée du Creux du Van: Présence des endophytes racinaires *Phialocephala fortinii* s.l. et *Acephala applanata* sur le pergélisole du Creux du Van. Actes de la societé jurassienne d'émulation 2007:107-126

- Queloz V, Grünig CR, Sieber TN, Holdenrieder O (2005) Monitoring the spatial and temporal dynamics of a community of the tree-root endophyte *Phialocephala fortinii* sl. New Phytol 168(3):651–660
- Queloz V, Duo A, Sieber TN, Grünig CR (2010) Microsatellite size homoplasies and null alleles do not affect species diagnosis and population genetic analysis in a fungal species complex. Mol Ecol Resour 10(2):348–367. doi:10.1111/j.1755-0998.2009.02757.x
- Queloz V, Sieber TN, Holdenrieder O, McDonald BA, Grünig CR (2011) No biogeographical pattern for a root-associated fungal species complex. Glob Ecol Biogeogr 20(1):160–169. doi:10.1111/j.1466-8238.2010.00589.x
- R_Development_Core_Team (2010) R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna
- Reininger V, Sieber TN (2012) Mycorrhiza reduces adverse effects of dark septate endophytes (DSE) on growth of conifers. Plos One 7(8):e42865. doi:10.1371/journal.pone.0042865
- Reininger V, Sieber TN (2013) Mitigation of antagonistic effects on plant growth due to root co-colonization by dark septate endophytes and ectomycorrhiza. Environ Microbiol Rep 5(6):892–898. doi:10.1111/ 1758-2229.12091
- Reininger V, Grünig CR, Sieber TN (2011a) Are plant communities shaped by fungal root endophytes? Phytopathology 101(6): S151–S152
- Reininger V, Grünig CR, Sieber TN (2011b) Microsatellite-based quantification method to estimate biomass of endophytic *Phialocephala* species in strain mixtures. Microb Ecol 61(3):676–683. doi:10. 1007/s00248-010-9798-z
- Reininger V, Grünig CR, Sieber TN (2012) Host species and strain combination determine growth reduction of spruce and birch seedlings colonized by root-associated dark septate endophytes. Environ Microbiol 14(4):1064–1076. doi:10.1111/j.1462-2920. 2011.02686.x
- Sieber TN (2002) Fungal Root Endophytes. In: Waisel Y, Eshel A, Kafkafi U (eds) Plant roots : The Hidden Half. 3rd edn. Marcel Dekker, New York, pp 887–917
- Sieber TN (2007) Endophytic fungi in forest trees: are they mutualists? Fungal Biol Rev 21(2/3):75–89
- Sieber TN, Grünig CR (2006) Biodiversity of fungal root-endophyte communities and populations in particular of the dark septate endophyte *Phialocephala fortinii*. In: Schulz B, Boyle C, Sieber TN (eds) Microbial Root Endophytes, vol 9, Soil Biology Series. Springer, Berlin, pp 107–132
- Sieber TN, Grünig CR (2013) Fungal root endophytes. In: Eshel A, Beeckman T (eds) Plant Roots—The Hidden Half, 4th edn. CRC Press, Taylor & Francis Group, Boca Raton, FL, USA, pp 38.31–38.49
- Tellenbach C, Sieber TN (2012) Do colonization by dark septate endophytes and elevated temperature affect pathogenicity of oomycetes? FEMS Microbiol Ecol 82:157–168
- Tellenbach C, Grünig CR, Sieber TN (2010) Suitability of quantitative real-time PCR to estimate the biomass of fungal root endophytes. Appl Environ Microbiol 76(17):5764–5772. doi:10.1128/aem. 00907-10
- Tellenbach C, Grünig CR, Sieber TN (2011) Negative effects on survival and performance of Norway spruce seedlings colonized by dark septate root endophytes are primarily isolate-dependent. Environ Microbiol 13(9):2508–2517. doi:10.1128/aem.00907-10