Eur J Plant Pathol (2011) 131:603–620
DOI 10.1007/s10658-011-9834-y

Dynamics of the root/soil pathogens and antagonists in organic and integrated production of potato

Leszek Lenc · Hanna Kwaśna · Czesław Sadowski

Accepted: 30 June 2011 / Published online: 30 July 2011

Abstract Microbial communities in the root, rhizoplane, and rhizosphere and non-rhizosphere soil in potato, in organic and integrated production systems, were compared at the emergence and flowering phases of plant development. Microorganisms were identified on the basis of their morphology. The dominant groups included *Clonostachys* + *Gliocladium* + *Trichoderma, Fusarium* + *Gibberell*a + *Haematonectria* + *Neonectria*, *Paecilomyces, Penicillium* and *Phoma*. Microbial density at the flowering phase was often significantly greater in roots and non-rhizosphere soil than in the rhizoplane and rhizosphere. Diversity of the communities often remained stable or was greater at the emergence phase. The density of bacteria changed with time. The density of *Pseudomonas* often decreased while *Streptomyces* significantly increased with time. Changes in densities of pathogens and antagonists decreased the suppressiveness of the habitat towards soil-borne potato pathogens at the flowering phase. The study contributes information that will help to: (a) understand the epidemiology of some potato diseases, (b) make decisions on the economic and ecological aspects of chemical control in potato, (c) develop strategies for manipulation of the soil microbial environment as a viable crop management technique, and (d) develop prognosis models for potato diseases in central Europe.

Keywords Biological control · Fungi · Integrated farming · Microbiota · Organic farming · Emergence phase · Flowering phase

H. Kwaśna (✉)
Department of Forest Pathology,
Poznań University of Life Sciences,
Ul. Wojska Polskiego 71 c,
60-625 Poznań, Poland
e-mail: kwasna@up.poznan.pl

L. Lenc · C. Sadowski
Department of Phytopathology and Molecular Mycology,
University of Technology and Life Sciences,
ul. Kordeckiego 20,
85-225 Bydgoszcz, Poland

Introduction

Soil quality and health are central to farming. Soil health has physical, chemical and biological components. Soil health monitoring is rarely practised. In the USA, farmers use test kits to demonstrate effects of management on soil health. An earthworm count and soil respiration are the biological indicators used (Ditzler and Tugel 2002). Soil basal respiration is one of the oldest and still the most frequently used parameter for quantifying microbial activity in soils. It is related to carbon availability and is generally greater at the soil surface (Saffigna et al. 1989). Soil health may, however, be measured with other parameters, including: (a) organic matter or total organic C content, or (b) structure and dynamics of the microbiota (Lemańczyk and Łukanowski 2000; Lemańczyk and Sadowski 2002). Since the microbiota responds

more rapidly to changes in organic matter input or rate of decomposition than to the soil organic matter as a whole (Powlson and Jenkinson 1981; Powlson et al. 1987) it is among the most sensitive indicators of soil quality.

Microbiota in the plant root zone are determined by: (a) root exudates, which vary qualitatively and quantitatively during plant development, (b) physical and chemical properties of soil, which vary continuously because of cultivation practices, (c) synthetic and organic fertilizers and chemical pesticides applied, and (d) relationships among microorganisms. The role of the pathogenic microbiota is well known. The saprotrophic microbiota performs only beneficial functions, including: (a) decomposition and transformation of organic matter, (b) providing a labile source of nutrients (C, N, P, S), (c) providing a temporary sink for C, N, P, S, (d) establishing bio-geochemical cycles, (e) formation of symbiotic associations with plants, and (f) acting as biological control agents.

The soil microbial biomass responds as a whole to changes in agricultural practices. Changes in structure of the microbiota may lead to: (a) changes in its important functions, (b) early warning of the direction of short- or long-term biochemical processes (Saffigna et al. 1989). Understanding and managing microbial biodiversity, and recognizing its contributions, are essential and crucial to sustainable agricultural development and for overall organization of the ecosystem.

Measurements of microbial activity in soils are based on the presence of intact and active microbial cells. They reflect the physiological state of the organisms. Therefore, counts of organisms can be used to recognize and understand the effects of phenological development of the host plant on the structure of its microbiota. Studies on microbial dynamics are biologically appealing because they: (a) promote biological and epidemiological realism, (b) allow recognition of primary and secondary inoculum potential, and (c) help to model or monitor the spread of disease in a continuously changing habitat.

The objective of this work was to examine and analyse microbial communities of potato at two plant development phases, emergence and flowering, in organic and integrated farming systems. The methods were intended to: (a) indicate shifts within the microbial community structure and functioning, and (b) investigate the impact of environmental fluctuations on density and diversity of the microbiota in potato roots and soil. The ultimate objective is eventually to allow implementation of crop management practices that optimize the soil microbial environment for reduced disease, increased production, and long-term sustainability.

Materials and methods

Description of location

The potato crops were grown in Osiny, Poland (51° 52′ 02″N, 22° 05′ 25″E). The soil was sandy loam, with characteristics given in Table 1. The total field area was 17 ha. It included 5 ha under an organic system and 4 ha under an integrated system, located 200 m apart. In each system potatoes were grown on a 1 ha area in rotation.

Table 1 Characteristics of soil in organic and integrated potato production systems in Osiny

Soil characteristics	2005		2006		2007	
	Organic	Integrated	Organic	Integrated	Organic	Integrated
pH in H_2O	6.31	6.87	6.79	6.64	6.70	6.12
pH in KCl	5.51	6.14	5.95	6.01	6.05	5.64
Humus content (%)	1.54	1.31	1.39	1.25	1.50	1.56
Soil nitrogen NO_3+NH_4 (mg/kg)						
Spring	62.3	87.7	75.8	91.2	66.0	69.4
Autumn	77.8	109.1	88.7	106.9	126.9	128.6
Soil phosphorus P_2O_5 (mg/kg)	7.40	17.13	11.17	15.00	10.69	14.93
Soil potassium K_2O (mg/kg)	5.51	12.53	9.28	13.53	8.87	17.03
Soil magnesium Mg (mg/kg)	6.67	7.30	7.57	9.35	9.71	8.30

Description of cultivation systems

Crop management procedures used in the organic and integrated systems of potato production are given in Table 2. The first cover crop was applied after the wheat harvest. Manure and compost were applied in October, immediately before the winter ploughing, followed by spring planting of potatoes (in the last third of April). In the organic system, copper oxychloride and copper hydroxide were used against fungal pathogens, and *Bacillus thuringiensis* against Colorado beetle (*Leptinotarsa decemlineata* Say). In the integrated system cymoxanil + mancozeb, dimethomorph + mancozeb, metalaxyl-M + mancozeb and chlorine hydroxide of propamocarb + chlorothalonil were applied against pathogens (mostly *Phytophthora*),

Table 2 Crop management procedures used in organic and integrated systems of potato production

Treatment	Organic system	Integrated system
Preceding crops	1999—potato	2000—potato
	2000—spring wheat	2001—spring wheat
	2001—clover+forage grasses	2002—faba bean (*Vicia faba* L.)
	2002—clover+forage grasses	2003—winter wheat
	2003—winter wheat	
Cover crop	2004—faba bean+pea (*Pisum sativum* L.) (350+20 kg/ha)	2004—white mustard (*Sinapis alba* L.) (22 kg/ha)
	2005—white mustard (20 kg/ha)	2005—white mustard (20 kg/ha)
	2006—lupin (*Lupinus* sp.)+ buckwheat (*Fagopyrum esculentum* Moench) + lacy phacelia (*Phacelia tanacetifolia* BENTH.) + white mustard (150+40+5+5 kg/ha)	2006—white mustard (20 kg/ha)
Tillage	2004	2004
	Autumn—winter plough (26–28 cm deep)	Autumn—winter plough (26–28 cm deep)
	2005	2005
	Spring—aggregate tillage (2×), earthing up (4×), harrowing (3×)	Spring—aggregate tillage (2×), earthing up (3×), harrowing (2×)
	Autumn—post-harvest tillage (gruber) (1×), harrowing (1×), winter plough (24–26 cm deep)	Autumn—post-harvest tillage (gruber) (2×), harrowing (2×), winter plough (24–26 cm deep)
	2006	2006
	Spring—aggregate tillage (1×), earthing up (4×), harrowing (1×)	Spring—aggregate tillage (1×), earthing up (2×), harrowing (1×)
	Autumn—first plough (8–10 cm deep), harrowing (2×), winter plough (24–26 cm deep)	Autumn—first plough (6–8 cm deep), harrowing (1×), winter plough (24–26 cm deep)
	2007	2007
	Spring—cultivator tillage (1×), earthing up (2×), harrowing (8×)	Spring—aggregate tillage (1×), cultivator tillage (1×), earthing up (3×), harrowing (5×)
Chemical fertilizers	Spring 2005—potassium sulphate (50 kg K_2O/ha)	Autumn 2004—ammonium nitrate (34 kg N/ha)
	Spring 2006—potassium sulphate (50 kg K_2O/ha)	Spring 2005—complex of NPK 1-4-6- (200 kg/ha)
	Spring 2007—potassium sulphate (75 kg K_2O/ha) + triple superphosphate (96 kg P_2O_5/ha)	Summer 2005—ammonium nitrate (34 kg N/ha)
		Autumn 2005—ammonium nitrate + trace of Mg (40 kg N/ha)

Table 2 (continued)

Treatment	Organic system	Integrated system
		Spring 2006—complex of NPK 2-6-6- (250 kg/ha)
		Summer 2006—ammonium nitrate + trace of Mg (30 kg N/ha)
		Spring 2007—complex of NPK 2-6-6- (250 kg/ha)
Organic fertilizers	Autumn 2004—manure (250 kg/ha)	Autumn 2004—manure (250 kg/ha)
	Autumn 2005—compost (300 kg/ha)	Autumn 2005—compost (320 kg/ha)
	Autumn 2006—compost (200 kg/ha)	Autumn 2006—compost (200 kg/ha)
Chemical control	Copper oxychloride (Miedzian Extra 350 SC)	Cymoxanil + mancozeb (Curzate M 72.5 WP)
	23 June 2005 (2.0 l/ha), 8 August 2005 (2.0 l/ha)	24 June 2005 (2.0 kg/ha)
	22 June 2006 (3.0 l/ha)	10 July 2007 (2.5 kg/ha)
	8 June 2007 (2.5 l/ha)	Dimethomorph + mancozeb (Acrobat MZ 69 WP)
	Copper hydroxide (Funguran-OH 50 WP)	23 July 2005 (2.0 kg/ha)
	23 July 2005 (2.0 kg/ha)	Metalaxyl-M + mancozeb (Ridomil Gold MZ 68 WG)
	10 August 2006 (2.0 kg/ha)	8 August 2005 (2.5 kg/ha)
	18 June 2007 (2.0 kg/ha)	10 August 2006 (2.0 kg/ha)
	Bacillus thuringiensis (Nowodor 02 SC)	18 June 2007 (2.0 kg/ha), 29 July 2007 (2.0 kg/ha)
	17 June 2005 (2.0 l/ha), 30 June 2005 (2.0 l/ha), 6 July 2005 (2.0 l/ha)	Chlorine hydroxide of propamocarb + chlorothalonil (Tattoo C 750 SC)
	22 June 2006 (2.5 l/ha), 26 June 2006 (2.5 l/ha), 3 July 2006 (2.0 l/ha), 12 July 2006 (2.0 l/ha)	30 June 2006 (2.5 l/ha)
		Thiamethoxam (Actara 25 WG)
	8 June 2007 (3.0 l/ha), 12 June 2007 (3.0 l/h), 18 June 2007 (2.5 l/ha)	21 June 2005 (0.06 kg/ha), 06 July 2005 (0.07 kg/ha)
		21 June 2006 (0.08 kg/ha), 26 June 2006 (0.1 kg/ha)
		11 June 2007 (0.08 kg/ha), 20 June 2007 (0.1 kg/ha)
		Fluazifop-P-butyl (Fusilade Forte 150 EC)
		23 June 2005 (1.0 l/ha)
		6 June 2006 (1.0 l/ha)
		Linuron (Afalon dispersion 450 SC) +
		clomazone (Command 480 EC)
		10 May 2006 (1.0+0.1 l/ha)
		15 May 2007 (1.0+0.1 l/ha)
Removing of weeds	Manually during vegetation	Manually during vegetation

thiamethoxam against Colorado beetle, and fluazifop-P-butyl, linuron and clomazone against weeds. Before planting, the soils were ploughed and then cultivated using appropriate machinery to create a deep tilth into which the tubers were planted in ridges and then earthed-up. Solid cattle manure enriched with grasses

and clover was applied. It contained 9.31% organic matter, 0.4% N, 0.1% P, 0.33% K, 0.85% Ca, 0.09% Mg and 0.018% Na.

Collection of samples

Roots and non-rhizosphere soil of potato cv. Drop grown in the organic and integrated systems were collected at the emergence and flowering phases in 2005–2007. Roots were collected from 100 randomly chosen plants from each of the crops. Twenty individual samples of non-rhizosphere soil were collected from the A horizon of the ploughed soil (0–20 cm deep) in each system. Roots were shaken for collection of rhizosphere soil.

Isolation of microorganisms

Roots were washed in running water for 30 min, rinsed 10 times x 3 min in sterile distilled water, dried in sterilized blotting paper, cut into 0.5–1 cm pieces and placed on potato dextrose agar (PDA). Sixty root pieces from each cultivation system were placed in 10 Petri dishes (six pieces per Petri dish). Ten grams of washed 0.5–1 cm root pieces were shaken in a mixture of sterile water (90 ml) + sterile quartz sand (30 g) for 10 min. For isolation of the rhizoplane fungi the suspension was serially diluted and 1 ml of suspension from each 10^{-2} and 10^{-3} dilution was poured into the bottom of an empty Petri dish and covered with liquid (50°C) Johnson-Martin's agar (JMA; 5 g peptone, 1 g KH_2PO_4, 0.5 g $MgSO_4.7H_2O$, 10 g glucose, 0.03 g rose bengal, 0.0025 g aureomycin, 20 g agar, 1 l distilled water). For isolation of rhizosphere soil fungi the individual samples of rhizosphere soil were mixed together, and 10 g of the mixed soil was shaken with 90 ml sterile distilled water for 10 min. The suspension was serially diluted and 1 ml of suspension from each 10^{-4} and 10^{-5} dilution was poured into the bottom of an empty Petri dish and covered with liquid JMA. Thirty replicates from each dilution were made. Isolation of non-rhizosphere soil fungi followed a modification of Warcup's soil plate method (Mańka 1974). A sub-sample of soil (1 g) was mixed with 149 g of sterile quartz sand and 27 mm^3 of mixture were put into a Petri dish and covered with liquid JMA. Thirty replicates from each soil were made. All plates were incubated for 10–30 days at 25°C.

Bacteria were isolated from the 10^{-3} dilution of 1 g of roots or 1 g of rhizosphere or non-rhizosphere soil. Hagedorn and Holt (1975) medium was used for *Arthrobacter* (4 d incubation, 28°C), Simon and Ridge (1974) medium for fluorescent *Pseudomonas* (4 d incubation, 28°C) and Williams and Davies (1965) medium for *Streptomyces* (10 d, 25°C).

Counts of fungi and bacteria were expressed as the number of isolates in a sample or number of colony forming units (*CFU*) in 1 g of roots or 1 g of soil.

Identification of microorganisms

Culture plates were examined microscopically and the identities of sporulating Oomycota and Fungi were confirmed. Non-sporulating colonies were transferred to PDA slants and incubated at 20°C under diffused daylight until sporulation occurred. Oomycota and Fungi were identified by their morphology on PDA, synthetic nutrient agar (SNA), Czapek yeast autolysate agar (CYA) and 2% malt extract agar (MEA).

The rhizoplane is defined as the part of a plant's root that lies adjacent to/in contact with the soil, where many microorganisms adhere to it. The rhizosphere is defined as: (a) the soil environment directly under the influence of living roots, and (b) the niche where complex microbial communities are supported by nutrients released by root exudates, mucilage, and sloughed-off root cells (Kent and Triplett 2002). The density of microbiota is defined as the number of isolates in a sample or number of colony-forming units in 1 g of the sample. Diversity is defined as the number of species in a sample. Frequency is defined as the percentage of isolates of a species in the total number of isolates. A species, or group of related species, were considered as: (a) dominant, where frequency was >5%, and most characteristic of the community, usually determining the presence, abundance, and type of other species; (b) influential but non-dominant, where frequency =1–5%, exerting an important modifying effect; and (c) non-key, where frequency was <1%, and non–essential but contributing to the community. Evaluation of the densities of *Arthrobacter, Pseudomonas* and *Streptomyces* was considered important because *Arthrobacter* is able to fix atmospheric nitrogen, and *Pseudomonas* and certain species of *Streptomyces* are known to enhance plant growth and suppress severity of various diseases, although *S. scabies* is pathogenic. *Alternaria* spp., *Arthrinium phaeospermum, Aspergillus niger* van Tie-

ghem, *Botrytis cinerea* Pers., *Cephalotrichum stemonitis* (Pers.) Nees, *Colletotrichum coccodes, Dendryphion nanum* (Nees ex Fr.) Hughes, *Fusarium* spp., *Geotrichum candidum* Link, *Gibellulopsis nigrescens*, *Gibberella* spp., *Haematonectria haematococca* (Berk. & Broome) Samuels & Rossman, *Neonectria radicicola* (Gerlach & L. Nilsson) Mantiri & Samuels, *Phoma* spp., *Pythium* spp., *Rhizopus* spp., *Thanatephorus cucumeris, Trichothecium roseum* (Pers.) Link and *Ulocladium* spp. were considered as potentially pathogenic, secondary invaders or participants in synergistic enhancement of pathogenicity. *Acremonium* spp., *Aureobasidium pullulans, Chaetomium cochlioides* Palliser, *C. globosum* Kunze, *Clonostachys* spp., *Epicoccum nigrum* Link, *Gliocladium* spp., *Humicola grisea* Traaen var. *grisea, Mortierella* spp., *Mucor* spp., *Myrothecium roridum* Tode, *Paecilomyces* spp., *Trichoderma* spp. and *Umbelopsis* spp. were considered as potential antagonists of potato pathogens.

Statistical analysis

The statistical significance of differences in number of isolates in two different samples was determined by a χ^2-test.

Community structures were analysed. Isolates of the same species were grouped and the frequency of each species was determined for each plant growth phase. A number of diversity indices were calculated for each community (Magurran 1988). These indices included three different species richness indicators: (a) the total number of species in the community, (b) Margalef's index (D_{Mg}), which shows richness from the ratio between number of species and their ln function, and (c) Shannon's diversity index (H'), a general diversity index that considers both species richness and evenness. Three different indices were also calculated for evenness and dominance: (a) Shannon's evenness index (E), which is the ratio of Shannon's diversity index to the maximum possible value with the observed number of species, (b) Simpson's index (D), which gives the probability that two isolates chosen at random will be from the same species, and (c) Berger–Parker's index (d), which is the relative abundance of the most abundant species. The similarity between fungal communities at two phases of development was determined by calculating the qualitative Sorensen's similarity index (C_N) from the number of co-occurring species.

Results

The total number of oomycetous and fungal isolates in potato in Osiny, in 2005–2007, at the emergence and flowering phase was 59–112 (roots), 65–630 (rhizoplane), 29–554 (rhizosphere soil) and 189–513 (non-rhizosphere soil) (Table 3). The total number of species was 7–15 (roots), 8–27 (rhizoplane), 7–41 (rhizosphere soil) and 19–34 (non-rhizosphere soil). Density of microorganisms at the flowering phase was often significantly greater in roots and non-rhizosphere soil and significantly smaller in the rhizoplane and rhizosphere. Diversities of the communities often remained stable or were greater at the emergence phase. The density of bacteria fluctuated in time (Table 4). The density of *Pseudomonas* often decreased while that of *Streptomyces* significantly increased in time.

Ten groups of dominating fungi included *Aspergillus* (mostly *A. fumigatus* Fresen. and *A. niger*), *Chaetomium* (mostly *C. cochlioides*, *C. crispatum* Fuck., *C. funicola* Cooke and *C. indicum* Corda), *Clonostachys* + *Gliocladium* (*C. rosea* f. *catenulata* (J.C. Gilman & E.V. Abbott) Schroers, *C. rosea* (Link) Schroers, Samuels, Seifert & W. Gams f. *rosea* and *C. solani* (Harting) Schroers & W. Gams) (f. *solani*), *Colletotrichum coccodes*, *Fusarium* + *Gibberella* + *Haematonectria* (mostly *F. culmorum* (W. G. Sm.) Sacc., *F. oxysporum* Schlecht. emend. Snyd. et Hans., *G. avenacea* R.J. Cook, *G. intricans* Wollenw. and *H. haematococca*), *Mortierellales* + *Mucorales* (mostly *Absidia glauca* Hagem, *Mortierella alpina* Peyronel, *M. hyalina* W. Gams var. *hyalina*, *M. zonata* Linnem. ex W. Gams, *Mucor mucedo* Fresen., *Rhizopus arrhizus* A. Fisch. var. *arrhizus, R. stolonifer* (Ehrenb.) Vuill., *Umbelopsis vinacea* (Dixon-Stew.) Arx and *Zygorhynchus moelleri* Vuill.), *Paecilomyces* (mostly *P. lilacinus* (Thom) Samson and *P. varioti* Bainier), *Penicillium* spp., *Phoma* (mostly *P. eupyrena* Sacc., *P. exigua* Desm. var. *exigua* and *P. glomerata* (Corda) Wollenw. & Hochapfel) and *Trichoderma* (*T. hamatum* (Bon.) Bain., *T. harzianum* Rifai, *T. koningii* Oudem., *T. polysporum* (Link ex Pers.) Rifai, *T. pseudokoningii* Rifai and *T. viride* Pers. ex Gray).

Twenty six taxa of the influential species included *Acremonium* (mostly *A. strictum* W. Gams), *Cephalotrichum* (mostly *C. stemonitis*), *Coniothyrium* (mostly *C. cerealis* E. Müll.), *Geomyces* (mostly *G. pannorum* (Link) Sigler & J.W. Carmich.), *Geotrichum* (mostly

Table 3 Frequency of microorganisms in potato in Osiny in 2005-2007

Taxon	Developing phase	Roots						Rhizoplane						Rhizosphere soil						Non-rhizosphere soil					
		2005		2006		2007		2005		2006		2007		2005		2006		2007		2005		2006		2007	
		O[1]	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I
	Dominating groups or species																								
Aspergillus spp.	E[2]	0	0	0	0	0	0	0^{b}	0.7	1.0	0	5.1^{b}	1.8	0.4	0.8^{b}	0	0.4	0.7	0	0^{a}	2.6^{a}	1.0	0.4	0.3	0
	F	0	0	1.2	0	0	0	4.6^{b}	1.4	1.1	0	0.3^{b}	1.1	0	10.3^{b}	0	0	0.3	0	35.2^{a}	25.1^{a}	0.3	0.6	0	0
Chaetomium spp.	E	0	0	0	0	0	0	10.8	0	0	0	0	0.5	0.8^{b}	0.4	0.5	0.7	0.4	0	0.5	0	0.7	0.9	0	0
	F	0	0	0	0	0	0	6.1	2.8	0	0	0	0.2	9.8^{b}	3.5	0	3.0	0	0.2	4.5	0.5	0.3	2.3	0.2	0.2
Clonostachys + *Gliocladium*	E	1.7	1.4	0	2.4	0^{b}	0	6.2^{b}	48.5^{a}	6.0^{v}	1.6	9.4	2.6	6.0^{v}	21.8^{a}	5.1^{b}	10.0^{b}	3.4^{b}	3.4	2.1	1.1	4.7	1.3	3.4	0
	F	3.5	0	0	1.2	5.3^{b}	0	0^{b}	0^{a}	0^{v}	0	8.0	1.9	0^{v}	0^{a}	0^{b}	1.0^{b}	12.8^{b}	5.3	0.5	5.4	3.9	0.8	6.3	1.5
Colletotrichum coccodes (Wallr.) S.J. Hughes	E	0	0	0	0	0^{a}	0^{b}	1.5	0	0^{a}	0	0^{a}	0^{a}	0	0	0^{b}	0	0.4^{a}	0.5^{a}	0	0	0	0	0	0
	F	0	0	0	0	25.0^{a}	4.1^{b}	0	0	29.2^{a}	0	50.3^{a}	24.1^{a}	0	0	7.2^{b}	0	16.4^{a}	12.8^{a}	0	0	0	0.6	0	0
Fusarium + *Gibberella* + *Haematonectria*	E	76.3	84.1	61.0^{b}	63.4^{b}	56.2	53.1	26.1^{a}	32.9	30.7^{b}	22.2^{a}	25.8^{b}	5.7^{a}	14.1^{a}	11.4	13.3	5.8^{a}	8.7	18.0^{b}	9.3	6.9^{a}	19.3^{b}	15.4	15.7	5.1
	F	73.2	84.3	88.0^{b}	91.8^{b}	41.1	45.9	3.1^{a}	48.0	49.5^{b}	58.7^{a}	13.3^{b}	26.2^{a}	0^{a}	17.3	17.0	27.6^{a}	11.3	4.3^{b}	18.0	24.9^{a}	32.6^{b}	27.2	18.9	11.7
Mortierellales + *Mucorales*	E	0	1.4	1.7	3.7	5.4^{b}	1.3	1.5	2.1	5.5	11.4^{b}	2.5	0.9	0.4	0.9	3.6^{b}	9.3	6.5	6.4	1.5	3.2	5.7^{b}	8.4	1.8	3.6
	F	0	0	0	1.2	0^{b}	2.0	0	0	1.1	3.8^{b}	1.7	1.4	0	0	0^{b}	4.5	2.6	2.2	0.9	0	0.6^{b}	11.8	3.6	5.3
Paecilomyces spp.	E	0	0	0	0	2.7	0	1.5	0	0	0.4	0	1.7	0	0^{b}	1.3	7.7	1.7	14.8^{b}	0	0	0	0^{b}	2.1	7.1
	F	0	0	0	0	0	0	1.5	2.8	1.1	2.5	0	0.4	0	6.9^{b}	1.3	9.1	0.7	2.1^{b}	0	0.3	0.9	5.7^{b}	0.4	1.1
Penicillium spp.	E	15.2	8.5	20.3^{b}	11.0	28.8	44.3	30.8^{b}	9.3^{b}	36.8^{a}	38.5	46.6^{a}	78.5^{a}	44.8^{b}	30.3	36.5	33.2	50.5^{b}	47.9	62.4^{b}	46.6	32.3	36.7	51.4	69.6
	F	10.5	2.9	6.0^{b}	5.8	16.9	30.6	53.9^{b}	26.8^{b}	10.1^{a}	33.7	16.8^{a}	34.5^{a}	68.6^{b}	41.4	34.0	47.3	32.5^{b}	54.2	32.0^{b}	32.7	34.1	25.8	45.2	62.4
Phoma spp.	E	0	0	1.7	2.5	0	0	4.6	2.9	8.0^{b}	2.4	1.3	2.2	9.7	19.3^{b}	15.0^{b}	7.1^{b}	2.7	0.8^{b}	3.1	3.2	13.5^{a}	8.4^{b}	1.1	2.7
	F	0	0	0	0	0.9	0	3.1	1.4	0^{b}	0	0.5	2.5	5.9	6.9^{b}	2.0^{b}	0^{b}	1.0	5.4^{b}	0	0	0^{a}	0.9^{b}	0.8	3.9
Trichoderma spp.	E	6.8	0	11.4^{a}	14.6^{a}	0^{b}	0^{b}	13.9	0	4.0	13.8^{a}	4.4	1.3	18.2^{b}	5.9	5.5	8.8^{b}	3.5	3.3	6.2	17.9^{b}	16.9	13.0	15.2	7.6
	F	2.3	1.4	0^{a}	0^{a}	8.1^{b}	9.2^{b}	6.1	1.4	2.3	0^{a}	1.4	2.5	5.9^{b}	3.4	2.6	0.5^{b}	7.0	3.3	4.6	4.7^{b}	12.9	8.0	14.4	9.0
	Influential species																								
Acremonium spp.	E[2]	0	1.4	0	0	0	0	0	0	0	1.2	0	0	1.2	0	0.5	2.9	0.7	0.3	0	0.5	0	0.9	0	0.2
	F	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0	0	0.3	1.1	0.2	0
Acrostalagmus luteoalbus (Link) Zare, W. Gams & Schroers	E	0	0	0	0	0	0	0	0	0	0	0	0.4	0	2.1	0	0.5	2.4	0	0	1.1	0.7	1.3	0.3	0
	F	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.2	0	0	0.3	0	0.3	0.3	0.4
Alternaria alternata (Fr.) Keissl.	E	0	2.8	0	1.2	1.4	0	0	0	0	0	0	0	0	0.4	0	0	0	0	0	0	0	0	0	0.2
	F	3.5	1.4	0	0	0.9	2.0	3.1	1.4	0	0	0	0.9	0	0	0	0	0	1.2	0	0	0	0	0	0
Arthrinium phaeospermum (Corda) M.B. Ellis	E	0	0	0	0	0	0	0^{b}	0	0	0	0	0	0	0	0	0.2	0	0	0	0.5	0	0	0.5	0
	F	0	0	0	0	0	0	6.2^{b}	0	0	0	0	0	0	0	0	0	0.3	0	0	0.6	0.3	0.3	0	0
Aureobasidium pullulans (de Bary) Arnaud	E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.2	0.2	0	0	0	0	0	0	0	0
	F	0	0	0	0	0	0	1.5	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Cephalotrichum	E	0	0	0	0	0	0	0	0	0	0.4	2.5	0	0	0	1.6	4.1	1.4	0.8	0	0	0	0.4	0	0

Table 3 (continued)

Taxon	Developing phase	Roots						Rhizoplane						Rhizosphere soil						Non-rhizosphere soil					
		2005		2006		2007		2005		2006		2007		2005		2006		2007		2005		2006		2007	
		O[1]	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I
spp.	F	0	0	0	0	0	0	0	0	0	0	0.3	0	0	3.5	1.3	0.5	0.2	0.6	0	0	0	0.6	0	0.2
Cladosporium herbarum Link ex Fries	E	0	0	0	0	0	0	0	0	1.5	0.4	0	0	0	0	0.7	0.7	0	0	0	0	0	0	0	0
	F	0	0	0	0	0	0	0	0	0	0	0.6	0.4	0	0	0	0	0	0.4	0	0	0	0	0	0
Coniothyrium spp.	E	0	0	0	0	0	0	0	0	0	0	0	0	0.8	0	0	0	0	0	3.6	0.5	0	0	0	0
	F	0	0	0	0	0	0	0	0	2.3	0	0	0	0	0	2.6	0	0	0	0	0	0.3	0.9	0	0
Epicoccum nigrum Link	E	0	0	1.7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.2	0
	F	0	0	0	0	0	0	0	0	0	0	0	0.4	0	0	0	0	0	0	0	0	0	0	0	0
Geomyces spp.	E	0	0	0	0	5.5[b]	0	0	0	0.5	6.1[b]	0	0	1.2	1.3	5.0[b]	4.5[b]	0	0	0	1.6	1.0	0	0	0.2
	F	0	0	0	0	0[b]	0	0	0	0	0[b]	0	0	0	0	0[b]	0[b]	0.7	0	0	0	0	0	1.0	0.8
Geotrichum spp.	E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.6[a]	0	0.4	0	0	1.1	0.3	0	0	0
	F	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	30.1[a]	0	0	0.4	0	0	1.8	0	0	0
Gibellulopsis nigrescens (Pethybr.) Zare, W. Gams & Summerb.	E	0	0	0	0	0	0	0	0	0	0	0[b]	2.5	0	0	2.4	0.2	10.4	2.8	0	0	0	5.3[b]	3.9	2.9
	F	0	0	0	0	0	0	0	1.4	0	0	4.3[b]	1.3	0	0	0.6	1.5	8.9	5.6	0	0	0	0[b]	1.0	1.0
Gliomastix spp.	E	0	0	0	0	0	0	0	0	0	0	0	0	0.4	0	0.9	1.8	1.0		1.0	0	0	0	0	0.2
	F	0	0	0	0	0	0	0	0	1.1	0	0	0	0	0	0	0	0.7	0.4	0	0	0.6	0.3	0	0.2
Gonytrichum macrocladum (Sacc.) Hughes	E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.5	0	0.4	0	0	0	0	0	0	0
	F	0	0	0	0	0	0	0	0	0	0.4	0	0	0	0	0	0	0.3	0	0	0	0	1.1	0.2	0
Gymnoascus spp.	E	0	0	0	0	0	0	1.5	0	0	0	0	0	0.4[b]	0.4	0.2	0	0	0	0	0	0.4	0	0.3	0.2
	F	1.2	0	1.2	0	0	0	0	1.4	0	0	0	0	5.9[b]	3.4	0	0	0	0	2.1	1.0	1.8	1.7	0.5	0
Humicola spp.	E	0	1.4	0	0	0	0	0[b]	0	0.5	0	0	0	0.8	0	0.2	0.5	0.4	0.5	2.1	0	2.0	2.2	0.5	0
	F	0	0	0	0	0	0	4.6[b]	0	1.1	0	0	0.2	0	0	1.3	0.5	0.5	0	0.5	1.9	3.9	3.1	0.5	0.2
Leptosphaeria coniothyrium (Fuckel) Sacc.	E	0	0	0	0	0	0	0	0	0	0	0.6	0.5	0.4	1.7	0.7	0	1.0	0	0	1.1	0.3	0	0	0.2
	F	0	0	0	0	0	0	0	0	1.1	0	1.0	0	0	0	0	0	0	0.6	0.3	1.9	1.5	1.7	0	0.2
Microascus brevicaulis S.P. Abbott	E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	2.4	0	0	0.5	0	3.1	0.3	0.2
	F	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2.5	0.5	0	0	0	0.3	1.1	0.5	0
Monocillium indicum Saksena	E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.5	0	0	0	0	1.1	0	0	0	0
	F	0	0	0	0	0	0	0	2.8	0	0	0	0	0	0	0	0	0	0	0.3	0	0	0	0	0
Myrothecium roridum Tode	E	0	0	0	0	0	0	0	0	0	0	0	0	0	0[b]	0	0	0	0	0	0	0	0	0	0
	F	0	0	0	0	0	0	0	0	0	0	0	0	0	3.4[b]	0	0	0	0	0	0	0	0	0	0
Neonectria radicicola (Gerlach & L. Nilsson) Mantiri & Samuels	E	0	0	0	0	0	0	0	0	1.0	0	0.6	0	0	0	0	0	0	0	0	0	0.3	0	0	0
	F	0	1.4	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0
Periconia macrospinosa Lefebvere et	E	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1.0	0	0.5	0	0	0	0	0
	F	0	0	0	0	0.9	0	0	1.4	0	0	0	0	0	0	0	0	0.7	0.2	0	0	0.3	0	0	0

Table 3 (continued)

Taxon	Developing phase	Roots						Rhizoplane						Rhizosphere soil						Non-rhizosphere soil					
		2005		2006		2007		2005		2006		2007		2005		2006		2007		2005		2006		2007	
		O[1]	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I
Johnson *Pythium* spp.	E	0	0	1.7	0	0	0	0	0	0	0.8	0	0	0	3.8[b]	0	0	0	0	3.6[b]	0.5	1.0	0	2.4	0
	F	0	0	1.2	0	0.9	0	0	0	0	0	0	0	0	0[b]	0	1.0	0	0	0[b]	0.3	0.9	0.6	6.0	0
Thanatephorus cucumeris (A.B. Frank) Donk	E	0	0	0	1.2	0	0	1.6	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
	F	0	0	0	0	0	3.1	0	0	0	0	0	0.8	0	0	0	0	0	0	0	0.3	0	0	0	0.2
Thielavia terricola (J.C. Gilman & E. V. Abbott) C.W. Emmons	E	0	0	0	0	0	0	0	0	0	0	0	0	0[b]	0	0	0	0	0	0	0	0	0	0	0
	F	0	0	0	0	0	0	0	0	0	0	0	0	3.9[b]	0	0	0	0	0	0.3	0	0	0	0	0
Torula spp.	E	0	0	0	0	0	0	0	3.6	0	0	0	0	0	0	0	0.2	0	0	0	0	0	0	0	0
	F	0	0	0	0	0	0	0	1.4	0	0	0	0	0	0	0	0	0		0.8	0	0	0	0	0
Total number of isolates	E	59[b]	71	59[b]	82	73[b]	79	65	140[a]	201[a]	247[a]	159[a]	228[a]	248[a]	238[a]	554[a]	443[a]	289[a]	390[a]	194[a]	189[a]	300	226[a]	381	451[a]
	F	86[b]	70	83[b]	85	112[b]	98	65	71[a]	89[a]	80[a]	630[a]	523[a]	51[a]	29[a]	153[a]	199[a]	416[a]	513[a]	377[a]	318[a]	332	349[a]	398	513[a]
Total number of species	E	7	8	9	12	9	7	14	9	19	24[b]	18	20	23[b]	21	39[a]	41[a]	35	24	19	28	31	30	28	24
	F	11	7	8	6	15	15	13	15	12	8[b]	24	27	7[b]	12	14[a]	15[a]	29	26	21	21	32	34	29	25

Explanations

[1] *O* organic

I integrated

[2] *E* emergence

F flowering

[a] the ratio for emergence and flowering phase is significantly different from 1:1 at $P=0.001$

[b] the ratio for emergence and flowering phase is significantly different from 1:1 at $P=0.05$

Table 4 Density of bacteria, oomycetous and fungal pathogens and antagonists in potato in Osiny in 2005-2007

Taxon	Phase	An average number of colony forming units (*cfu*) in 1 g of roots or 1 g of soil							
		Roots		Rhizoplane		Rhizosphere		Non-rhizosphere soil	
		Organic	Integrated	Organic	Integrated	Organic	Integrated	Organic	Integrated
Arthrobacter	E[1]			6,909 [2ac]	5,426^{ac}	14,190^{ac}	14,805^{ac}	4,356^{a}	3,431^{ac}
	F			2,018^{ac}	7,274^{ac}	14,887^{ac}	17,657^{ac}	4,279^{a}	2,646^{ac}
Pseudomonas	E			99^{ac}	168^{ac}	1,370^{a}	2,013^{ac}	941^{ac}	1,957^{ac}
	F			320^{bc}	268^{bc}	1,278^{a}	414^{a}	215^{bc}	170^{bc}
Streptomyces	E			1,306^{ac}	269^{ac}	4,872^{ac}	6,973^{ac}	9,712^{ac}	6,633^{ac}
	F			2,777^{ac}	4,698^{ac}	15,551^{ac}	14,380^{ac}	11,831^{ac}	9,562^{ac}
Pathogens (total)	E	209^{bc}	262^{bd}	1,622^{bc}	1,489^{bc}	33,778^{ac}	27,333^{ac}	6,767^{ac}	4,600^{ac}
	F	357^{c}	326^{d}	5,656^{ac}	4,178^{ac}	21,556^{ac}	25,000^{ac}	9,967^{c}	9,733^{c}
A. alternata	E	2	5	0^{c}	0^{c}	0^{a}	111^{ac}	0^{a}	33^{ac}
	F	7	5	22^{ac}	67^{ac}	0^{a}	667^{ac}	0	0^{c}
A. phaeospermum	E	0	0	0^{c}	0	0^{ac}	111^{ac}	67^{ac}	33^{ac}
	F	0	0	44^{ac}	0^{a}	111^{ac}	0^{ac}	33^{ac}	100^{ac}
A. niger	E	0	0	78^{bc}	44^{bc}	222^{c}	222^{c}	0^{ac}	100^{ac}
	F	0	0	0^{c}	0^{c}	111^{ac}	0^{ac}	933^{ac}	467^{ac}
B. cinerea	E	0	0	0	0	0	0	0	0
	F	0	2	0	0	0	0	0	0
C. stemonitis	E	0	0	44^{ad}	0^{a}	1,444^{ac}	2,333^{ac}	0^{a}	33^{ac}
	F	0	0	22^{ad}	0^{a}	333^{ac}	444^{ac}	0^{a}	100^{ac}
C. coccodes	E	0^{c}	0	0^{c}	0^{c}	111^{ac}	222^{ac}	0	0^{c}
	F	48^{ac}	7^{a}	3,811^{ac}	1,400^{ac}	8,778^{ac}	7,333^{ac}	0^{a}	67^{ac}
D. nanum	E	0	0	0	0^{c}	222^{ac}	0^{a}	33^{ac}	0^{a}
	F	0	0	0^{a}	22^{ac}	0^{c}	0	0^{c}	0
F. culmorum	E	2^{d}	0	0	0^{c}	1,000^{ac}	111^{a}	100^{ad}	0^{a}
	F	9^{d}	0	144^{ac}	0^{a}	333^{ac}	111^{a}	67^{ad}	0^{a}
F. oxysporum	E	80^{a}	199^{a}	578^{a}	856^{ac}	6,000^{ac}	10,444^{ac}	1,467^{c}	1,533^{c}
	F	80^{a}	167^{a}	533^{a}	1,856^{ac}	3,222^{ac}	8,222^{ac}	3,667^{ac}	6,000^{ac}
F. sporotrichioides	E	0	0	0	0	0	0	0^{c}	0
	F	0	0	0	0	0	0	33^{ac}	0^{a}
G. candidum	E	0	0	0^{d}	0	222^{ac}	0^{ac}	0^{a}	67^{ac}
	F	0	0	11^{bd}	0^{b}	0^{ac}	222^{ac}	0	0^{c}
G. nigrescens	E	0	0	0^{ac}	67^{a}	4,778^{ac}	1,333^{ac}	500^{ac}	833^{ac}
	F	0	0	300^{ac}	89^{a}	4,222^{ac}	3,556^{ac}	133^{c}	167^{c}
G. avenacea	E	2	7	0^{a}	133^{ac}	0^{a}	111^{ac}	33^{ac}	0^{a}
	F	0	2	0^{a}	22^{ac}	0	0^{c}	0^{c}	0
H. haematococca	E	119^{ac}	46^{ac}	678^{a}	200^{ac}	7,111^{ac}	2,556^{ac}	2,400^{ac}	733^{ac}
	F	208^{ac}	136^{ac}	689^{a}	522^{ac}	3,333^{ac}	667^{ac}	3,900^{ac}	1,800^{ac}
N. radicicola	E	0	0	0	0	0	0	0	0
	F	0	2	0	0	0	0	0	0
Phoma spp.	E	2	3	233^{ac}	167^{a}	12,444^{ac}	8,444^{ac}	1,533^{ac}	1,167^{ac}
	F	2	0	56^{ac}	156^{a}	1,111^{ac}	3,556^{ac}	267^{ac}	867^{ac}

Table 4 (continued)

Taxon	Phase	An average number of colony forming units (*cfu*) in 1 g of roots or 1 g of soil							
		Roots		Rhizoplane		Rhizosphere		Non-rhizosphere soil	
		Organic	Integrated	Organic	Integrated	Organic	Integrated	Organic	Integrated
Pythium spp.	E	2	0	0^{a}	22^{ac}	0^{a}	$1{,}000^{ac}$	633^{ac}	33^{ac}
	F	3	0	0	0^{c}	0^{a}	222^{ac}	900^{ac}	100^{ac}
Rhizopus spp.	E	0	0	0^{c}	0	222^{c}	222^{c}	0^{c}	0
	F	0	0	22^{ac}	0^{a}	0^{c}	0^{c}	33^{ac}	0^{a}
T. cucumeris	E	0	2	11^{bd}	0^{bc}	0	0	0	0^{c}
	F	0	5	0^{ad}	44^{ac}	0	0	0^{a}	67^{ac}
T. roseum	E	0	0	0	0	0	0	0^{a}	33^{ac}
	F	0	0	0	0	0	0	0	0^{c}
U. consortiale	E	0	0	0	0	0^{a}	111^{ac}	0	0
	F	0	0	0	0	0	0^{c}	0	0
Antagonists (total)	E	32	35	567^{a}	$1{,}422^{ac}$	$18{,}889^{ac}$	$33{,}111^{ac}$	$5{,}667^{b}$	$5{,}900^{bc}$
	F	28	25	633^{a}	444^{ac}	$10{,}111^{ac}$	$8{,}556^{ac}$	$5{,}500^{a}$	$6{,}600^{ac}$
A. strictum	E	0	2	0^{ad}	33^{ac}	889^{ac}	$1{,}556^{ac}$	0^{ac}	133^{a}
	F	0	0	11^{bd}	0^{bc}	0^{c}	0^{c}	33^{ac}	133^{a}
A. pullulans	E	0	0	0^{d}	0	111^{c}	111^{c}	0	0
	F	0	0	11^{bd}	0^{b}	0^{c}	0^{c}	0	0
C. cochlioides + *C. globosum*	E	0	0	0	0	0	0	0^{a}	33^{a}
	F	0	0	0	0	0	0	0^{a}	33^{a}
C. rosea f. *catenulata*	E	0	0	156^{ac}	622^{ac}	$2{,}778^{ac}$	$6{,}111^{ac}$	133^{ac}	33^{ac}
	F	9	0	278^{ac}	78^{ac}	$4{,}000^{ac}$	556^{ac}	333^{ac}	0^{ac}
C. rosea f. *rosea*	E	0	3	0	0	0	0	67^{ac}	0^{a}
	F	0	0	0	0	0	0	33^{ac}	0^{a}
E. nigrum	E	2	0	0	0^{c}	0	0	33^{ac}	0^{a}
	F	0	0	0^{a}	22^{ac}	0	0	0^{c}	0
G. virens	E	0	0	0	0	0^{a}	222^{ac}	0	0
	F	0	0	0	0	0	0^{c}	0	0
G. cerealis	E	0	0	0^{d}	0	0	0	0^{c}	0
	F	0	0	11^{bd}	0^{b}	0	0	33^{ac}	0^{a}
H. grisea	E	0	2	11^{bc}	0^{bd}	333^{ac}	444^{ac}	400^{ad}	167^{ac}
	F	0	0	44^{ac}	11^{ad}	444^{ac}	111^{ac}	467^{bd}	567^{bc}
Mortierella spp.	E	3	0	22^{a}	122^{ac}	$1{,}111^{ac}$	$2{,}333^{ac}$	200^{a}	467^{ac}
	F	0	3	22^{b}	44^{bc}	333^{ac}	667^{ac}	233^{a}	700^{ac}
Mucor spp.	E	5	5	100^{d}	111^{c}	$2{,}778^{c}$	$2{,}889^{c}$	533^{bc}	600^{bc}
	F	0	5	67^{ad}	22^{ac}	778^{ac}	444^{ac}	267^{ac}	0^{ac}
M. roridum	E	0	0	0	0	0	0^{c}	0	0
	F	0	0	0	0	0^{a}	111^{ac}	0	0
Paecilomyces spp.	E	3	0	11^{a}	56^{a}	$1{,}333^{ac}$	$10{,}222^{ac}$	267^{ac}	$1{,}067^{ac}$
	F	0	0	22^{a}	67^{a}	556^{ac}	$3{,}444^{ac}$	167^{ac}	900^{ac}
T hamatum + *T. harzianum* + *T. koningii* + *T. viride*	E	0	0	256^{bc}	333^{bc}	$9{,}222^{ac}$	$7{,}000^{ac}$	$3{,}833^{ad}$	$3{,}100^{ac}$
	F	0	2	133^{c}	156^{c}	$4{,}000^{ac}$	$2{,}111^{ac}$	$3{,}567^{ad}$	$2{,}833^{ac}$

Table 4 (continued)

Taxon	Phase	An average number of colony forming units (*cfu*) in 1 g of roots or 1 g of soil							
		Roots		Rhizoplane		Rhizosphere		Non-rhizosphere soil	
		Organic	Integrated	Organic	Integrated	Organic	Integrated	Organic	Integrated
Trichoderma other	E	19	20	11[ac]	78[ac]	333[c]	333[c]	200[ac]	133[a]
	F	19	15	33[ac]	0[ac]	0[c]	0[c]	333[ac]	133[a]
U. vinacea	E	0	3	0[a]	67[ad]	0[a]	1,889[ac]	0[ac]	167[a]
	F	0	0	0[a]	44[ad]	0[a]	1,111[ac]	33[ac]	1,300[a]
Penicillium spp.	E	72	85	1,867[ac]	3,189[ac]	51,000[ac]	45,111[ac]	13,800[a]	16,167[ac]
	F	56	63	1,667[ac]	2,522[ac]	24,667[ac]	42,667[ac]	13,800[a]	17,133[ac]

[1] *E* emergence

F flowering

[2] in bacteria *cfu* 10^{-3}

[a] the ratio for organic system and integrated system is significantly different from 1:1 at $P=0.001$

[b] the ratio for organic system and integrated system is significantly different from 1:1 at $P=0.05$

[c] the ratio for emergence and flowering phase is significantly different from 1:1 at $P=0.001$

[d] the ratio for emergence and flowering phase is significantly different from 1:1 at $P=0.05$

G. candidum), *Gliomastix* (mostly *G. cerealis* (Kart.) Dickinson and *G. murorum* (Corda) S. Hughes var. *murorum*), *Gymnoascus* (mostly *G. reessii* Baran.), *Humicola* (*H. fuscoatra* Traaen var. *fuscoatra* and *H. grisea* var. *grisea*).

The non-key species included *Acremoniella fusca* Kunze, *Botrytis cinerea. Cephalosporium* sp., *Chlamydomyces* sp., *Dendryphion nanum*, *Emericellopsis terricola* van Beyma, *Graphium* spp., *Melanospora lagenaria* (Persoon) Fuckel, *Melanospora* sp., *Metarhizium anisopliae* (Metschn.) Sorokīn, *Monographella nivalis* (Schaffnit) E. Müll. var. *nivalis*, *Papulaspora irregularis* Hotson, *Preussia aemulans* (Rehm) Arx, *Pyrenochaeta* sp., *Sporothrix* spp., *Thielavia terricola* (J.C. Gilman & E.V. Abbott) C. W. Emmons, *Torula herbarum* (Pers.) Link, *T. roseum* and *Ulocladium consortiale* (Thüm.) E.G. Simmons.

Acremoniella fusca, Aspergillus fischeri Wehmer, *Gliocladium virens* Miller, *M. nivalis* var. *nivalis, Mortierella candelabrum* van Tiegh. et LeMonnier, *M. lignicola* (G.W. Martin) W. Gams & R. Moreau, *M. stylospora* Dixon-Stew., *Paecilomyces carneus* (Duché & R. Heim) A.H.S. Br. & G. Sm., *Papulaspora irregularis* Hotson, *Phoma medicaginis* Malbr. & Roum. var. *medicaginis, P. terricola* Boerema, *P. aemulans, Sporothrix* spp., *Torula herbarum* (Pers.) Link and *T. roseum* occurred only at the emergence phase.

Botrytis cinerea, Chaetomium cochlioides, C. globosum, *Fusarium poae* (Peck) Wollenw., *F. sporotrichioides* Sherb, *Gibberella tricincta* El-Gholl, McRitchie, Schoult. & Ridings, *Gliomastix cerealis* (Kart.) Dickinson, *Gliomastix* sp., *M. lagenaria, Melanospora* sp., *M. anisopliae, Mortierella bisporalis* (Thaxter) Björling, *M. parvispora* Linnem., *Mucor circinelloides* Tiegh., *Myrothecium roridum*, *Phoma terricola* Boerema, *Pyrenochaeta* sp., *Verticillium* sp.and *U. consortiale* occurred only at flowering.

The total number of soil-borne potato pathogens in roots, rhizoplane, non-rhizosphere soil and partly in the rhizosphere had increased at the flowering phase (Table 4). This effect resulted from the increased density of *A. alternata*, *C. coccodes, F. oxysporum, H. haematococca, Pythium* spp. and *T. cucumeris* but not of *F. culmorum, G. nigrescens, G. avenacea* and *Phoma* spp. The total number of the potato antagonists had often decreased at the flowering phase. The changes in density of the individual microorganisms in time were not correlated with the system of farming.

The relatively small number of fungal taxa and the infrequent occurrence of many taxa resulted in relatively

small diversity indices based on species richness (D_{Mg}) and the proportional abundance of species (H') (Table 5). Species richness was often similar at emergence and flowering, but tended to be less in rhizosphere soil at and greater in non-rhizosphere soil at flowering than at emergence, with no clear effects of farming system. The dominance of the single taxa in communities resulted in small values for Shannon's evenness index (E) and high values for dominance indices (D and d). Evenness tended to be less in roots at flowering than at emergence and less in roots than in the rhizoplane, rhizosphere or non-rhizosphere soil. Dominance tended to be greater at flowering than at emergence in roots (integrated system) and rhizosphere. Sorensen's qualitative similarity index (C_N) for the emergence and flowering phases suggests that there was more similarity in communities in roots than in the rhizoplane, rhizosphere or non-rhizosphere soil.

Discussion

Potatoes grow in the presence of a huge amount of microorganisms. During cultivation, plants temporarily stimulate or inhibit the development of particular soil-borne species. Identifying them and understanding their life history and susceptibility to environmental changes are important if the impact of pathogens is to be minimized. Recognition and understanding relationships between host plant and pathogen/antagonist is also important. It may help to predict conditions that require control actions and so prevent economic losses. Control measures against soil-borne potato pathogens, such as soil treatment (fumigation) or tuber seed treatment, have to be planned before planting. Therefore the ability to identify and evaluate the potential risk is extremely important.

Colletotrichum coccodes (wilt and tuber black dot), *Fusarium* (fusarium wilt and tuber dry rot), *Gibellulopsis-Verticillium* (wilt), *Haematonectria* (fusarium dry rot), *Phoma* (gangrene), *Pythium* (pythium leak, root rot), *Streptomyces* (common scab) and *T. cucumeris* (black scurf and rhizoctonia stem canker) were pathogens recorded in the potato root/soil habitat in both the organic and integrated cultivation systems in Osiny in 2005–2007. The diseases they cause are the most important worldwide and can be soil-borne. Soil-borne pathogens typically damage plants through infection of below-ground parts of the plant, i.e. roots, stems and stolons. In some cases their spores, if carried by water or wind, can infect above ground plant parts. Infection can result in rotted roots, plugged vascular tissue, girdled underground stems, and plant death. The crop can be disfigured or damaged. Loss can result from two separate causes: reduced yield and reduced quality.

Microorganisms use water-soluble carbon compounds such as carbohydrates as their source of nutrition and energy. Large amounts of manure, composts and cover crops applied every year in both farming systems provided (partly in spring) considerable carbon input. Carbon was also provided from the plant rhizosphere. Both sources influence the density and diversity of the surrounding microbial community, with consequent effects on nutrient cycling and pathogen inhibition. A positive correlation exists between the concentration of soluble C fractions and microbial density.

All forms of carbon require high temperature to react even with oxygen. A positive role of temperature in effective nourishment of microorganisms has been emphasized (Kawasaki et al. 1969; Morita and Buck 1974; Piperno and Oxender 1968). Higher carbon consumption and utilization at higher temperatures (at the flowering phase) seemed to stimulate the growth of microorganisms, mostly in the non-rhizosphere soil. A similar increase in microbial density in time was expected in the rhizosphere. It occurred only once, however, in 2007. A significant (P=0.001) decrease was observed earlier. This seemed to result from preferences of fungi for plant-specific root exudates followed by competition among microorganisms.

Some genera that dominated early in the potato root/soil habitat i.e. *Clonostachys, Fusarium, Penicillium* and *Trichoderma*, are members of strong fungal associations with a generally broad ecological range, present in many natural or disturbed habitats (Lemańczyk and Sadowski 2000). These genera are primary colonizers because of their strong adaptive features, mostly: (a) capacity for rapid growth and invasion of the available substrate, (b) enzymatic flexibility, and (c) resistance to environmental hazards (Frankland 1981; Cabello and Arambarri 2002).

The microorganisms included groups of dominant, influential and non-key species. They represented a pattern that resulted from the plant's phenology, local periodic growing conditions and inter- and intra-

Table 5 Diversity indices for microbial communities from roots, rhizoplane, rhizosphere and non-rhizosphere soil of potato

Taxon	Developing phase	Roots						Rhizoplane						Rhizosphere soil						Non-rhizosphere soil					
		2005		2006		2007		2005		2006		2007		2005		2006		2007		2005		2006		2007	
		O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I	O	I
Species richness indices																									
Margalef's index (D_{Mg})	E	1.47	1.64	1.96	2.49	1.86	1.37	3.11	1.61	3.39	4.35	3.35	3.49	3.99	3.47	6.02	6.56	5.82	3.68	3.41	5.15	5.25	5.35	4.54	3.76
	F	2.24	1.41	1.58	1.12	2.96	3.05	2.87	3.28	2.45	1.36	3.56	4.15	1.52	3.26	2.58	2.45	4.47	4.00	3.37	3.29	5.34	5.63	4.67	3.84
Shannon's diversity index ($H^{'}$)	E	0.94	1.16	1.36	1.71	1.43	1.24	1.98	1.63	1.95	2.33	1.94	1.08	2.09	2.29	2.62	2.72	2.15	1.93	1.60	2.12	2.44	2.45	1.94	1.43
	F	1.36	0.70	1.19	0.89	2.08	1.79	1.78	1.97	1.75	1.25	1.84	1.92	1.15	2.01	1.83	1.61	2.39	1.85	1.91	2.15	2.29	2.53	2.11	1.56
Evenness or dominance indices																									
Shannon's evenness index (E)	E	0.13	0.14	0.15	0.14	0.15	0.17	0.14	0.18	0.10	0.09	0.10	0.05	0.09	0.10	0.06	0.06	0.06	0.08	0.08	0.07	0.07	0.08	0.06	00.5
	F	0.12	0.10	0.14	0.14	0.13	0.11	0.13	0.13	0.14	0.15	0.07	0.07	0.16	0.16	0.13	0.10	0.08	0.07	0.09	0.10	0.07	0.07	0.07	0.06
Simpson's index (D)	E	0.54	0.43	0.37	0.28	0.32	0.35	0.43	0.25	0.18	0.16	0.24	0.61	0.22	0.14	0.15	0.13	0.27	0.27	0.40	0.23	0.14	0.16	0.28	0.49
	F	0.43	0.69	0.37	0.53	0.15	0.24	0.29	0.18	0.21	0.36	0.29	0.22	0.48	0.18	0.22	0.30	0.15	0.31	0.21	0.17	0.17	0.13	0.23	0.40
Berger–Parker's index (d)	E	0.72	0.61	0.57	0.51	0.49	0.44	0.30	0.38	0.36	0.38	0.46	0.78	0.44	0.30	0.36	0.33	0.50	0.47	0.62	0.46	0.32	0.36	0.51	0.69
	F	0.65	0.82	0.46	0.70	0.25	0.38	0.53	0.26	0.29	0.50	0.50	0.34	0.68	0.41	0.33	0.47	0.32	0.54	0.32	0.32	0.34	0.25	0.45	0.62
Sorensen's qualitative similarity index (C_N)		0.027	0.028	0.028	0.023	0.021	0.022	0.030	0.018	0.013	0.012	0.005	0.005	0.013	0.014	0.005	0.006	0.005	0.004	0.007	0.007	0.006	0.006	0.005	0.004

species relationships. The group of dominant species included pathogens, e.g. *C. coccodes, Fusarium* + *Gibberell*a + *Haematonectria* + *Neonectria* and *T. cucumeris*, and their antagonists, e.g. *Clonostachys* + *Gliocladium* + *Trichoderma* and *Penicillium* spp.

Colletotrichum coccodes was present in/on roots and almost absent in non-rhizosphere soil, although it is known to survive free in soil or on colonized plant debris for 2–8 years (Farley 1976; Dillard 1990; Dillard and Cobb 1993; 1998). Its density increased very significantly at the flowering phase. This fungus is a secondary pathogen. Colonization of roots by *C. coccodes* is restricted in the early stages of plant growth and the extent of its infection is a function of time; the longer the time the more extensive infection (Ingram and Johnson 2010). Multiple primary infections occur from microsclerotia that become prevalent on host tissues late in the growing season. It is often associated with senescing potato plants. Its long-term persistance becomes a problem in the absence of effective control measures. No specific fungicides have been developed to control *C. coccodes.* Chemicals that proved effective in vitro are usually unsucceseful in the field (Marais 1990; Read and Hide 1995; Read et al. 1995). Crop rotation designed to reduce soil-borne inoculum of *C. coccodes* has limitations. *Colletotrichum coccodes* can alkalinize the colonized decaying tissue through secretion and accumulation of ammonia (Alkan et al. 2008), which: (a) facilitates the pathogen's virulence and its transformation from the quiescent-biotroph to active-necrotroph, and (b) eliminates other microfungi. The low frequency of *G. nigrescens* (syn. *V. nigrescens* Pethybr.) in roots and rhizoplane where *C. coccodes* dominated seems to have resulted from such interactions (Gilpatrick 1969; Tenuta 2001).

Fusarium + *Gibberell*a + *Haematonectria* dominated early, *Fusarium* + *Gibberell*a (mostly *F. oxysporum*) usually more often in the integrated system and *Haematonectria* in the organic system. Their sometimes higher density at flowering, when temperatures were higher, agrees with reports of others. *Fusarium oxysporum* is reported to be the most frequent pathogen of potato at higher temperatures (Upstone 1970; Thanassoulopoulos and Kitsos 1985; Hide 1986; Singh et al. 1987; Tivoli et al. 1988; Theron 1991; Manici and Cerato 1994). *Fusarium* and *Haematonectria* are known for their good persistence in roots and soil, often in the form of dormant chlamydospores that are resistant to temperature and moisture deficiencies (Windels 1993; Suárez-Estrella et al. 2004; Paparu et al. 2008). Formation of *H. haematococca* chlamydospores is favoured by higher temperatures (Schippers and Old 1974; Li et al. 1998). The ease with which *F. oxysporum* infects the potato vascular tissues suggests that its continuous presence in/on roots may increase the incidence and spread of fusarium wilt and tuber dry rot (Manici and Cerato 1994).

We observed an increased density of *T. cucumeris* in time, in agreement with a report of Chand and Logan (1984). This seems to result from accumulation of sclerotia by the fungus. This fungus uses endogenous C for germination and infection making it partly independent of other nutrient sources.

Streptomyces was assumed to occur mainly as a pathogen of potato (*S. scabies* (Thaxter) Waksman and Henrici, and *S. turgidiscabies* Miyajima, Tanaka, Takeuchi et Kuninaga, Lenc 2006) although species were not identified. *Streptomyces* spp. are, however, also prolific producers of a broad range of antibiotics; in agricultural systems, species have been shown to suppress diverse plant pathogens, via antibiosis or resource competition. Both mechanisms are likely to be influenced by resource availability (Schlatter et al. 2009). In our studies, the density of *Streptomyces* always increased at flowering. High nutrient inputs applied in both cultivation systems may have resulted also in its greater inhibitory effect, a consequence of positive selection and increased density of antibiotic-producing isolates (Schlatter et al. 2009). Soil nutrient availability and microbial population densities are likely to be key determinants of phenotypic composition among *Streptomyces.*

The density of the *Clonostachys* + *Gliocladium* + *Trichoderma* and *Penicillium* spp. group had often decreased at the flowering phase. This indicates their limited resistance to adverse environments. *Trichoderma* spp. are relatively intolerant of low moisture (Harman and Kubicek 1998). Dryer weather at flowering seemed to affect its decrease. *Clonostachys* was generally compatible with *Trichoderma* although individual species behaved differently. *Clonostachys rosea* may suppress *T. harzianum* and *T. viride* but not *T. koningii.* A similar relationship between *C. rosea* and *Trichoderma* has been observed elsewhere (Piper et al. 2000; Krauss and Soberanis 2001)

The usual decrease of the *Phoma* population, particularly of *P. exigua,* at the flowering phase results

mostly from its environmental requirements, the specific disease cycle and competition. An initial presence of *P. exigua* with diseased tubers was followed by its decline because of its: (a) preference for lower temperatures (in loam, the fungus survives at 15°C for 8 months, at 10°C for 2 years and at 5°C for 3 years), (b) non-specificity for the root habitat (it usually invades stems), and (c) microbial interactions (in autoclaved soil its initial population remained constant for 3–4 months, Adams 1979).

An increased density of *Aspergillus* species, mostly of *A. fumigatus* and *A. niger*, at the flowering phase in 2005 seemed to result from the key role of *A. fumigatus* in recycling of C and N in compost. This ability results from its: (a) thermotolerance (it thrives at>37°C), (b) sporulation efficiency (it produces many conidia in the extremely hostile habitat of compost), (c) germination efficiency (conidia survive and germinate at 60°C), (d) degradation of many components of organic waste (sugars, fatty acids, proteins, cellulose, pectin, xylan), and (e) nutritional versatility (senses and utilizes a variety of C and N sources). *Aspergillus* (as well as *Penicillium* species) is often involved in postharvest spoilage. Their toxins are regarded as a storage concern (Pitt 2002; Scudamore and Livesey 1998). Accumulation of *Aspergillus* in the later phases of potato development increases the risk of the tuber contamination.

The shifts in populations described above would tend to decrease the suppressiveness of the habitat towards soil-borne potato pathogens at the flowering phase.

Saprotrophic fungi, by their uptake of mineral nutrients and decomposition of detritus, are essential for nutrient cycling and formation of ecosystems. A few taxa that had increased density at the flowering phase, i.e. *Alternaria*, *Arthrinium*, *Chaetomium* and *Ulocladium*, are known secondary saprotrophic colonizers of potato tissues (Shukla et al. 1990). Although *Mucor mucedo* and *Torula herbarum*, according to Shukla et al. (1990), belong to this group, they were more frequent at the emergence phase. Greater density of *Geomyces*, *Mortierella* and *T. polysporum* at the emergence phase resulted from their respective preferences for low temperature and high moisture. *Geomyces* spp. have low-temperature adapted fatty acids in their cell membrane that allow them to grow in colder seasons (Finolti et al. 1993). *Mortierella* spp. and *T. polysporum* prefer very humid and moist soils with high organic contents (Domsch et al. 1993). *Mortierella* species exhibited typical ruderal behaviour: rapid mycelial growth, rapid colonization of newly available resources, limited enzymatic range, rapid and prolific asexual reproduction, and lysis of mycelium following nutrient depletion and survival by spores (Dix and Webster 1995).

The general hypothesis of species diversity assumes that most communities exist in a state of non-equilibrium, where competitive equilibrium is prevented by periodic population decreases or increases and environmental fluctuations (Huston 1979). Increases in growth rates of successful competitors are expected to decrease diversity. Such correlations were observed in this study. In roots and rhizoplane, domination by *Clonostachys, Fusarium*, *Penicillium* and often *Haematonectria*, rarely *C. coccodes*, seemed to decrease microbial diversity measured by the number of species. The slightly greater numbers of species at flowering and the greater number of specific species for the flowering phase (19), compared with the number of specific species at emergence (15) indicates a tendency for a habitat to differentiate new niches in time.

The conservation and enhancement of soil microbial diversity are part of the foundation of sustainable farming practices. If the soil microbial biodiversity is permanent it can improve biodiversity in other parts of the environment (bodies of water and the broader agricultural landscape). Similar numbers of species were often recorded at the emergence and flowering phases but the biodiversity was not permanent; the microbiota varied qualitatively.

Conclusions

This study on dynamics of microbiota in potato provides new information that: (a) increases understanding of the epidemiology of some potato diseases, (b) can contribute to decision making, based on economic and ecological considerations, for chemical control in potato crops (active ingredient and timing), (c) can contribute to development strategies for manipulation of the soil microbial environment as a viable crop management technique, and (d) can contribute to development of prognosis models for potato diseases in central Europe.

References

Adams, M. J. (1979). Factors affecting survival of *Phoma exigua* var. foveata in soil. *Transactions of the British Mycological Society, 73*, 91–97.

Alkan, N., Fluhr, R., Sherman, A., & Prusky, D. (2008). Role of ammonia secretion and pH modulation on pathogenicity of *Colletotrichum coccodes* on tomato fruit. *Molecular Plant -Microbe Interactions, 21*, 1058–1066.

Cabello, M., & Arambarri, A. (2002). Diversity in soil fungi from undisturbed and disturbed *Celtis tala* and *Scutia buxifolia* forests in the eastern Buenos Aires province (Argentina). *Microbiological Research, 157*, 115–125.

Chand, T., & Logan, C. (1984). Post-harvest development of *Rhizoctonia solani* and its penetration of potato tubers in Northern Ireland. *Transactions of the British Mycological Society, 82*, 615–619.

Dillard, H. R. (1990). Survival of *Colletotrichum coccodes* in New York. *Phytopathology, 80*, 1026.

Dillard, H. R., & Cobb, A. C. (1993). Persistence of *Colletotrichum coccodes* on tomato roots and in soil. *Phytopathology, 83*, 1345.

Dillard, H. R., & Cobb, A. C. (1998). Survival of *Colletotrichum coccodes* in infected tomato tissue and in soil. *Plant Diseases, 82*, 235–238.

Ditzler, C. A., & Tugel, A. J. (2002). Soil quality fiield tools: Experience of USDA-NRCS soil quality Institute. *Agronomy Journal, 94*, 33–38.

Dix, N. J., & Webster, J. (1995). *Fungal ecology*. London: Chapman and Hall.

Domsch, K. H., Gams, W., & Anderson, T.-H. (1993). *Compendium of soil fungi*. London: Academic.

Farley, J. D. (1976). Survival of *Colletotrichum coccodes* in soil. *Phytopathology, 66*, 640–641.

Finolti, E., Moretto, D., Marsella, R., & Mercantini, R. (1993). Temperature effects and fatty acid patterns in *Geomyces* species isolated from Antarctic soil. *Polar Biology, 13*, 127–130.

Frankland, J. C. (1981). Mechanisms in fungal successions. In D. T. Wicklow & G. C. Carroll (Eds.), *The fungal community, its organization and role in the ecosystem* (pp. 403–426). New York: Marcel Dekker.

Gilpatrick, D. (1969). Role of ammonia in the control of avocado root rot with alfalfa meal soil amendment. *Phytopathology, 59*, 973–978.

Hagedorn, C., & Holt, J. G. (1975). Ecology of soil arthrobacters in Clarion–Webster toposequences of Iowa. *Applied Microbiology, 29*, 211–218.

Harman, G. E., & Kubicek, C. P. (1998). *Trichoderma and gliocladium, enzymes, biological control and commercial applications*. London: Taylor and Francis.

Hide, G. A. (1986). *Phoma* and *Fusarium* rots on imported 'new' potatoes. *Plant Pathology, 35*, 126–127.

Huston, M. (1979). A general hypothesis of species diversity. *American Naturalist, 113*, 81–101.

Ingram, J., & Johnson, D. (2010). Colonization of potato roots and stolons by *Colletotrichum coccodes* from tuberborne inoculum. *American Journal of Potato Research, 87*, 382–389.

Kawasaki, T., Miyata, I., Esaki, K., & Nose, Y. (1969). Thiamine uptake in *Escherichia coli:* I. General properties of thiamine uptake system in Escherichia coli. *Archives of Biochemistry and Biophysics, 131*, 223–230.

Kent, A. D., & Triplett, E. W. (2002). Microbial communities and their interactions in soil and rhizosphere ecosystems. *Annual Review of Microbiology, 56*, 11–236.

Krauss, U., & Soberanis, W. (2001). Biocontrol of cocoa pod diseases with mycoparasite mixtures. *Biological Control, 22*, 149–158.

Lemańczyk, G., & Łukanowski, A. (2000). Fungal communities and health status of winter wheat roots cultivated after lupine and its mixtures. *Phytopathologia Polonica, 20*, 139–154.

Lemańczyk, G., & Sadowski, C. K. (2000). The effect of different forecrops on the occurrence of *Fusarium* spp. in winter wheat rhizosphere. *Phytopathologia Polonica, 20*, 131–138.

Lemańczyk, G., & Sadowski, C. K. (2002). Fungal communities and health status of roots of winter wheat cultivated after oats and oats mixed with other crops. *BioControl, 47*, 349–361.

Lenc, L. (2006). *Rhizoctonia solani* and *Streptomyces scabies* on sprouts and tubers of potato grown in organic and integrated systems, and fungal communities in the soil habitat. *Phytopathologia Polonica, 42*, 13–28.

Li, S., Hartman, G. L., & Gray, L. E. (1998). Chlamydospore formation, production, and nuclear status in *Fusarium solani* f. sp. *glycines* soybean sudden death syndrome-causing isolates. *Mycologia, 90*, 414–21.

Magurran, A. E. (1988). *Ecological diversity and its measurement*. Princeton: Princeton University Press.

Manici, L. M., & Cerato, C. (1994). Pathogenicity of *Fusarium oxysporum* f.sp. *tuberosi* isolates from tubers and potato plants. *Potato Research, 37*, 129–134.

Mańka, K. (1974). Zbiorowiska grzybów jako kryterium oceny wpływów środowiska na choroby roślin. (Fungal communities as a criterion for estimating the effect of the environment on plant diseases). *Zeszyty Problemowe Postepów Nauk Rolniczych, 160*, 9–23.

Marais, L. (1990). Efficacy of fungicides against *Colletotrichum coccodes* on potato tubers. *Potato Research, 33*, 275–81.

Morita, R. Y., & Buck, G. E. (1974). Low temperature inhibition of substrate uptake. In R. R. Colwel & R. Y. Morita (Eds.), *Effect of ocean environment on microbial activities*. Baltimore: University Park Press.

Paparu, P., Dubois, T., Gold, C. S., Niere, B., Adipala, E., & Coyne, D. (2008). Screenhouse and field persistence of nonpathogenic endophytic *Fusarium oxysporum* in *Musa* tissue culture plants. *Microbial Ecology, 55*, 561–568.

Piper, S., Martınez, A., Hidalgo, E., & Krauss, U. (2000). Effect of formulation on population dynamics of mycoparasites on the surface of cocoa pods. In C. L. Bong, C. H. Lee, & F. S. Shari (Eds.), *Proceedings of the INCOPED 3rd international seminar on cocoa pest and diseases* (pp. 21–26). Kota Kinabalu: Sabah.

Piperno, J. R., & Oxender, D. L. (1968). Amino acid transport system in *Escherichia coli* K12. *Journal of Biological Chemistry, 243*, 5914–5920.

Pitt, J. I. (2002). Biology and ecology of toxigenic *Penicillium* species. Mycotoxins and food safety. *Advances in experimental medicine and biology, 504*, 29–41.

Powlson, D. S., & Jenkinson, D. S. (1981). A comparison of the organic matter, biomass, and mineralizable nitrogen contents of ploughed and direct-drilled soils. *Journal of Agricultural Sciences, Cambridge, 97*, 713–721.

Powlson, D. S., Brookes, P. C., & Christensen, B. T. (1987). Measurement of soil microbial biomass provides an early indication of changes in total soil organic matter due to straw incorporation. *Soil Biology and Biochemistry, 19*, 159–164.

Read, P. J., & Hide, G. A. (1995). Effects of fungicides on the growth and conidial germination of *Colletotrichum coccodes* and on the development of black dot disease of potatoes. *Annals of Applied Biology, 126*, 437–447.

Read, P. J., Storey, R. M., & Hudson, D. R. (1995). A survey of black dot and other fungal tuber blemishing diseases in British potato crops at harvest. *Annals of Applied Biology, 126*, 249–258.

Saffigna, P. G., Powlson, D. S., Brookes, P. C., & Thomas, G. A. (1989). Influence of sorghum residues and tillage on soil organic matter and soil micro- bial biomass in an Australian Vertisol. *Soil Biology and Biochemistry, 21*, 759–765.

Schippers, B., & Old, K. M. (1974). Factors affecting chlamydospores formation by *Fusarium solani* f. sp. *cucurbitae* in pure cultures. *Soil Biology and Biochemistry, 6*, 153–160.

Schlatter, D., Fubuh, A., Xiao, K., Hernandez, D., Hobbie, S., & Kinkel, L. (2009). Resource amendments influence density and competitive phenotypes of *Streptomyces* in soil. *Microbial Ecology, 57*, 413–420.

Scudamore, K. A., & Livesey, T. (1998). Occurrence and significance of mycotoxins in forage crops and silage: a review. *Journal of the Science of Food and Agriculture, 77*, 1–17.

Shukla, A. K., Tiwari, B. K., & Mishra, R. R. (1990). Decomposition of potato litter in relation to microbial population and plant nutrients under field condition. *Pedobiologia, 34*, 287–298.

Simon, A., & Ridge, E. H. (1974). The use of ampicillin in a simplified selective medium for the isolation of fluorescent *Pseudomonas*. *Journal of Applied Bacteriology, 37*, 459–460.

Singh, B. P., Nagaich, B. B., & Saxena, S. K. (1987). Fungi associated with dry rot of potatoes, their frequency and distribution. *Indian Journal of Plant Pathology, 5*, 142–145.

Suárez-Estrella, F., Vargas-Garcia, M. C., Lopez, M. J., & Moreno, J. (2004). Survival of *Fusarium oxysporum* f. sp. *melonis* on plant waste. *Crop Protection, 23*, 127–133.

Tenuta, M. (2001). The role of nitrogen transformation products in the control of soil-borne plant pathogens and pests. Ph. D. Thesis. University of Western Ontario, London, Ontario.

Thanassoulopoulos, C. C., & Kitsos, G. T. (1985). Studies on *Fusarium* wilt of potatoes. 1. Plant wilt and tuber infection in naturally infected fields. *Potato Research, 28*, 507–514.

Theron, D. J. (1991). Prediction of potato dry rot based on tile presence of *Fttsarittm* in soil adhering to tubers at harvest. *Plant Diseses, 75*, 126–130.

Tivoli, B., Torres, H., & French, E. R. (1988). Inventaire, distribution et agressivité des espéces ou variétés de *Fusarium* rencontrées sur la pomme de terre ou dans son environnement dans différentes zones agroécologiques du Pérou. *Potato Research, 31*, 681–690.

Upstone, M. E. (1970). A corky rot of Jersey Royal potato tubers caused by *Fusarium oxysporum*. *Plant Patholology, 19*, 165–167.

Williams, S. T., & Davies, F. L. (1965). Use of antibiotics for selective isolation and enumeration of *Actinomycetes* in soil. *Journal of General Microbiology, 38*, 251–261.

Windels, C. E. (1993). *Fusarium* species stored on silica gel and soil for ten years. *Mycologia, 85*, 21–23.