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SHORT COMMUNICATION

Changes in rhizosphere populations of selected physiological groups of bacteria related to substitution of specific pairs of chromosomes in spring wheat

Summary

Rhizosphere population characteristics of two cultivars of spring wheat (*Triticum aestivum* L. emend Thell.), Rescue (R) and Cadet (C), and the related chromosome substitution lines, C–R*5B* and C–R*5D*, were investigated. Replacement of the chromosome pair, *5B*, in Cadet with *5B* from Rescue made many of the rhizosphere microbial characteristics of C–R*5B* similar to or the same as those in the rhizosphere of the donor parent, Rescue. In contrast, substitution of the functionally related chromosome pair, *5D*, did not cause marked changes in the rhizosphere microbial population, demonstrating the specificity of the plant's control over factors governing the rhizosphere microbial environment.

Introduction

Many rhizosphere studies have been concerned with the elucidation of factors in the root zone environments that stimulate or depress the growth of certain groups of soil micro-organisms [1 9]. The growth of these rhizosphere microbes is influenced by the sloughing-off of root cells, physical-chemical balances, and the exudation of metabolites from roots [9], all directly or indirectly influenced by the plant [10 11 12].

Rhizosphere microflora characteristics have been shown to differ for a variety of plants [1 9], but little is known of any genetic basis for these differences. Neal *et al.*[8] working with a disomic chromosome substitution line of spring wheat, showed that specific alteration of host-plant genotype mediates selective changes in the growth and activity of rhizosphere microbes. This communication presents further evidence of such a relationship.

Materials and methods

Lines of spring wheat, *Triticum aestivum* L. emend Thell., selected for study were Cadet (C), a commercial cultivar moderately resistant to common root rot; Rescue (R), a commercial cultivar very susceptible to common root rot; and two homoeologous chromosome substitution lines, C–R*5B* and C–R*5D*, identical to the recipient parent, Cadet, except for the substitution of *5B* and *5D* chromosome pairs, respectively, from the donor parent, Rescue. C–R*5B* is susceptible to root rot whereas C–R*5D* is not [7].

TABLE 1

Total populations and selected physiological groups of micro-organisms in rhizosphere and non-rhizosphere soil*

Rhizosphere soil	Disease reaction**	Bacteria (× 10^6)	Cellulolytic (× 10^3)	Pectinolytic (× 10^4)	Amylolytic (× 10^6)	Ammonifying (× 10^6)	Nitrate-reducing (× 10^5)
Cadet***	Resistant	165.4b††	4.7b	4.1d	2.4c	18.1c	1.2b
Rescue***	Susceptible	335.2a	131.2a	570.2a	38.1b	116.1b	3.8b
C–R5*B*†	Susceptible	325.9a	146.9*a*	270.4b	70.3a	221.2a	2.6b
C–R5*D*†	Resistant	180.4b	3.2b	62.2c	4.4c	15.6c	14.6a
Non-rhizosphere	–	32.1c	0.2c	0.3e	2.0c	1.1d	1.2b

* Per gram of soil, oven-dry basis. Each value represents a geometric mean of three replicates.
** Relative resistance to common root rot[7].
*** Recipient and donor parental varieties, respectively.
† Substitution lines, identical to Cadet except for substitution of chromosome pair, *5B* and *5D*, respectively.
†† Data in each column followed by same letter do not differ statistically ($P = 0.01$).

The general experimental procedures were as previously described [8]. After growing for 7 weeks in the greenhouse, the plant roots were removed and estimates made of the total rhizosphere microbial population and of those microorganisms capable of ammonification, nitrate reduction, and hydrolysis of starch [8], cellulose [15], and pectin [5] by the plate dilution frequency technique [2]. Cellulolytic, pectinolytic, and amylolytic bacteria were specifically selected for enumeration because they may play a role in determining the reaction of wheat to common root rot. The soil was assayed for root rot before seeding and found to be essentially 'disease-free.' The replicated data were subjected to log transformation and analysis of variance. The significance of the difference between the means was determined by Duncan's multiple range test.

Results

The pronounced increase in the total bacterial population of each rhizosphere over that of non-rhizosphere soil demonstrated the typical rhizosphere effect (Table 1). The increase was more pronounced in the rhizosphere of the root-rot-susceptible Rescue and C–R5*B* than in the root-rot-resistant Cadet and C–R5*D*. The bacterial counts were not significantly different between Cadet and C–R5*D* nor between Rescue and C–R5*B*.

More cellulolytic, amylolytic, pectinolytic, and ammonifying bacteria were found in the rhizospheres of Rescue and C–R5*B*, than in the rhizospheres of Cadet and C–R5*D*. The numbers of cellulolytic and pectinolytic micro-organisms were low relative to the number of amylolytic bacteria enumerated in each of the rhizosphere soils. Cadet, Rescue, and C–R5*B* showed no rhizosphere effect in the numbers of nitrate-reducing microbes. The number of nitrate-reducing microbes in the rhizosphere of C–R5*D* was, however, significantly greater than that in the non-rhizosphere soil and in the rhizosphere soils of the other varieties.

Discussion

The data presented substantiate the generally accepted view that rhizosphere soil supports micro-organisms that differ numerically and physiologically from soil devoid of living plant roots. The proportionately greater rhizosphere effect exerted by the root-rot-susceptible varieties, Rescue and C–R*5B*, than by the resistant varieties, Cadet and C–R*5D*, confirms the findings of others [1 3 4 6 8 9 14].

The most interesting aspect of this study was the demonstration that the substitution of a pair of *5B* chromosomes from one cultivar for its homologue in another changed certain microbial characteristics of the rhizosphere in the direction of the donor parent, Rescue (Table 1). C–R*5B*, containing 20 pairs of chromosomes from Cadet and one pair from Rescue, resembled the donor parent, Rescue, in most of the rhizosphere microbial characteristics examined. The fact that the substitution of the homoeologous chromosome pair, *5D*, did not have this effect is evidence for the specificity of the plant's genetic control of the factors governing the rhizosphere environment.

In general, homoeologous chromosomes govern similar metabolic processes [13]. Presumably, then, although chromosome *5D* of Rescue in this instance did not cause the microbial characteristics of the rhizosphere of C–R*5D* to change from those of Cadet to those of Rescue, it nevertheless may carry genes controlling other rhizosphere microbial characteristics not yet investigated.

Chromosome *5B* has a major effect in differentiating resistance and susceptibility to common root rot [7]. In our previous studies, the substitution of *5B* from Apex for *5B* in S–615 not only made the latter resistant [7] but also caused substantial changes in the rhizosphere [8]. In the present study, the substitution of chromosome *5B* of Rescue for that in Cadet, which makes the latter susceptible [7], caused equally profound changes in the rhizosphere.

Since the experiments reported in this paper were conducted in an essentially 'disease-free' soil, we believe these changes in the rhizosphere microbial characteristics are directly attributable to the genetic changes in the plant, not secondarily to the presence of disease as suggested for maize (*Zea mays* L.) [3 4]. Whether or how these changes in the rhizosphere microbial population are causally related to the reaction of the plant to common root rot remains to be seen.

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