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Short communication

Reaction of Some *Coffea arabica* Genotypes to Strains of *Colletotrichum kahawae*, the Cause of Coffee Berry Disease

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Abstract

Pathogenicity tests were performed on 11 genotypes of *Coffea arabica* using single-isolate suspensions of *Colletotrichum kahawae* obtained from 90 monoconidial isolates. The objective of this study was to estimate the proportion of pathogenic variation corresponding to differences in aggressiveness and virulence (races). A large part of the variation in the pathogen population was due to aggressiveness. The differential effects were too small to suggest conclusively that races exist. This paper discusses the possible causes for the observed small differential interaction and suggests breeding strategies that not only prevent possible adaptation of the pathogen to resistant varieties but also limit variation for resistance due to differences in aggressiveness of the pathogen.

Zusammenfassung

Reaktion einiger *Coffea-arabica*-Genotypen auf Stämme von *Colletotrichum kahawae*, dem Erreger der Kaffeekirschenkrankheit

Bei 11 *Coffea-arabica*-Genotypen wurden Pathogenitätstests vorgenommen, wobei Einzelisolat-Suspensionen von 90 *Colletotrichum-kahawae*-Monokonidienisolaten zum Einsatz kamen. Das Ziel dieser Untersuchung bestand darin, den Anteil der Variation des Pathogens zu schätzen, der für Unterschiede bei Aggressivität und Virulenz verantwortlich ist (Rassen). Ein großer Teil der Variation in der Population des Pathogens beruhte auf Aggressivität. Die Unterschiede waren zu klein, um eindeutig zu belegen, daß Rassen existieren. Dieser Artikel diskutiert die möglichen Gründe für die beobachteten geringen Unterschiede und schlägt Züchtungsstrategien vor, die eine mögliche

Anpassung des Pathogens an resistente Sorten verhindern und zudem die Variation bezüglich der Resistenz aufgrund von Unterschieden bei der Aggressivität des Pathogens begrenzen.

Introduction

Coffee is one of the most important agricultural commodities upon which the economy of more than 50 producer countries depend (Rodrigues Jr. et al., 1975). In Kenya, coffee is important because of its contribution to foreign exchange earnings, farm incomes and employment opportunities. Economic production of Arabica coffee in Kenya is greatly hindered by coffee berry disease (caused by *Colletotrichum kahawae*).

It is believed that breeding for resistance to coffee berry disease (CBD) may provide a sustainable long-term control of the disease. The Coffee Research Foundation, in Ruiru, Kenya has developed an Arabica coffee cultivar, 'Ruiru 11', which combines resistance to CBD and leaf rust (caused by *Hemileia vastatrix*) with high yield, fine quality and compact growth that is amenable to intensive planting. The years following the release of the variety have been devoted to the improvement of the genetic base of resistance, but this faces the problem of possible pathogen variation. In a study with isolates from Angola, Malawi and Kenya, Rodrigues Jr. et al. (1991) found that Angolan and Malawian strains of *C. kahawae* possessed different characteristics to those of the Kenyan strain. The isolates were highly aggressive on the cultivar 'Catimor', which is used in Kenya as a mother parent in the production of the disease-resistant hybrid variety, 'Ruiru 11'. Rodrigues Jr. et al. (1992) concluded that physiologic races of the CBD pathogen might exist among the Ango-

Table 1

A list of *C. kahawae* isolates, their sampling locations, altitude (in parenthesis) and host variety

Location	Host variety/isolates	
	Ruiru II	SL 28
Gatanga, Thika District (1670 m)	R1.1-7	S1.8-9
Karatina, Nyeri District (1981 m)	R2.1-7	S2.8-9
Kiriaini, Muranga District (1760 m)	R3.1-7	S3.8-9
Kangema, Muranga District (1700 m)	R4.1-7	S4.8-9
Yara, Kiambu District (1767 m)	-	S5.1-9
Kitale, Trans-Nzoia District (1890 m)	R6.1-9	=
Koru, Kericho District (1615)	-	S9.1-9
Kisii, Kisii District (1680 m)	R10.1-9	-
Bahati, Nakuru District (1830 m)	-	S11.1-9
Jacaranda, Thika District (1603 m)	-	S12.1-9

lan, Malawian and Kenyan isolates. The objective of this study was therefore to determine the extent of pathogen variation within the Kenyan population.

Materials and Methods

Green infected berries were obtained from 10 locations in the coffee growing districts of Kenya. A list of the isolates, their distribution and altitudes of the sampling sites are presented in Table 1. At each location, nine berries were sampled from which nine single conidia isolates were derived (one isolate per berry) making a total of 90 isolates for the 10 locations. The isolates were grown for 7 days in three replications and then stored at 4 °C for a period of up to 6 weeks to allow for the growth of test seedlings.

Eleven genotypes of *Coffea arabica*, including 'Rume

Sudan', 'Pretoria', 'Hibrido de Timor', 'K7', 'Padang', 'SL 28', 'SL 34', 'Caturra', 'Erecta', 'Mokka' and 'Laurina' were selfed to generate experimental seeds. Batches of 100 seeds of each genotype were sown in three replications in moist sterilized sand in plastic boxes with closely fitting transparent lids. Conidia suspensions were prepared from 10-day-old monoconidial cultures of each isolate and standardized to 2×10^6 conidia/ml. The 6-week-old seedlings were inoculated, incubated and individually scored after 3 weeks for disease symptoms developed on the hypocotyl stem on a scale of 1 (no symptoms) to 12 (seedlings completely dead) as described by van der Vossen et al. (1977). The susceptible 'SL 28' genotype was used as the control. A mean grade of infection for each replication was subjected to an analysis of variance. The genotype \times isolate interaction was considered an important indicator for the presence/absence of races. The contribution of each isolate (W_i) and genotype (W_j) to the total interaction component were computed according to Denoyes and Baudry (1995) as follows:

$$W_i = \left[\frac{\text{Variance of the interaction due to an isolate}}{\times 100} \right] / (\text{total variance of the interaction})$$

$$W_j = \left[\frac{\text{Variance of the interaction due to a genotype}}{\times 100} \right] / (\text{total variance of the interaction})$$

The more the contribution, the greater the isolate or genotype takes part in the interaction.

Results

Pathogenicity tests revealed that all isolates had compatible reactions with the genotypes tested (Table 2). One

Table 2

The disease scores and relative contributions to isolate \times genotype interaction by individual isolates and genotypes

Disease score	Isolate	Genotype	Relative contribution to isolate \times genotype effect	Isolates	Genotypes
1-3	-	-	< 3%	R1.1-7, S1.8-9, R2.1-7, S2.8-9, R3.1-7, S3.8-9, R4.1-7, S4.8-9, S5.1-9, R6.1-9, S9.1-8, R10.1-9, S11.1-5, S11.7-8, S12.1-4, S12.6-9	-
4-6	R1.6	-	3-5%	S9.9, S11.6, S11.9, S12.5	'Hibrido de Timor', 'SL 28', 'SL 34', 'Caturra', 'Erecta', 'Laurina'
7-9	R1.5, S1.8-9, R2.1-7, S2.9, R3.2, S3.8-9, R4.2-3, R4.5-7, S4.8, S5.2, S5.5-6, S5.8, R6.1-8, S9.4-9, R10.1-3, R10.5-8, S11.4-6, S12.1, S12.5-6	'Rume Sudan', 'Pretoria', 'K7', 'Padang'	6-10%	-	'Mokka'
10-12	R1.1-4, R1.7, S2.8, R3.1, R3.3-7, R4.1, R4.4, S4.9, S5.1, S5.3-4, S5.7, S5.9, R6.9, S9.1-3, R10.4, R10.9, S11.1-3, S11.7-9, S12.2-4, S12.7-9	'Hibrido de Timor', 'SL28', 'SL34', 'Caturra', 'Erecta', 'Mokka', 'Laurina'	> 10%	-	'Rume Sudan', 'Pretoria', 'K7', 'Padang'

isolate, R1.6, was less aggressive (disease score 4–6) while the others were highly aggressive (10–12) or intermediate (7–9). Susceptible reactions were observed in the control genotype 'SL 28' as well as 'Hibrido de Timor', 'SL34', 'Caturra', 'Erecta', 'Mokka' and 'Laurina'. There were no genotypes in the highly resistant classes 1–3 or in the medium resistant classes 4–6. Partial resistance was observed in genotypes 'Rume Sudan', 'Pretoria', 'K7', and 'Padang'. The contribution of most isolates to the total isolate \times genotype interactions were less than 3% except for isolates S9.9 (3%), S11.6 (5%), S11.9 (3%) and S12.5 (3%). The partial contributions of individual genotypes to the total isolate \times genotype interactions were high for 'Rume Sudan' (16%), 'Pretoria' (14%), 'K7' (16%) and 'Padang' (17%). The individual contributions of the remaining genotypes were less than 10%.

Discussion

The small contribution of isolates to the differential interaction is an indication that the Kenyan population of *C. kahawae* has not developed into physiologic races. The apparent absence of races was probably due to the fact that the pathogen co-evolved with genetically narrow-based host species. The greatest diversity of *C. arabica* species is found in the highlands of South-west Ethiopia. CBD was, however, never found in Ethiopia until 1971 (van der Graaff, 1981). This implies that there was hardly any substructuring of the pathogen population on the basis of the host selection pressure that could have resulted in variability for virulence. The host selection pressure is still of minor importance because resistant varieties such as 'Ruiru 11' have not been widely grown. It can be observed that isolates with high contribution to the differential interaction were not from the 'Ruiru 11' cultivar. The genetic uniformity of the pathogen may have also been perpetuated by its asexual nature of reproduction. There is no conclusive evidence for the existence of a sexual stage in the pathogen. Despite the genetic uniformity within the Kenyan population of *C. kahawae*, Rodrigues Jr. et al. (1992) observed that isolates of diverse origin could be different physiologic races. It is therefore important to observe strict quarantine regulations when exchanging coffee plants among countries where CBD is endemic. In this study, no isolates from other countries were tested because of the risk of introducing pathotypes that were hitherto not present in

Kenya. The highest contribution to the differential interaction was observed in the genotypes, 'Rume Sudan', 'Pretoria', 'K7' and 'Padang'. Although the inheritance of resistance in Padang is not known, the other genotypes have major gene resistance to CBD on two separate loci, R- and k- (van der Vossen and Walyaro, 1980). The third known gene for CBD resistance on the T-locus is carried by 'Hibrido de Timor' and its hybrid derivative, 'Catimor'. In this study, 'Hibrido de Timor' was apparently susceptible when tested with all isolates. It is unlikely that the T gene of resistance could have succumbed to the entire range of isolates from diverse origins. The susceptibility could be as a result of segregation in the genotype.

Although no races were detected in this study, the Kenyan coffee breeding programme has been geared towards the development of varieties with broad-based resistance. It is generally believed that gene pyramiding minimizes variation for resistance and could prevent pathogen adaptation to resistant varieties.

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