

Spatial distribution of *Rhizoctonia oryzae* and rhizoctonia root rot in direct-seeded cereals

T.C. Paulitz, H. Zhang, and R.J. Cook

Abstract: *Rhizoctonia oryzae* causes root rot and stunting of wheat, barley, and other small grains, and is widely distributed in eastern Washington State. The spatial distribution of both the pathogen and the disease were studied over two seasons in a 36-ha field north of Pullman, Wash. The field was direct seeded with spring barley in 2000, then divided and planted to winter wheat and spring wheat in 2001. The incidence of crown-root rot and root colonization by *R. oryzae* were measured on plants taken from 95 sites 30–100 m apart on a nonaligned grid, localized by global positioning system. The incidence of crown-root rot was low, averaging 18, 16, and 13% on the spring barley, spring wheat, and winter wheat, respectively. The incidence of root colonization by *R. oryzae* was even lower, averaging 4, <1, and 2% on the spring barley, spring wheat, and winter wheat, respectively. The frequency distributions were highly skewed, with a high frequency of zero or low values. The distributions were fit to a beta-binomial distribution, indicating an aggregated or overdispersed distribution. Because of the highly skewed data, traditional geostatistical approaches did not show spatial correlation. However, a spatial generalized linear mixed model did show spatial correlation and was used to interpolate values to produce pathogen and disease distribution maps. This large-scale mapping of soilborne pathogens may have applications in precision agriculture.

Key words : global positioning system, spatial generalized linear mixed model, beta-binomial distribution, precision agriculture, geostatistics.

Résumé : Le *Rhizoctonia oryzae* cause le rhizoctone noir et l'arrêt de croissance chez le blé, l'orge et d'autres petites semences, et est largement distribué dans l'est de l'État de Washington. La répartition géographique de l'agent pathogène et de la maladie fut étudiée durant deux saisons dans un champ de 36 ha au nord de Pullman, Washington. Le champ fut planté en orge de printemps par ensemencement direct en 2000, puis subdivisé et planté en blé d'automne et blé de printemps en 2001. La fréquence de la pourriture du collet et de la colonisation des racines par le *R. oryzae* fut mesurée sur des plantes provenant de 95 sites distants de 30 à 100 m sur une grille non alignée, localisés par système de positionnement global. La fréquence de la pourriture du collet fut faible, respectivement aux environs de 18, 16 et 13% sur l'orge de printemps, le blé de printemps et le blé d'automne. La fréquence de la colonisation des racines par le *R. oryzae* fut encore plus basse, avec des moyennes respectives de 4, <1 et 2% sur l'orge de printemps, le blé de printemps et le blé d'automne. Les distributions des fréquences étaient très asymétriques, avec beaucoup de valeurs nulles ou faibles. Les distributions s'ajustaient à une courbe de distribution bêta-binomiale, ce qui indique une distribution agrégative ou surdispersée. À cause des données très asymétriques, les approches géostatistiques classiques n'ont pas montré de corrélation spatiale. Cependant, un modèle linéaire généralisé mixte (GLMM) spatial a révélé une corrélation spatiale et fut utilisé pour interpoler les valeurs servant à produire des cartes de distribution de l'agent pathogène et de la maladie. Cette cartographie à grande échelle de champignons pathogènes telluriques peut avoir des applications en agriculture de précision.

Mots clés : système de positionnement global, modèle linéaire généralisé mixte spatial, distribution bêta-binomiale, agriculture de précision, géostatistique.

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Introduction

Rhizoctonia root rot, caused by mixtures of *Rhizoctonia solani* Kühn AG-8 and *R. oryzae* Ryker and Gooch, can be a major yield limitation in direct-seeded (no-till) cereals. *Rhizoctonia solani* AG-8, cause of root rot and bare patch, was discovered in Australia in the 1930's (Samuel and Garrett 1932) and in the Pacific Northwest in the mid 1980's (Weller et al. 1986). This pathogen can become especially damaging in direct-seed systems (Weller et al. 1986; Pumphrey et al. 1987; MacNish 1985a; Rovira and Venn 1985), yet growers are increasingly interested in direct-seed systems in eastern Washington State, because of lower costs of production, the soil and water conservation benefits, and reduced use of fossil fuels. Much of the wheat production in that state is on steep hillsides, and the conventional wheat – summer fallow rotation leads to significant loss of soil from wind and water erosion. *Rhizoctonia oryzae* was first detected in eastern Washington State and adjacent northeastern Oregon in the late 1980's (Ogoshi et al. 1990), but was considered to be only weakly pathogenic (Ogoshi et al. 1990; Smiley and Uddin 1993). However, work by Mazzola et al. (1996) showed that 12 out of 19 strains were pathogenic in natural soil at 12°C. Recent work (Paulitz et al. 2002a) demonstrated that *R. oryzae* was predominant in the higher rainfall areas with silt loam soils and was highly pathogenic to wheat, barley, pea (Paulitz 2002b), and other broadleaf rotation crops. *Rhizoctonia oryzae* does not cause bare patches, but does cause damping-off, stunting, reduction in tillering and root production, and reduction in yield.

There are some important questions concerning the spatial distribution of *Rhizoctonia* spp. in cereals. In the case of *R. solani* AG-8 causing bare patches, the patchy distribution is easy to visualize in the field and to map (MacNish 1985b; Cook et al. 2002). However, since *R. oryzae* does not produce disease as patches, its distribution cannot be easily visualized. Other studies of the spatial distribution of *Rhizoctonia* have focused on foliar and stem diseases caused by *R. solani* that are easy to recognize and score. These include summer blight on white clover (Nelson and Campbell 1993a, 1993b), foliar blight on soybean (Yang et al. 1991), hypocotyl rot on beans (Campbell and Pennypacker 1980), patch disease in turfgrass (Martin et al. 1983; Yuen et al. 1994), and sheath blight in rice (Savary et al. 2001).

Most of the work on spatial distribution of diseases caused by soilborne pathogens has focused on smaller scales, usually on the order of 10 to 100 m, or an area of 1 ha or less. With the advent of GPS (global positioning system) technologies, it is possible to do spatial sampling on a larger scale, with a resolution of around 1 m, with the intent of integrating this information with a precision-agriculture approach to crop, pest, and disease management. Precision agriculture has been defined as “the application of technologies and principles to manage spatial and temporal variability associated with all aspects of agricultural production for the purpose of improving crop performance and environmental quality” (Pierce and Nowak 1999). The idea behind precision agriculture is the proper placement of agricultural inputs at the right time and place to match the crop requirements on a localized basis. Fertilizer placement and timing

is especially important, because of the impaired ability of plants with diseased or missing roots to take up nutrients. Weed control in cereals is also important because *Rhizoctonia* spp. can use volunteers or weeds to build up inoculum that can serve as a “green bridge” to the crop (Smiley et al. 1992; Roget et al. 1987).

In 1999, the Cunningham Agronomy Farm, owned by Washington State University, was established north of Pullman, Wash., and dedicated to a large-scale direct-seed, precision-agriculture cropping system study. Three hundred and sixty-nine sites were GPS-located on a 36-ha site within this farm to capture landscape variability due to the topography. An interdisciplinary research effort has developed and mapped a large database of soil characteristics, available seasonal water, drainage, pH, weed seed banks, and annual yield and protein content of grain based on these 369 georeferenced sites.

The purpose of this work was to look at the spatial distribution or pattern of *R. oryzae* over the 36-ha site, by sampling at 95 randomly selected sites. Incidence data from root isolations and root-rot assessments were fit to discrete distributions to detect randomness or clustering. However, in fitting frequency distributions such as binomial, beta-binomial, or Poisson, it is assumed that incidence data collected at different spatial locations are independent. This assumption is vital to maximum likelihood estimation of model parameters and to the goodness-of-fit test. However, spatial correlation often exists in most practical situations, i.e., given a spatial location of high incidence, the incidence at a nearby neighbor is also likely to be high.

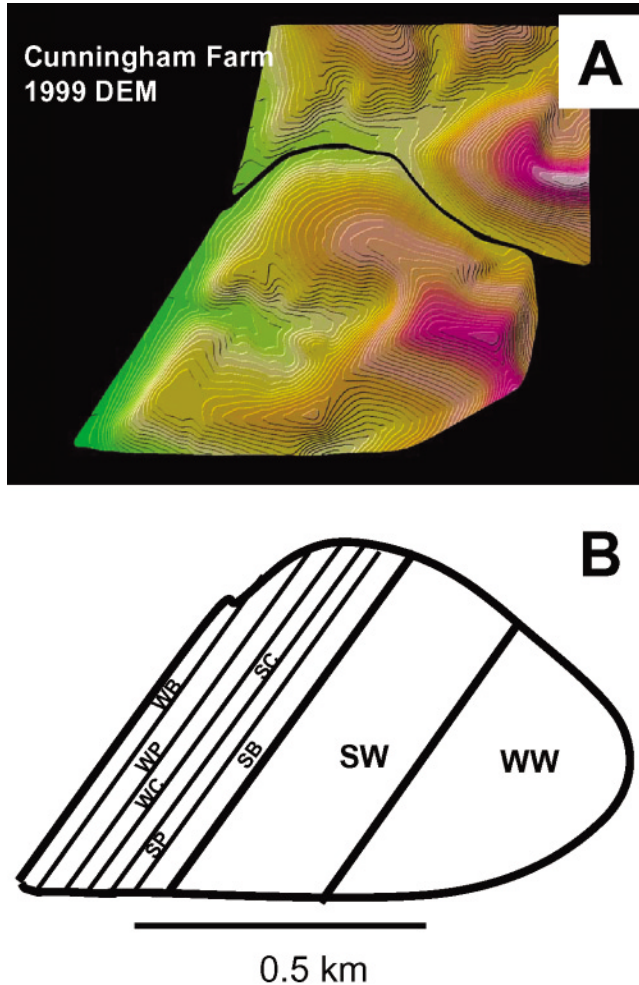
In the traditional literature, spatial correlation is often characterized by the variogram, defined as one half of the mean squared difference between observations at two locations of certain distance units apart. Spatial correlation has not been considered in most work on spatial point patterns. This paper is an attempt to incorporate spatial correlation into the analysis of spatial point pattern by employing spatial generalized linear mixed models (GLMM) developed in the last few years (Diggle et al. 1998; Zhang 2002a, 2002b, 2003). This spatial GLMM approach also allows for interpolation of incidence rates at unsampled sites. One advantage of this approach for interpolation over some classical kriging methods is that it effectively incorporates the sample size, i.e., the total number of roots sampled at each site into the interpolation, which cannot be done with classical kriging methods such as ordinary kriging and indicator kriging. Another advantage of the spatial GLMM approach is that it reveals spatial correlation more effectively than the classical geostatistical methods, especially when the incidence data are extremely skewed, such as the data from our work.

Materials and methods

Site characteristics

The study was conducted on the Cunningham Agronomy Farm, a 57-ha farm located 10 km north of Pullman, Wash., at 117°5'W, 46°47'N (Fig. 1A). The site ranges from 771 to 823 m in elevation, typical of the hilly Palouse region. Latah, Palouse, Thatuna, and Naff silt loams are all present on the site, with A horizon depths ranging from 20 to

Fig. 1. (A) Topographical map of the Cunningham Agronomy Farm (D.M. Huggins, unpublished). Elevation range, 773–817 m; contour interval, 1 m. (B) Crop rotations in 2001. SB, spring barley; WB, winter barley; SC, spring canola; WC, winter canola; SP, spring pea; WP, winter pea; SW, spring wheat; WW, winter wheat.



100 cm. This research farm was established in 1999, and 369 GPS sites were established on a grid over the 36-ha portion of the southwestern part of the farm. From 1999 to 2002, these sites have been sampled to determine soil characteristics, including pH, texture, water infiltration and content, weed seed banks, and annual grain yield and protein content. This 36-ha section was direct seeded with dark northern spring wheat (*Triticum aestivum* L. 'WPB926') on 10–14 April 1999 at a rate of 134 kg·ha⁻¹. All cereal crops were seeded at a depth of 1.25–2.5 cm, with double-disk openers and a row spacing of 25 cm, using a Great Plains direct-seed drill. N, P, and K fertilizer were applied as a deep band with the drill so as to place these nutrients directly beneath the seed at a rate of 162, 22, and 34 kg·ha⁻¹, respectively, for the crop in 1999. In 2000, the area was direct seeded with spring barley (*Hordeum vulgare* L. 'Baronesse') on 17–20 April, using the same drill, at a rate of 134 kg·ha⁻¹. N, P, and K were applied at 110, 22, and 16 kg·ha⁻¹, respectively, with the drill beneath the seed.

In fall 2000, the 36-ha plot was divided into three approximately 12-ha fields (Fig. 1B). The eastern third of the area was direct seeded with winter wheat 'Madsen' on 20–24 October 2000, at a rate of 112 kg·ha⁻¹, with N, P, and K applied at 196, 22, and 17 kg·ha⁻¹, respectively. The center third of the area was direct seeded with spring wheat 'Hank' on 24 March 2001 at a rate of 112 kg·ha⁻¹, with N, P, and K applied at 157, 22, and 35 kg·ha⁻¹, respectively. The western strip was further subdivided into six 2-ha strips, one of which was direct seeded to winter barley ('Hundred') on 19 October 2000 at a rate of 100 kg·ha⁻¹, with N, P, and K at 157, 22, and 17 kg·ha⁻¹, respectively, and another with spring barley ('Baronesse') on 26 March 2000, at a rate of 103 kg·ha⁻¹, with N, P, and K at 110, 22, and 16 kg·ha⁻¹, respectively. The other four strips were seeded with winter pea (*Pisum sativum* L.), spring pea, winter canola (*Brassica napus* L. var. *napus*), and spring canola. Root-colonization data from all crops were included in the mapping interpolation for 2001. However, in 2001, data for crown-root rot were taken only from the winter and spring wheat and winter and spring barley plots, not from the broadleaf crops.

Data collection

Fifteen barley plants were dug from each site on 6 June 2000. The sites were located with a Mid-Tech RX 400P a differential GPS unit (Midwest Technologies, Inc., Springfield, Ill.). This differential GPS unit uses the wide area augmentation system (WAAS) satellite and has a horizontal accuracy of 1 m with 95% confidence. Roots were washed, and seminal and crown roots were counted on each plant, along with the number that had symptoms of *Rhizoctonia* infection, including brown root tips, brown lesions, spear tipping, or where the cortex was rotted away leaving the stele. On 26 and 27 July 2000, five additional plants were removed from each of the same 95 sites. Roots were washed and plated on agar medium containing 1 µg·mL⁻¹ benomyl to inhibit fungal growth and 100 µg·mL⁻¹ chloramphenicol to inhibit bacterial growth. From each plant, ten 1- to 2-cm lengths of roots were placed on the medium of each plate, for a total of 50 root segments for each georeferenced site. After 24 h, plates were examined under a dissecting microscope and root segments with characteristic colonies of *Rhizoctonia* were counted. Hyphal tips were taken from all the positive root segments and transferred to potato dextrose agar to confirm the identifications. Identifications were also confirmed by examination of hyphae at × 400 for the presence of right-angle branching, constriction of branch hyphae at the point of attachment to the main hyphae, wide hyphal diameter, and dolipore septa. On 22 May 2001, five plants were removed from each georeferenced site in all rotations. Roots of all rotation crops were washed and rated for percent root colonization based on plating, as described above. Roots of cereals were rated for crown-root rot (percent incidence of crown roots showing *Rhizoctonia* infection based on symptoms).

Data analysis

Incidence of crown-root rot on the cereals, based on the presence or absence of symptoms, was calculated for each site. Incidence of root colonization for each site was calculated based on the number of plated root segments giving

rise to *Rhizoctonia* colonies. We use two approaches to analyze the incidence patterns: the frequency distribution analysis and the spatial GLMM approach. The latter but not the former takes into consideration possible spatial correlation.

Frequency distribution analyses and indices

To see whether the data were random or clustered, beta-binomial (BBD) and binomial (BD) distributions were fitted to the data, with the help of the computer program BBD, Windows version (Madden and Hughes 1994). A good fit to the BBD suggests an aggregated or overdispersed spatial pattern of disease and pathogen incidence. A good fit with the BD suggests a random distribution. The goodness-of-fit of the observed frequency distributions compared with the expected distributions was tested with the Kolmogorov–Smirnov test statistic. A $\theta > 0$ from the BBD indicates aggregation. The $C(\alpha)$ test served to determine if there was overdispersion, which could be described by the BBD. The index of dispersion (D) was also calculated for the data. This index is similar to the variance/mean ratio for count data, and $D > 1$ indicates spatial aggregation.

Mapping, spatial correlation, and interpolation

The beta-binomial approach can effectively model spatial heterogeneity but does not utilize the spatial configuration or location of the incidence data. For this report, we modeled spatial heterogeneity while incorporating the spatial dependence of the incidence data.

An analogy can be drawn between the spatial GLMM and the beta-binomial model. When n units are sampled at a location, it is reasonable to assume that the number of diseased units, denoted by Y , is binomial with index n and binomial probability p . However, the binomial probability may change from location to location. In the beta-binomial approach, the heterogeneity of the binomial probability is modeled through a beta distribution. More specifically, the binomial probabilities at the sampling locations are assumed to be independently and identically distributed from a beta distribution. In the spatial GLMM, the binomial probabilities p are assumed to depend on some stationary normal process b whose values change from location to location, e.g.,

$$[1] p = \exp(\beta + b) / [1 + \exp(\beta + b)]$$

Hence this approach models not only the spatial heterogeneity but also the dependence of the incidence values. In this work, the logistic link, which is the most popular choice of link functions for binomial data (McCullagh and Nelder 1989), was employed. The distribution of the normal process b was characterized by a variogram. In this work, the exponential variogram was used, which has the parametric form:

$$[2] \gamma(h) = \theta_1 + \theta_2[1 - \exp(-h/\theta_3)], \quad \text{for } h \geq 0$$

The variance of b is $\theta_1 + \theta_2$. A positive variance of b indicates extra-binomial variation. The partial sill θ_2 reflects the strength of the spatial correlation. The sill is a constant value of the variance that stabilizes beyond the range (the lag distance at which there is no spatial dependence or correlation). The spatial GLMM was fit to the data from

crown-root rot and root colonization, with the assistance of the exponential variogram for root colonization and the spherical variogram for the crown-root rot. Maximum likelihoods of the parameter β and those parameters in the variogram of b were estimated with the Monte Carlo EM algorithm, as discussed in Zhang (2002a). Once the parameters were estimated, the optimal interpolation in the sense of mean squared error could be evaluated (Diggle et al. 1998; Zhang 2003).

Results

Frequency distributions and indices

The incidence of root colonization by *R. oryzae* was highly skewed, with a high frequency of zero values (Fig. 2). Most of the plants that were infected had low percentages of colonization. In 2000, the average incidence of root colonization was only 4% on spring barley (Fig. 2A) and, in 2001, it was <1% on spring wheat (Fig. 2B) and 1.9% on winter wheat (Fig. 2C). *Rhizoctonia oryzae* was not detected at most sites in 2000 or 2001. In 2000, roots were positive for *R. oryzae* in only 27 out of 95 sites and, in 2001, in only 29 out of 95 sites.

The incidence of crown-root rot was less skewed (Fig. 3), but still did not show a normal distribution. In general, the percentage of crown roots showing symptoms was higher than the percentage of roots colonized by *R. oryzae*. The average incidence of diseased crown roots on spring barley (Fig. 3A), spring wheat (Fig. 3B), and winter wheat (Fig. 3C) was 18.2, 15.8, and 13.4%, respectively.

The frequency distributions of incidence of root colonization could be described by the BBD (Table 1 and Fig. 2), indicative of an aggregated, overdispersed spatial pattern. The binomial model did not fit the data set of root colonization for spring barley, but did for spring wheat, although the fit was better with the BBD. A probability could not be calculated for winter wheat in 2001, but the test statistic indicated a better fit of the BBD.

Data for incidence of crown-root rot from all cereal crops also fit a BBD, except for spring barley, for which these data fit a BD. The θ value of the BBD was >0 for all distributions, except for incidence of crown-root rot of spring barley, indicating overdispersion. D was >1 for all data sets, except for incidence of crown-root rot of spring barley, indicating spatial aggregation. For these same data sets, the $C(\alpha)$ tests showed that this overdispersion could be described by the BBD. For spring barley and spring wheat, incidence of root colonization showed a higher degree of overdispersion than did the incidence of crown-root rot.

Mapping, spatial correlation, and interpolation

Maximum likelihood estimates were made from data sets fit to the spatial GLMM (Table 2). In general, a small and negative β indicates an aggregated pattern. Root colonization was aggregated in both years (Table 2). The positive partial sills reveal the existence of spatial dependence in all data sets. There was considerable spatial variability in all data sets. For example, the estimates show that 95% of incidence rates of root colonization in 2000 varied between 0.013 and 32%, because of spatial heterogeneity. This interval was calculated by letting b vary within two standard de-

Fig. 2. Frequency distribution of incidence of root colonization by *Rhizoctonia oryzae* in (A) spring barley 2000, (B) spring wheat 2001, and (C) winter wheat 2001. Observed data are represented with predicted values from beta-binomial distribution (BBD) and binomial distribution (BD).

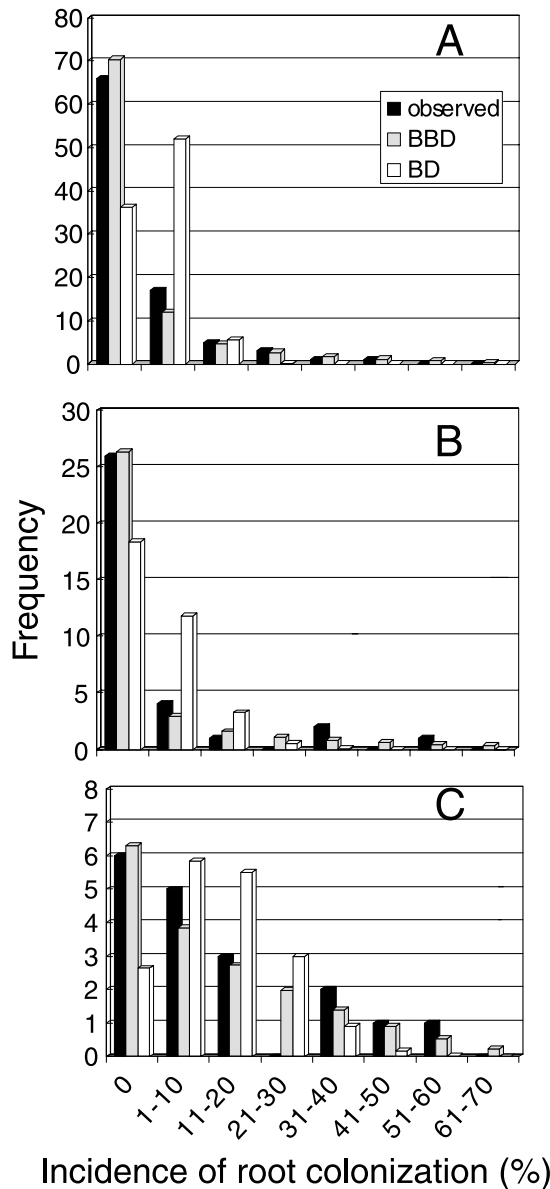
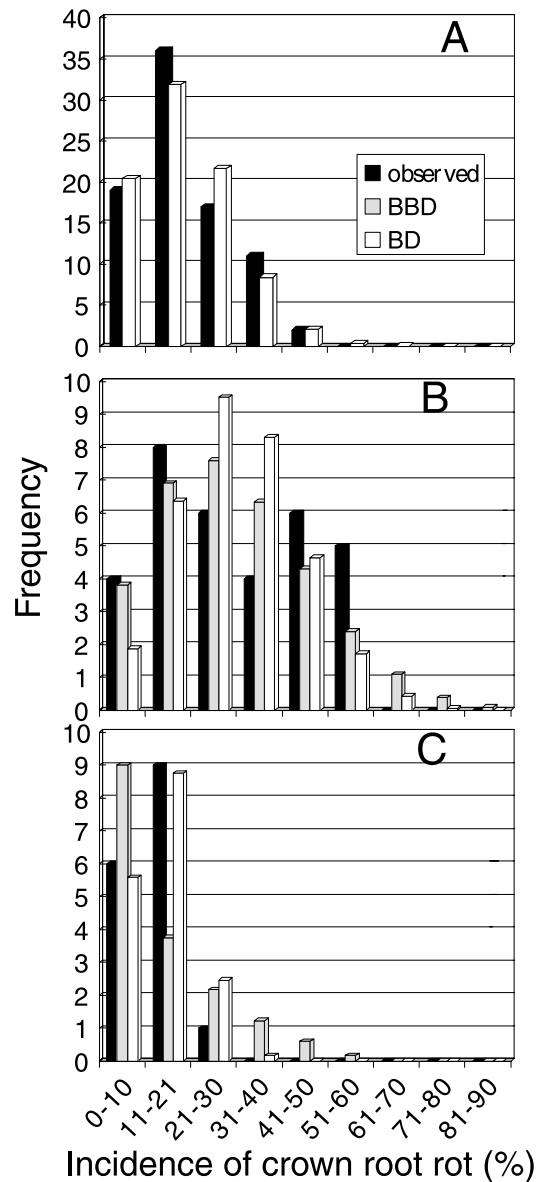


Fig. 3. Frequency distribution of incidence of crown-root rot in (A) spring barley 2000, (B) spring wheat 2001, and (C) winter wheat 2001. Observed data are represented with predicted values from beta-binomial distribution (BBD) and binomial distribution (BD).



viations from the mean 0, i.e., between -4.098 and 4.098 . The corresponding binomial probability,

$$[3] p = \exp(\beta + b) / [1 + \exp(\beta + b)]$$

will then vary between 0.013 and 32% for $\beta = -4.8493$.

Classical geostatistical methods did not work well to effectively reveal the spatial correlation. For example, no spatial correlation was evident from the classical geostatistical variogram of barley root-colonization data in 2000 (Fig. 4A). However, using a variogram derived from the spatial GLMM, spatial correlation was evident (Fig. 4B). The range, i.e., the distance at which the variance stabilizes, was approximately 200 m, indicating that points further apart were not spatially correlated.

Root-colonization maps derived from interpolations from the spatial GLMM are shown in Figs. 5 and 6. The pattern of distribution of root colonization, with this model, was remarkably similar both years. Most of the higher values were concentrated in the southwest corner of the field, with intermediate values along the southern and southeastern borders of the field. In contrast, higher incidences of crown-root rot were evident over larger areas of the field (Fig. 7), with the lowest incidences found in a strip along the higher terrain of the field and higher incidences in the lowland (draw) that extends to the center of the field from the west. This same general pattern of lower and higher values was revealed in the map of seminal-root rot from 2000 (data not shown). Despite the general similarity of patterns between 2000 and

Table 1. Statistics for the spatial patterns of incidence of crown-root rot and root colonization of direct-seeded cereals by *Rhizoctonia oryzae*.

	Estimated beta-binomial parameters					$C(\alpha)$ test		K-S statistic p^*	
	p	SE(p)	θ	SE(θ)	D	z	$p(z)$	BBD	BD
Root colonization by <i>Rhizoctonia oryzae</i>									
2000 spring barley	0.05	-1.00	0.49	-1.00	6.00	34.90	0	0.91	0.003
2001 spring wheat	0.08	-1.00	0.72	-1.00	3.61	11.20	0	1.00	0.52
2001 winter wheat	0.23	0.06	0.37	0.18	2.78	5.26	0	—	—
Crown-root rot[†]									
2000 spring barley	0.16	-1.00	0	‡	0.98	-0.21	1.00	‡	1.00
2001 spring wheat	0.27	0.03	0.07	0.05	1.57	2.28	0.01	1.00	0.90
2001 winter wheat	0.10	-1.00	0.33	-1.00	3.74	7.70	0	—	—

Note: Dashes indicate that p was not calculated because of a lack of degrees of freedom. SE, standard error.

* p value from Smirnov's χ^2 approximation of two-tailed Kolmogorov-Smirnov statistic.

[†]Incidence of crown roots showing *Rhizoctonia* symptoms.

[‡]Because $\theta = 0$, BBD distribution was the same as BD distribution.

Table 2. Maximum likelihood estimates of data sets fit to the spatial generalized linear mixed model for crown-root rot and root colonization of direct-seeded cereals by *Rhizoctonia oryzae*.

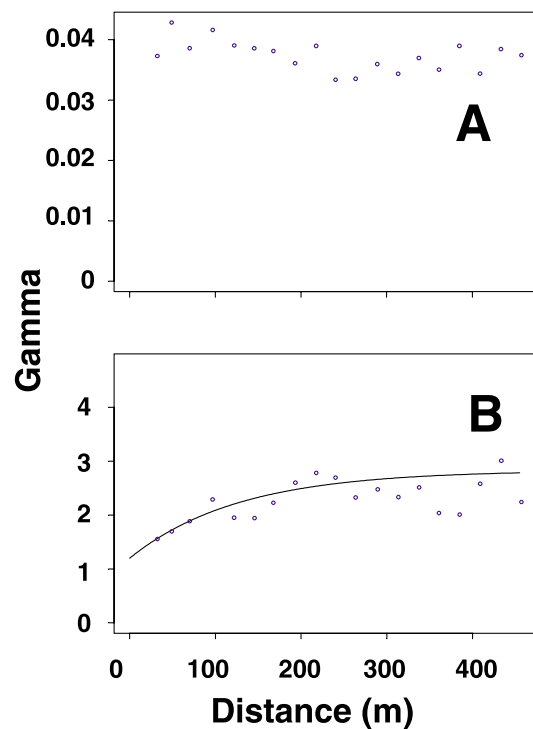
Data set	Estimates			
	β	θ_1	θ_2	θ_3
Crown-root rot				
2000	-1.6152	0.3451	0.1754	145.11
Root colonization by <i>Rhizoctonia oryzae</i>				
2000	-4.8493	2.5641	1.6346	127.02
2001	-4.4831	0.8612	1.1284	142.33

2001, the area of higher values was less in 2001, for both root colonization and crown-root rot.

Discussion

The GPS has been widely applied in ecology, forestry, entomology, weed science, soils, and agronomic cropping system studies (Kravchenko and Bullock 2000; Holmstrom et al. 2001; Luschei et al. 2001). Its use in plant pathology has been mainly for large-scale disease surveys or documentation of diseases spread over a large geographical area, such as for downy mildew of lettuce (Wu et al. 2001) or orchards affected by citrus canker in Florida (Gottwald et al. 2002). Global positioning system has not been favored to study soilborne pathogens, because most studies on the spatial distribution of these pathogens have been done at a finer scale. In our work, we adopted a scale more suitable for applications to precision agriculture, with sample sites no closer to each other than 30 m, over a 36-ha area. This work demonstrates that, at this scale, *R. oryzae* shows an aggregated distribution in direct-seeded cereals, based on both frequency distributions and indices, and the spatial GLMM approach.

The spatial GLMM approach incorporates spatial dependence into the model and may more closely describe the actual field values compared with other approaches. Spatial GLMM is valuable for the analysis of dependent spatial

Fig. 4. Variograms of incidence of root colonization by *Rhizoctonia oryzae* on spring barley, 2000. (A) Variogram using traditional geostatistics. (B) Variogram from spatial generalized linear mixed model. See equation 2 for a definition of γ .

point patterns and also allows for the interpolation of incidence values over the field so that the spatial pattern can be visualized. It distinguishes itself from other geostatistical methods in that it incorporates the binomial sample sizes into the interpolation and reveals spatial correlation where classical geostatistical methods fail.

Based on maps of root colonization, we found that *R. oryzae* was predominant in the southwest corner of the field, with other infested areas (based on infected roots) along the border of the field toward the lowest elevations of west-, south-, and east-facing slopes. There was also a high incidence of root colonization on the south-facing slope

Fig. 5. Spatial map of incidence of root colonization of direct seeded spring barley by *Rhizoctonia oryzae*, 2000. (A) Data points. (B) Interpolated map derived from spatial generalized linear mixed model.

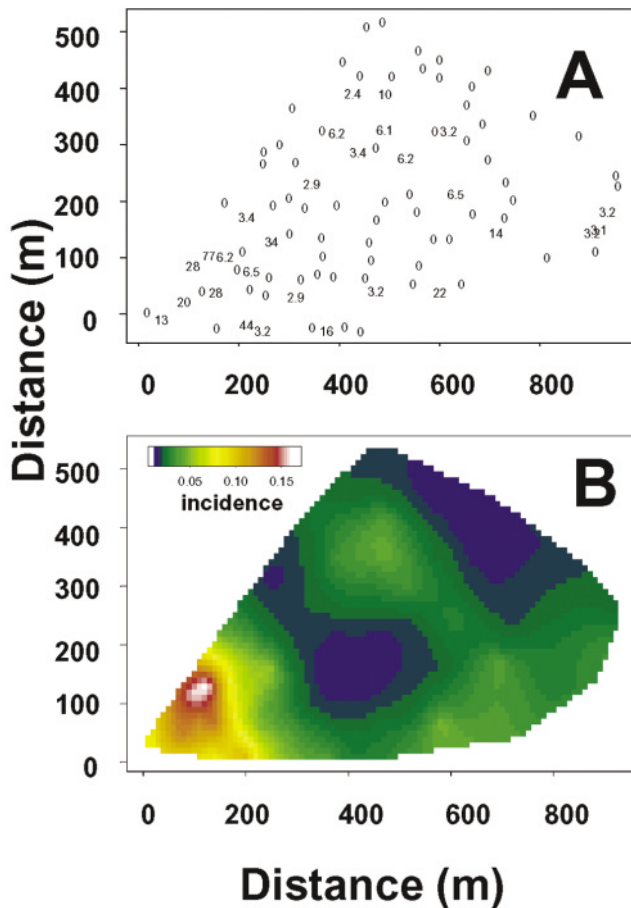
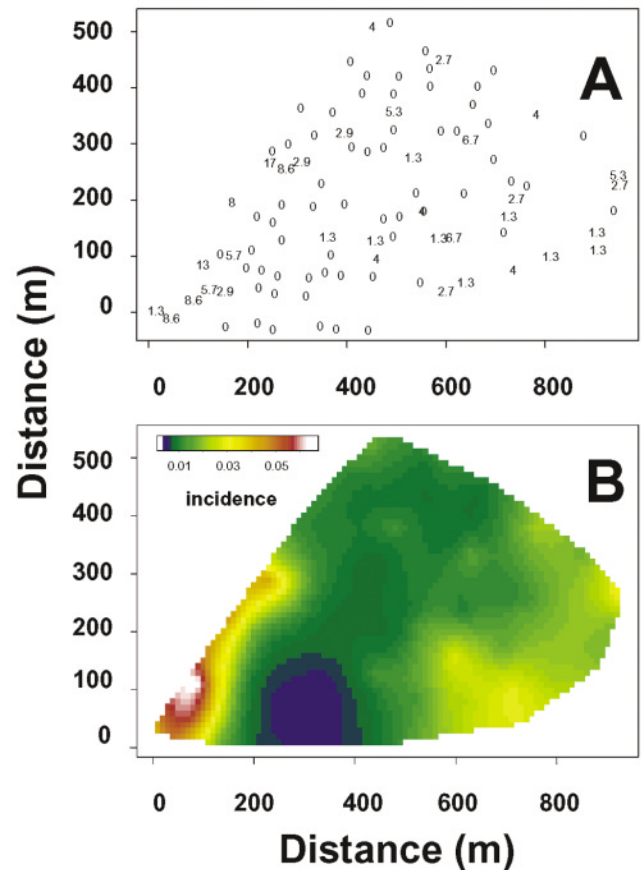


Fig. 6. Spatial map of incidence of root colonization of direct seeded winter and spring wheat by *Rhizoctonia oryzae*, 2001. (A) Data points. (B) Interpolated map derived from spatial generalized linear mixed model.

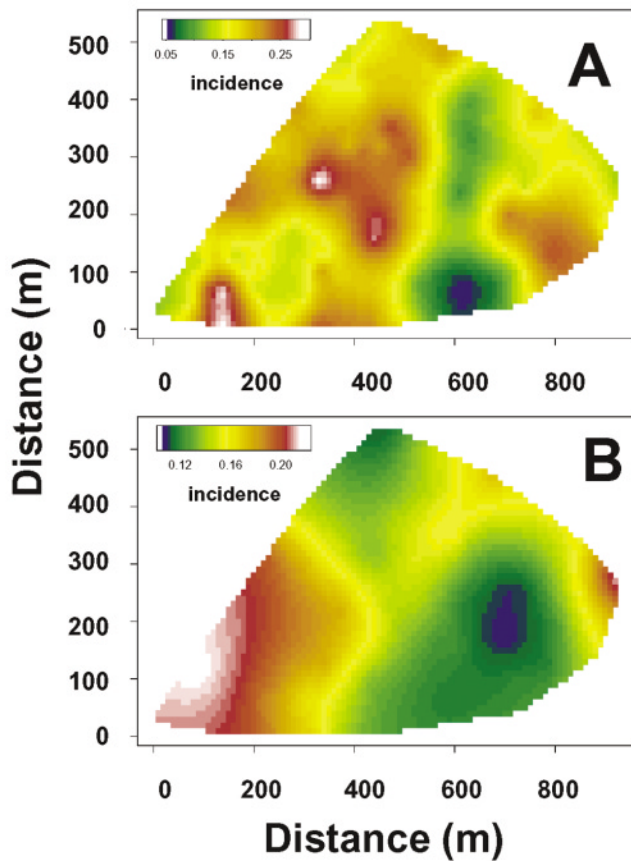


north of the bowl in the middle of the field. This may be due to more suitable soil, environmental, or other unknown edaphic factors. The fact that the pathogen was more prevalent on the borders of the field may indicate movement via roads around the west and southern borders. There was some correlation between areas where the pathogen was isolated from roots and areas with a high incidence of root rot based on visual symptoms. Surprisingly, the symptoms were more widespread than the pathogen, based on direct isolation on agar. The efficiency of culturing out *R. oryzae* from root systems is low because of competition from secondary colonists on the semi-selective medium. Many other fungi grew from the root segments. Thus the actual frequency of this pathogen is likely to be considerably more widespread in the soil and in roots than revealed in our data. Another possibility is that the root symptoms recorded as rhizoctonia root rot could be caused by pathogens other than *R. oryzae*. The incidence of symptoms on the seminal-root system was even higher than on crown roots (T.C. Paulitz, unpublished data).

MacNish (1985b) mapped bare patches caused by *R. solani* AG-8 in no-till wheat, oat, and barley and found that the size, shape, and distribution of the patches varied

between seasons. He proposed that the changes were due to a shift in the balance of suppressive or conducive soil factors. Patches were up to 16 m long and 8 m wide. Cook et al. (2002) mapped bare patches in a field in the 3rd and 4th years of direct seeding with three different rotations and also found that the size and shape of the patches was dynamic. In their study, patches were up to 40 m in diameter. Gilligan et al. (1996) employed bait plants to look at the spatial patterns of inoculum density and stem canker caused by *R. solani* in potatoes, and found spatial correlation and disease occurring in patches. Patches were a maximum of 10–15 m long, based on one-dimensional transects. Natural bare patches of *R. solani* AG 2-t in tulip fields extended up to 3 m long in beds 1.5 m wide (Schneider et al. 2001). *Rhizoctonia oryzae* may exist in patches of similar size, but this cannot be inferred from the present study since our sampling scale (30 m) was larger than the patches reported in the literature. The “hot areas” identified in this study may be aggregations of patches. The dynamic appearance and disappearance of these patches may account for the fact that, in 2001, only 9 of the 27 sites that yielded root colonization were also positive in 2000, and 23 of the 29 positive sites in 2001 were negative in 2000, yet the basic spatial pattern remained for both years.

Fig. 7. Spatial map of incidence of crown-root rot in (A) 2000 and (B) 2001, derived from spatial generalized linear mixed model.



These spatial data will also be useful for studies of disease impacts on yield, since yield data were also taken from hand-harvested 2 m × 2 m plots at each georeferenced site (D.M. Huggins, unpublished data). This will enable us to look at correlations between yield and disease over a wide range of disease levels, unlike the traditional disease survey or method of field plots infested with different levels of inoculum. Disease levels mapped at this spatial scale could also be useful for farmers practicing precision agriculture. Less susceptible cultivars could be seeded in “hot” areas, and seeding depth or fertilizer levels could be modified. Different rotation crops could be chosen, although both *R. solani* AG-8 and *R. oryzae* attack broadleaf crops such as pea and chickpea (Paulitz 2002b), which are common crops in rotation with wheat and barley. Fertilizer could be increased to compensate for root loss, or light tillage could be used within those areas with the most root disease; tillage reduces the amount of bare patch caused by *R. solani* AG-8 (Pumphrey et al. 1987; Roget et al. 1996), although its affect on *R. oryzae* is unknown.

In conclusion, *R. oryzae* shows an aggregated distribution in direct-seeded cereals. This disease can be mapped from large-scale sampling over a large area, using an adaptation of the spatial GLMM, which allows for highly skewed data that would not show spatial correlation with traditional geostatistics. These techniques may be adapted to other

soilborne pathogens and provide information for future applications in precision agriculture.

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