Rank Regression for Analyzing Ordinal Qualitative Data for Treatment Comparison

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ABSTRACT

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Ordinal qualitative data are often collected for phenotypical measurements in plant pathology and other biological sciences. Statistical methods, such as *t* tests or analysis of variance, are usually used to analyze ordinal data when comparing two groups or multiple groups. However, the underlying assumptions such as normality and homogeneous variances are often violated for qualitative data. To this end, we investigated an alternative methodology, rank regression, for analyzing the ordinal

data. The rank-based methods are essentially based on pairwise comparisons and, therefore, can deal with qualitative data naturally. They require neither normality assumption nor data transformation. Apart from robustness against outliers and high efficiency, the rank regression can also incorporate covariate effects in the same way as the ordinary regression. By reanalyzing a data set from a wheat *Fusarium* crown rot study, we illustrated the use of the rank regression methodology and demonstrated that the rank regression models appear to be more appropriate and sensible for analyzing nonnormal data and data with outliers.

Additional keywords: linear rank regression model.

In many plant studies, the measurements of interest are ordinal and count data (37,38,42). For example, noncontinuous data are frequently collected for quantitative trait loci analysis in plants. Ordinal data are also often used to measure disease severities and plant characteristics, such as seedling vigor and leaf glossiness (22,30,36). For ordinal data, the normality assumption is violated; therefore, ordinary parametric methods, such as *t* tests and analysis of variance (ANOVA), cannot be directly applied. Furthermore, equal variance assumption may not be satisfied in practice. Violation of these assumptions may cause incorrect variance estimates which, though not always, may lead to incorrect testing conclusions. In such cases, ordinal data are usually transformed to continuous data which are close to normal before being analyzed by parametric methods (25,28). However, it may not be easy, in practice, to find an appropriate transformation for the ordinal data.

An appealing alternative is the rank-based nonparametric method because of several well-known properties: relatively insensitive to outliers, no normality and equal variance assumptions, transform invariant, and more efficient and robust than the linear regression when the data are nonnormal (18–20,33,37). Rank-based methods play an important role in practice, and their theoretical properties have been thoroughly studied (18–20,24). In recent years, much progress has been made in advocating rank-based methods in plant research (11,32,34,41,48). For two-group or *k*-group comparison, the equivalence to the well known *t* test or one-way ANOVA is the so called Kruskal-Wallis test (26), which is the same as the traditional *t* test or ANOVA but with observations being replaced by their corresponding ranks. Rank transformation (RT) methods consist of replacing the measures by their ranks, and then applying the usual parametric methods to

their ranks (10). Many of the popular nonparametric methods may be treated as RT procedures. The RT approaches have some limitations due to the nonlinear nature of the RT (3,7,8,37). Nonparametric procedures for hypothesis testing by means of the distribution functions were developed to test the treatment effects (4), which do not assume that variances are equal and measurements are from a shift family distribution. These procedures were extended to unbalanced factorial designs (5), and a unified form was derived by combining results of some recent papers (8). Shah and Madden (37) illustrated the use of nonparametric approaches for ordinal data obtained from various factorial experimental designs, including a repeated measure design and a split-plot design. Their analysis presented the basic concepts behind the nonparametric analysis and showed how to qualify the experimental effects.

Various parametric and nonparametric methods developed for the ordinal data analysis are all under more or less restrictive conditions on the underlying distribution functions of the measurements (1,16,21,37,38). In this article, we will consider a regression model based on ranks which is a generalization of the aforementioned rank tests for analyzing the ordinal data. The rank regression to be introduced can be used not only to estimate the treatment effects but also to test hypotheses. For example, suppose that we are assessing the effect of a medical treatment in an experiment, randomly choose *N* subjects, and randomize *N*₁ subjects to the treatment group and others (*N*₂) to the control group. Let *X*_{*i*} = 1 if the *i*th subject is in the treatment group; otherwise, *X*_{*i*} = 0. We consider a simple linear rank regression model $Y_i = \beta_0 + X_i\beta_1 + \epsilon_i$, where parameter β_1 indicates the treatment effect and ϵ_i is the error term. In order to evaluate the treatment effect, we can test the hypothesis, $H_0: \beta_1 = 0$. If we assume ϵ_i are iid $N(0, \sigma^2)$ and estimate β_1 using the ordinary least squares method, the statistic $\hat{\beta}/SE(\hat{\beta})$ is essentially the *t* test. In plant pathology experiments, it is also very common to assess the relationship between disease response and various environmental variables, such as temperature and relative humidity (31). The

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mentioned nonparametric methods cannot handle such cases. However, such covariate effects can be easily taken into account using the rank regression model; therefore, comparisons are made after standardization of these covariates. The ordered logistic regression model (1,15,21), known as the proportional odds model, is also an appealing method to analyze the ordinal data, and the maximum likelihood estimates of the regression parameters can then be obtained. For the ordered logistic regression model, strong parametric assumptions are required. For example, the slopes are assumed to be the same for all categories (response probabilities have the same categorical pattern for different groups). The linear rank regression does not require any specification of the error distribution, and rank estimation is known to be robust against outliers and high efficiency (20,24,27,45). Furthermore, the rank regression allows for heterogeneous error variances and can be used for analysis of repeated measurements (24,46). When the distribution of measurements is nonnormal, a rank-based test is more powerful than the traditional t test. For example, to compare the sapling sizes of ash and maple in a forest of southern Québec, Potiv and Roff (32) used both a rank-based Mann-Whitney test (MWT) and a t test to analyze the data. The analysis shows that the sapling diameter follows a skewed distribution. The MWT test indicates that there is a highly significant difference, whereas the t test leads to ambiguous results. Wang and Fu (44) analyzed the water quality data from southeast Queensland using rank regression models. Compared with the linear model, their results demonstrate that the rank regression model is more robust and appropriate for analyzing nonnormal data and data with outliers.

We illustrate the rank regression model by analyzing a data set from a study on *Fusarium* crown rot (CR) disease (ordinal data, scored 0 to 5) and seedling lengths (continuous data). Specifically, we carry out model-free tests to investigate whether the differences between tall and dwarf isolines are significant for 12 pairs of near-isogenic lines (NILs) in wheat CR severity, and to test whether effects of exogenous gibberellin (GA) application on CR reaction exist. To reduce computational effort, the model-free test statistic is based on estimating functions instead of their resulting parameter estimates. All the significance tests for each genotype were derived from two rank-regression models so that all the covariate effects were taken into account in the tests, and all analysis was performed using statistical package R (free download from <http://www.r-project.org/>). Our computing codes are available at <http://www.maths.uq.edu.au/~uqywang9/>.

MATERIALS AND METHODS

Rank-based methods. The linear regression model is widely used to investigate the relationship between responses of interest and explanatory variables for continuous data. We now consider the typical linear regression model

$$Y = \beta_0 + X'\beta + \varepsilon \quad (1)$$

where Y is a continuous response variable, X is a $p \times 1$ explanatory variable, β_0 is the intercept, β is a $1 \times p$ regression parameter, and ε is the error term. Suppose that there are N subjects and each subject has n_i replications. The measurements are (Y_{ik}, X_{ik}) and $k = 1, \dots, n_i$; $i = 1, \dots, N$. The linear regression model is suitable for continuous measurements and the ordinal least squares (OLS) procedures are often used to obtain the estimates of the regression parameters by minimizing the sum of squared residuals. Diggle et al. (12) also provided various methods to handle repeated measurements.

In statistical inference, in order to test whether a covariate has a significant effect on the response variable, we can do hypothesis testing. Without loss of generality, we consider the following

hypothesis test:

$$H_0: \beta_k = \beta_{k0} \text{ versus } H_1: \beta_k \neq \beta_{k0} \quad (2)$$

where β_{k0} is a constant. Suppose that $\hat{\beta}_{Lk}$ is an estimator of β_k obtained by OLS. We can use the traditional test statistic $(\hat{\beta}_{Lk} - \beta_{k0})/SE(\hat{\beta}_{Lk})$, which follows a t distribution with one degree of freedom under the normality assumption. However, the normality assumption does not always hold in practice, and the estimates obtained by OLS are relatively sensitive to the outliers.

A useful alternative is the rank regression model, which is well known for robustness (i.e., insensitive to outliers and unusual data points) (18–20). The basic assumption for the rank regression model is that the median of $\varepsilon_{ik} - \varepsilon_{jl} = 0$; that is, $p(\varepsilon_{ik} \geq \varepsilon_{jl}) = p(\varepsilon_{ik} \leq \varepsilon_{jl})$ for any $i \neq j$. Therefore, the rank regression model relaxes the assumptions of normality and equal variance. We minimize the following function:

$$L(\beta) = \sum_{i=1}^N \sum_{j=1}^N \sum_{k=1}^{n_i} \sum_{l=1}^{n_j} |e_{ik} - e_{jl}| \quad (3)$$

to obtain an estimate β_R for β , where $\varepsilon_{ik} = Y_{ik} - \hat{\beta}_0 - X'_{ik}\hat{\beta}_R$. The intercept β_0 cannot be simultaneously estimated with β because the rank regression model does not shift to location (24,40); therefore, we use the median of $Y_{ik} - X'_{ik}\hat{\beta}_R$ as an estimator of β_0 .

For the hypothesis test 2, we can consider the Wald type statistic $(\hat{\beta}_{Rk} - \beta_{k0})/SE(\hat{\beta}_{Rk})$, where $\hat{\beta}_{Rk}$ is the rank estimator for β_k . Its asymptotic distribution is the standard normal distribution. Because the variance of $\hat{\beta}_{Rk}$ depends on the distribution of error terms, which may be unknown and difficult to estimate. In order to bypass the density estimate, Jung and Ying (24) proposed a model-free test statistic based on

$$S(\beta) = \sum_{i=1}^N \sum_{j=1}^N \sum_{k=1}^{n_i} \sum_{l=1}^{n_j} (X_{ik} - X_{jl})I(e_{ik} \geq e_{jl}) \quad (4)$$

where $I(\cdot)$ is an indicator function. Let $Q(\beta_{k0})$ be the minimum of $S(\beta)' \hat{V}^{-1} S(\beta)$ with respect to $(\beta_1, \dots, \beta_{k-1}, \beta_{k+1}, \dots, \beta_p)$ fixed $\beta_k = \beta_{k0}$, where $\hat{V}$ is a consistent estimator of $\text{var}\{S(\beta)\}$ given by

$$\hat{V} = \sum_{i=1}^N \hat{\phi}_i \hat{\phi}_i', \quad \hat{\phi}_i = \sum_{j=1}^N \sum_{k=1}^{n_i} \sum_{l=1}^{n_j} (X_{ik} - X_{jl}) \{I(e_{ik} \geq e_{jl}) - 1/2\} \quad (5)$$

Under the null hypothesis H_0 , $Q(\beta_{k0})$ has a χ^2_1 distribution asymptotically. Hence, the critical region of the hypothesis testing equation 2 is $\{Q(\beta_{k0}) \geq \chi^2_{1,1-\alpha}\}$, where $\chi^2_{1,1-\alpha}$ is the $(1 - \alpha)$ percentile of χ^2_1 distribution.

We now consider the hypothesis testing under the special design mentioned in the introduction and assume that each subject has n repeated measurements. Function 4 can be written as

$$S(\beta) = 2 \sum_{i=1}^N \sum_{j=1}^N \sum_{k=1}^n \sum_{l=1}^n X_{ik} I(e_{ik} \geq e_{jl}) - NN_1 n^2 \quad (6)$$

which is equivalent to the Wilcoxon rank sum statistic proposed by Ronser et al. (35).

To demonstrate the rank regression method numerically, we now consider a real data set from a wheat CR severity study, and investigate the effects of exogenous GA application on CR severity (29). Wallwork et al. (43) reported that taller plants gave better CR resistance than shorter ones in a population that segregated for plant height as well as CR resistance. These authors also mapped a quantitative trait locus conferring CR resistance near the dwarfing reduced height (*Rht*) gene *Rht1* (*Rht-B1b*) on the short arm of chromosome 4B. Recent results by the school of Liu also showed an association between plant height and CR severity

in both wheat and barley. However, in contrast to the previous report, it was the shorter plants that gave better CR resistance in both of these populations.

Fusarium CR assessments. CR disease is an important cereal disease caused by various *Fusarium* pathogens (2,6,9,39), and results from previous studies showed that applied GA and GA signaling pathways may be important in resistance to necrotrophic fungal pathogens in *Arabidopsis*. To test whether GA has any effect on CR severity in wheat, Liu et al. (29) assessed 19 genotypes in four independent trials, each consisting of two GA-treated and two mock-treated (with distilled water) experiments. In each experiment, 10 inoculated seedlings or controls were wrapped and grown in a single piece of moist paper towel as one replication. GA treatment was carried out by germinating grains in petri dishes on three layers of filter paper saturated with 25 ppm aqueous GA₃ (Sigma-Aldrich, catalog number G7645) solution. CR inoculation was conducted when the seedlings reached 0.5 to 1.0 cm in length by immersing in either distilled water (mock-inoculated controls) or the spore suspension of *Fusarium pseudograminearum* isolate CS3096 for ≈1 min, as described by Li et al. (28). Experiments on CR assessment were all carried out in a laboratory under constant temperature (23°C) and relative humidity (≈60%) with natural and fluorescent room lighting maintained for ≈12 to 14 h daily.

At the same time of CR assessment, seedling lengths of the mock-inoculation controls were measured for each tested genotype. In this study, CR severity was scored using a 0 to 5 scale, where 0 represents no symptom and 5 indicates the whole seedling is completely necrotic. In the paper of Liu et al. (29), a disease index was calculated for each line following the formula $(\sum_{s=0}^5 n_s S / 5N) \times 100$, where S is the scale value of each plant, n_s is the number of plants with score S , and N is the total number of plants assessed for each line, and parametric methods were used to analyze the transformed data (29). Results for significance tests were obtained using t tests based on the parameter estimates and their standard errors. We now provide analysis using the rank-based models in the following section.

Rank-based models for CR data. Let Y indicate measurements in the four experiments, such as CR scores or seedling lengths; let G be the gene indicator, taking 1 for the tall isolate and 0 for the dwarf isolate; let T be the treatment indicator, taking 1 for GA treatment and 0 for mock treatment; and let exp be the experiment indicator, taking 1 for experiment one and 2 for experiment two. We consider a linear rank regression model:

$$Y = \alpha_0 + G\alpha_1 - (1 - T)\alpha_2 + G(1 - T)\alpha_3 + exp \times \alpha_4 + \varepsilon \quad (7)$$

where ε is the error term and $\alpha_1, \alpha_2, \alpha_3$, and α_4 are four parameters corresponding to covariates $X = [G, (T - 1), G(1 - T), exp]^T$. Here, α_0 represents the baseline. Parameter α_1 measures the difference between the tall and dwarf isolines after GA treatment, and α_2 measures the difference between the GA and mock treatments for the dwarf isolate; $\alpha_2 - \alpha_3$ measures the difference between the GA and mock treatments for the tall isolate; $\alpha_1 + \alpha_3$

measures the difference between the tall and dwarf isolines after mock treatment; and α_4 represents the difference between two experiments. It is complex to test either $\alpha_2 - \alpha_3$ and $\alpha_1 + \alpha_3 = 0$. We therefore consider the following model:

$$Y = \beta_0 - (1 - G)\beta_1 + T\beta_2 + (1 - G)T\beta_3 + exp \times \beta_4 + \varepsilon \quad (8)$$

where $\beta_1, \beta_2, \beta_3$, and β_4 are four parameters corresponding to $X = [(G - 1), T, (1 - G)T, exp]^T$. Here, β_0 is the baseline; parameter β_1 measures the difference between the tall and dwarf isolines after mock treatment and β_2 measures the difference between GA and mock treatments for the tall isolate. Interpretations for parameters in models 7 and 8 are also listed in Table 1. We were only interested in testing whether the differences between tall and dwarf isolines for the 12 pairs of NILs are significant, and whether the effects of exogenous GA application on CR reaction exist for all 19 genotypes, which correspond to four hypothesis testings; that is, whether $\alpha_1, \alpha_2, \beta_1$, or $\beta_2 = 0$. As we can see, all the hypothesis tests are imbedded in models 7 and 8.

RESULTS

Preliminary analysis of the data sets. The 12 pairs of NILs for six different *Rht* genes (*Rht1, Rht2, Rht3, Rht4, Rht8*, and *Rht13*) in wheat were studied in the four trials. The tall genotype ‘Mironovskaya 808’ (M808) is the shared recurrent parent for six pairs of the NILs (Lan 1, Lan 2, Lan 3, Lan 4, Lan 8, and Lan13). Traditionally, we can use a t test to test whether the differences between tall and dwarf isolines are significant. However, Q-Q plots indicate that seedling lengths for the 19 genotypes are not close to normal distributions (Fig. 1). The boxplots show that there exist outliers in the measurements of CR scores as well as seedling lengths for some genotypes (Figs. 2 and 3). It can be seen that both the CR severity and seedling length increased after GA treatment for each genotype. Compared with their respective dwarf isolines, all of the tall isolines have higher CR severity and longer seedling lengths.

Rank-based analysis for seedling length. First, we apply models 7 and 8 to analyze the seedling length data (continuous data). Let Y be the measurements of the seedling lengths. We obtain the parameter estimates by minimizing function 3 using the function *optim* or *nlm* in package stats (R 2.10.0 version), and use $Q(\beta_{ko})$ to test whether the changes in seedling length are significant after GA treatment. As expected, compared with their respective dwarf counterparts, all 12 of the tall isolines had longer seedling lengths following either mock or GA treatment (Table 2, estimates for α_1 and β_1). The differences between the tall and dwarf isolines in seedling lengths increased after GA treatment and were statistically significant after either GA or mock treatments for all 12 NIL pairs. The changes following GA treatment were significant for all the tall genotypes (Table 2). It is interesting to note that the estimates for α_2 and β_2 are comparable with the estimated differences in Liu et al. (29) for all of the dwarf and tall genotypes, respectively. Compared with the results based

TABLE 1. Interpretations for parameters in models 7 and 8^a

Indicators		Model 7		Model 8	
G	T	$\alpha_0 + G\alpha_1 - (1 - T)\alpha_2 + G(1 - T)\alpha_3$		$\beta_0 - (1 - G)\beta_1 + T\beta_2 + (1 - G)T\beta_3$	
1	1	$\alpha_0 + \alpha_1$	α_1 is the difference between tall and dwarf isolines for GA treatment	$\beta_0 + \beta_2$	β_2 is the difference between GA and mock treatments for the tall isolate.
1	0	$\alpha_0 + \alpha_1 - \alpha_2 + \alpha_3$	α_2 is the difference between GA and mock treatments for dwarf isolate	β_0	β_0 is the baseline
0	0	$\alpha_0 - \alpha_2$		$\beta_0 - \beta_1$	β_1 is the difference between tall and dwarf isolines for mock treatment
0	1	α_0	α_0 is the baseline	$\beta_0 - \beta_1 + \beta_2 + \beta_3$	

^a G is the gene indicator, taking 1 for the tall isolate and 0 for the dwarf isolate; and T is the treatment indicator, taking 1 for GA (gibberellin application) treatment and 0 for mock treatment.

on a t test (29), the results on GA versus mock for Lan 2 and Kauz dwarf also become significant, although they both contain the potent GA-insensitive *Rht* genes (*Rht1* and *Rht2*, respectively).

Rank-based analysis for CR severity. We now use models 7 and 8 to analyze the CR severity data. Similarly, we minimize function 3 to obtain parameter estimates of interest, and use the statistic $Q(\beta_{k0})$ to test whether the differences between the tall and dwarf isolines for the 12 pairs of NILs in CR severity are statistically significant. Compared with their respective tall counterparts, all 12 of the dwarf isolines had better CR resistance after either mock or GA treatment (Table 3, parameter estimates for α_1 and β_1). The results are similar to those obtained using the traditional regression and t tests, except for those underlined. The resistance difference between Lan 4 and M808 for the mock group (Table 3, column under α_1) became significant using the rank-based method, which agrees well with the majority of the other genotypes (Lan 1 to 3), where significant difference in CR severity exists between the dwarf and tall isolines.

In order to test whether manipulation of shoot elongation has any effect on CR severity development, the *Rht* NILs were first treated with GA and then inoculated. The test results of (α_2 , β_2) (Table 3) indicate that CR severities increased for all 12 pairs NILs after GA treatment. The changes in CR severity after GA treatment for all of the tall genotypes were significant. In terms of test results, we obtained the same conclusions as the traditional t tests regarding to the significance levels marked by asterisks in most cases. The effects of GA or mock became significant for an additional six dwarf genotypes (Table 3, column under α_2), pro-

viding evidence in favor of that derived from the majority of the genotypes that GA treatment dramatically increased CR severity in wheat.

The diagnostic plots (Figs. 1 to 3) clearly show that the distributions of seedling lengths are nonnormal and outliers may exist in seedling lengths and CR scores. Therefore, the fundamental assumptions are violated. However, the traditional t test is also known as the “robust” test. This is why most of the results obtained from the rank regression (Tables 2 and 3) are in agreement with the previous study (t test).

DISCUSSION

In plant pathology experiments, plant disease severity is sometimes recorded using ordinal data. The traditional parametric methods are usually convenient and routinely used for ordinal data, sometimes after transformation. However, these methods may be inappropriate because their assumptions may not be met in practice. Although transformation will make violations of assumptions to a lesser extent, it is not always possible to find an appropriate transformation to meet the normality assumption, and with good interpretation of the final results.

There are several well-known methods for handling ordinal data, such as the ordered logistic regression model (1,15,21) and RT procedures (10). The former can be used to analyze ordinal data. However, a large number of measurements are required to fit this model when there are many different categories or experimental factors, and the assumption that the odds ratio is a constant for all categories may not be met in practice. Although the

Fig. 1. Normality test for seedling lengths in wheat of all the 19 genotypes based on Q-Q plots.

Fig. 2. Boxplots for crown rot scores of all 19 genotypes following mock and gibberellin application (GA) treatments.

Fig. 3. Boxplots for seedling lengths of all 19 genotypes following mock and gibberellin application (GA) treatments.

later method provides a useful tool to develop new nonparametric procedures to analyze the ordinal data, there are some limitations because of the nonlinear nature of the RT (4,5,8).

The use of the rank-based approach can be an appealing alternative in many cases. Nonparametric procedures have been considered by many researchers (4,5,7,8,37), which are always used to qualify the experimental effects. The principal aim of this article is to demonstrate the value in using the rank regression to analyze ordinal data, which can be easily extended to the other qualitative data. In contrast to the linear regression procedures, the essential change of the rank regression model is to replace the sum of squared residuals with the sum of absolute values of pairwise residuals. Therefore, the rank method is robust to outliers while it retains its high efficiency, even when the underlying distribution of the responses is nonnormal. We combined all the hypothesis tests into two regression models, and investigated the effects of exogenous GA application on CR reaction using rank-based methodology. The test statistic is based on estimating functions, which avoids estimating the variance of the parameter estimator and reduces the computational effort. The results obtained from the rank-based analysis seem to be more meaningful for both the CR severity and seedling length than those based on the *t* test. For example, it is well known that GA treatment increases plant height, although *Rht* can be divided into GA-sensitive and GA-insensitive (13,14,47). However, significant changes were detected for only 7 of the 12 dwarf genotypes based on the *t* test, and this was increased to 9 when the same data were analyzed using the rank-based approach. Similarly, previous

studies showed that GA treatment would increase susceptibility to necrotrophic pathogens (17,29). However, significant changes in CR severity following GA treatment were detected for only 4 of the 12 dwarf lines based on a *t* test (29) and an additional 6 genotypes were found to be significant from the same data set based on the rank-based test. Clearly, the rank-based approach generated results which conform better to the existing findings in the literature and, therefore, we believe the rank-based analysis can be more powerful for analyzing qualitative data. Compared with existing nonparametric methods, the rank regression model can not only test experimental effects but also demonstrate effects of other environmental covariates. Therefore, the rank regression model can extract much useful information from the covariates which have considerable influence on the response variable. The questions of interest can be usually converted to hypotheses, testing regression parameters corresponding to special covariate designs. Furthermore, rank-based methods can also be used to analyze repeated measurements and censored data (23,24,27).

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TABLE 2. Significant test results for analysis of seedling length data based on rank regression models^a

Near-isogenic line pair		Tall–Dwarf		GA–Mock	
Dwarf	Tall	α_1 (GA)	β_1 (Mock)	α_2 (Dwarf)	β_2 (Tall)
Lan 1	M808	14.50**	8.60**	1.50**	7.69**
Lan 2	M808	14.00**	7.51**	<u>1.00**</u>	7.97**
Lan 3	M808	21.00**	13.53**	0.29	7.49**
Lan 4	M808	4.53**	3.00**	6.23**	7.75**
Lan 8	M808	7.50**	4.76**	4.75**	7.50**
Lan 13	M808	6.51**	5.00**	5.99**	7.50**
Galvez dwarf	Galvez tall	9.00**	6.50**	2.50**	5.00**
Pavon dwarf	Pavon tall	6.08**	5.00**	2.92**	4.00**
Kauz dwarf	Kauz tall	7.17**	4.03**	<u>0.67*</u>	3.80**
Seri dwarf	Seri tall	9.14**	4.34**	0.71	5.50**
Nesser dwarf	Nesser tall	9.50**	6.67**	2.07**	5.00**
Aconchi 89	Aconchi tall	11.00**	6.76**	0.24	4.50**

^a Here, α_1 and β_1 are the genetic differences between the tall and dwarf isolines for the gibberellin application (GA) group and the mock group, respectively, and α_2 and β_2 are the treatment differences between the two treatments (GA and mock) for dwarf and tall isolines, respectively. Numbers in each column correspond to the estimates for the parameters α_1 , β_1 , α_2 , and β_2 ; * and ** indicate that the test is significant at $P < 0.05$ and 0.01 , respectively, based on χ^2_1 test. Numbers that are underlined indicate significance results different from those of Liu et al. (29).

TABLE 3. Significant test results for analysis of Fusarium crown rot severity data based on rank regression models^a

Near-isogenic line pair		Tall–Dwarf		GA–Mock	
Dwarf	Tall	α_1 (GA)	β_1 (Mock)	α_2 (Dwarf)	β_2 (Tall)
Lan 1	M808	56.16**	50.00**	<u>5.00**</u>	13.52**
Lan 2	M808	60.00**	50.01**	<u>5.00*</u>	14.96**
Lan 3	M808	50.00**	40.00**	<u>3.52*</u>	13.87**
Lan 4	M808	14.82**	10.05**	10.00**	14.96**
Lan 8	M808	50.03**	49.97**	9.97**	10.04**
Lan 13	M808	10.00**	20.02**	20.00**	10.00**
Galvez dwarf	Galvez tall	30.00**	30.00**	20.00**	20.00**
Pavon dwarf	Pavon tall	30.00**	20.00**	0.001	12.37**
Kauz dwarf	Kauz tall	30.00**	20.00**	0.00	10.00**
Seri dwarf	Seri tall	30.00**	30.00**	<u>10.00**</u>	10.00**
Nesser dwarf	Nesser tall	29.70**	10.00**	<u>0.31*</u>	20.01**
Aconchi 89	Aconchi tall	45.00**	45.00**	<u>5.00**</u>	5.00**

^a Here, α_1 and β_1 are genetic differences between the tall and dwarf isolines for the gibberellin application (GA) group and the mock group, respectively, and α_2 and β_2 are the treatment differences between the two treatments (GA and mock) for dwarf and tall isolines, respectively. Numbers in each column correspond to the estimates for the parameters α_1 , β_1 , α_2 , and β_2 ; * and ** indicate that the test is significant at $P < 0.05$ and 0.01 , respectively, based on χ^2_1 test. Numbers that are underlined indicate significance results different from those of Liu et al. (29).

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