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Reaction of commercial clones of cashew to powdery mildew in northeastern Brazil

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ABSTRACT

Cashew powdery mildew, caused by *Erysiphe quercicola*, is one of the main disease problems of cashew trees in Brazil. Thus, research to study the reaction of commercial cashew clones under different epidemiological stages of the disease is very important for identifying resistant clones. The objective of this research was to evaluate the reaction of commercial clones of cashew to powdery mildew by monitoring the disease during three disease cycles. The study was carried out at Embrapa Agroindústria Tropical, Pacajus Experimental Field, Ceará, Brazil, during 2012, 2013 and 2014 using eleven commercial clones of cashew (CCP 09, CCP 76, CCP 100, CCP 06, EMBRAPA 51, EMBRAPA 50, BRS 265, BRS 189, BRS 274, BRS 275 and BRS 226). Powdery mildew severity on inflorescences was estimated using a descriptive scale of severity consisting of scores ranging from 0 to 4. The transformed data were used to estimate the area under the disease progression curve (AUDPC) and the rate of infection. Based on similarities in disease severity estimates with time, clones were clustered using multivariate clustering analysis. Epidemics of cashew powdery mildew differed between the three cycles in terms of duration and severity. The clones were classified into four clusters of similar clones, defined by the graphical analysis on the basis of the powdery mildew severity. Clones BRS 274, BRS 275, CCP 1001 and BRS 226 attained lower AUDPC and clones BRS 189 and CCP 06 showed higher AUDPC. The results show evidence of partial resistance to powdery mildew among commercially grown cashew clones. Clones BRS 274, BRS 275, BRS 226 and CCP 1001 were the most resistant, while CCP 06 and BRS 189 clones were the most susceptible to powdery mildew. The AUDPC seems to be suitable for discriminating between genotypes, whereas the rate of disease progression may be used for establishing a threshold in the evaluation of other control methods, as it does not clearly differentiate between disease reactions.

1. Introduction

The cashew industry is one of the main sources of employment and income for northeastern Brazil. Cashew crops have been improving, not only in terms of management practices, but also the release and adoption of improved cloned varieties, especially the dwarf types of tree. These improved varieties may have contributed to narrowing the genetic variability within orchards which are susceptible to epidemic outbreaks of what were once minor diseases.

Cashew powdery mildew (CPM), in spite of being considered a minor disease for a very long time, is currently one of the main disease problems of cashew trees in Brazil, mainly due the resulting significant reduction in yield and quality of products. The disease is caused by the anamorphic state of *Erysiphe quercicola* [named *Pseudoidium anacardii* (Noack) U. Braun & R.T.A.Cook], formerly known as *Oidium anacardii* (Cardoso et al., 2017). Former occurrence reports (Cardoso et al., 2012; Freire et al., 2002) described as a fine, grayish-white, powdery cover on the surface of mature leaves in very specific environmental conditions, such as shade and leaves protected from wind. In several African countries, however, this disease has been of great economic importance since the middle of the last century and is considered to be the main disease of cashews in some East African countries (Martin et al., 1997; Shomari, 1996). In recent years, there has been an increasing incidence of powdery mildew in young and immature leaves, inflorescence, fruits and pseudo-fruit trees in commercial orchards containing common and dwarf cashew trees in Ceará and Piauí States, as is already the case in

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African countries (Cardoso et al., 2014, 2017). Since the main target of the disease is the inflorescences, this has had serious effects on cashew yields and quality of cashew apple and nut.

Symptoms of CPM first appear when new shoots emerge, which depends on cashew genotype, and dry and windy environmental conditions. These environmental and host conditions are commonly prevalent in northeast Brazil after the rainy season. In this region, CPM symptoms may be seen by June or July, with young leaves and inflorescences becoming covered with whitish spots which comprise a mass of fungal tissue (mycelia and conidia). Similar pattern between CPM on young leaves and inflorescences was reported early (Sijaona et al., 2001; Shomari and Kennedy, 1999). The fungus rapidly spread over the leaves and their stalks, flower scales, buds and young fruits. As the symptoms progress, a darkening of these spots may be seen, with purplish brown spots similar to ash like color. In the inflorescences, expression of the fungus may cause flowers to drop off prematurely. The flowers that succeed into mature fruit will produce cracked peduncles, scabby fruits and deformed nuts (Cardoso et al., 2013).

Cashew powdery mildew has been effectively controlled by massive applications of sulfur powder (Cardoso et al., 2012; Nathaniels et al., 2003; Sijaona, 1984; Topper and Boma, 1994). However, chemical control is associated with legal, practical and environmental problems, including the need for legislative approval by environmental agencies, acquisition of application equipment and cost of labor. Genetic resistance is deemed as an alternative approach for economic and environmental strategies for long-term control of the disease. Early studies on this subject have suggested the potential use of resistance genotypes for integration into disease management (Faenza et al., 1982; Nathaniels, 1990, 1996; Sijaona et al., 2001). The main constraints of screening methods include the irregularity in budding time among different genotypes and differences in environmental conditions at the time of plant vulnerability to infection which makes comparisons among cashew genotypes subject to errors. Sijaona et al. (2001) reported that the disease developed on inoculated young leaves at 48 h after inoculation, however mature leaves were apparently immune to infection. Several methods for assessing resistance to CPM have been conducted under laboratory and field conditions (Nathaniels, 1996; Sijaona et al., 2001). Inoculation of detached leaves, seedling plants and flower panicles has been compared and infection of seedlings proved successful under field conditions (Sijaona et al., 2001). However, no method has been reported for evaluating adult cloned plants under field conditions. At present, there are 14 cashew clones which are commercially available for growers in Brazil, but no scientific report is available on their reaction to CPM, although a preliminary report has been published (Pinto et al., 2017).

An interesting approach to screening for disease resistance would be to monitor the reactions of genotypes over time by clustering of disease progression curves with similar temporal patterns, as they cluster into similar curves (Laurindo et al., 2015). In determining the number of clusters of cashew clones according to their reaction to powdery mildew, the statistical method of root mean square standard deviation (RMSSTD) is advantageous because it allows the number of clusters of cashew clones defined in the dendogram to be distinguished objectively (Liu et al., 2013). According to Sharma (1996), the smaller the number of clusters formed using the RMSSTD method, the more homogeneous the clusters will be.

Parameters which are commonly used in experiments to compare reactions of plant genotypes to disease epidemics are the area under the disease progression curve and the infection rate (Campbell and Madden, 1990; Moreira et al., 2013; Silva et al., 2007).

In view of the few studies available on resistance of cloned cashew varieties to polycyclic diseases, such as powdery mildew, and the increasing importance of this disease in Brazil, the objectives of this research were to determine the reaction of commercially grown clones of cashew to powdery mildew and to establish a reliable method for analyzing disease reaction data.

2. Material and methods

The study was carried out in cashew orchards located in the experimental field at Embrapa Agroindústria Tropical, Pacajus, Ceará, Brazil (4°11′38,6″S, 38°29′51,5″W). This experimental field is mainly composed of cashew plants and holds a huge collection of cashew germplasm from all over the country. Historical records of CPM in this area show a high frequency and severity, indicating a favorable environment for this disease (Cardoso et al., 2013). Eleven commercially grown clones were used, consisting of nine dwarf types (CCP 06, CCP 09, CCP 76, CCP 1001, EMBRAPA 50, EMBRAPA 51, BRS 189, BRS 226 and BRS 265), one common type (BRS 274) and one hybrid type (BRS 275). Trees were originally planted as sources of scions for grafting and were arranged in six rows of nine plants each, spaced at 7 × 7 m. Approximately three months before the beginning of each evaluation cycle, all plants were pruned to minimize the effect of different budding times among the clones. Cropping practices followed those commonly used by growers where no fungicidal applications were involved (Oliveira, 2008).

The reaction to natural infection with powdery mildew was monitored biweekly throughout each epidemic cycle (2012, 2013 and 2014). Assessment of disease on flower panicles of ten central plants for each clone was estimated accordingly to a disease severity score. The score ranged from 0 to 4: 0 = absence of symptoms; 1 = < 10% colonization of panicles; 2 = 11–25% colonization of panicles; 3 = 26–50% colonization of panicles; and 4 = > 50% colonization of panicles (Cardoso et al., 2012; Sijaona et al., 2001). Four homogeneous inflorescences from each selected plant were randomly selected for assessment and labeled at each cardinal point. The same plants were evaluated throughout the study. A completely randomized experimental design was used, arranged as 11 × 3 factorial (*i.e.* eleven clones and three epidemic cycles) with 10 replicates. Data consisted of the average of four inflorescences per plant representing an experimental unit for each set of ten plants per clone. Whenever a marked inflorescence reached the mature stage, this was replaced by a new nearby inflorescence; this reduced errors due to irregularity of budding among the different genotypes. Consequently, more than one set of flowering was evaluated each year. Field evaluation was carried out from July to December of each year, except for 2012 when evaluation started in August.

The data obtained were used to estimate the disease severity index (DSI) for the inflorescence, according to the formula $DSI = \Sigma (ni \times i)/N$, where i represents severity (0–4), ni is the number of inflorescences with severity i and N is the total number of inflorescences. Disease severity was used to estimate both the area under the disease progress curve (AUDPC) and the infection rate (r) per clone and per season (Campbell and Madden, 1990). Infection rates were estimated as the regression of the natural logarithm of $x/(1\text{-}x)$ plotted against t, where x = DSI and t = time, according to the logistic model described by Campbell and Madden (1990). Temporal progress curves of DSI were plotted by clone and by year using the PROC PRINTCOMP package. Since the number of samples (*i.e.* inflorescences) was fairly large and the variance was highly heterogenic, the data for the clones were separated into clusters. Severity data among clusters were analyzed, using the PROC PRINTCOMP package to reduce the amount of data and PROC CLUSTER for cluster analyses (SAS®/STAT; SAS®, 2008). Dendrograms were constructed using the centroid-based method and the Euclidean distance. The graphical method based on the RMSSTD index (Sharma, 1996) was used to determine the optimal number of clusters in the dendrogram. Descriptive graphs of similar profiles were constructed for each cluster to represent the temporal evolution of CPM within clones as a function of the evaluation period.

Analyses of variance (ANOVA) of AUDPC and the infection rate were conducted to determine resistance among clones using generalized linear models (GLM) with logarithmic transformed data to ensure variance homogeneity and normality. When ANOVA showed significant