Evaluation of Coffee Genotypes to Coffee Thread Blight Disease in Southwestern Ethiopia

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Abstract

Thread blight is one of the fungal pathogens that cause severe damage to *Coffea arabica* in Southwest Ethiopia. However, there are very few research findings on its management in Ethiopia. Therefore, the current work was designed with the objective to evaluate *Coffea arabica* genotypes for their reaction to the disease. For this purpose, a field experiment was conducted to evaluate the resistance of 126 *C. arabica* genotypes against the disease at Mettu, Ethiopia. The experiment was arranged in 8x8 simple lattice designs with two replications. Out of 126 *C. arabica* genotypes tested, 14 (11%) of them showed highly resistant reaction, while 28 genotypes (22%) were moderately resistant. Additionally, 26, 29 and 12% of the genotypes were moderately susceptible, susceptible and highly susceptible to *C. koleroga*, respectively. The current study demonstrates the role of host resistance to manage the disease, and it could be considered as potential component in integrated management of the disease. Future research should be directed towards studying the resistance mechanisms of the accessions for possible resistance gene transfer to released coffee varieties.

Keywords: *Corticium Koleroga*, Genotype, Resistance reaction, Severity, Susceptible

Introduction

Arabica coffee (*Coffea arabica*) is one of the highly preferred international beverages and is the most important trade commodity in the world next to petroleum (Torok *et al.*, 2018). Ethiopia was ranked as the first largest *C. arabica* producer in Africa and the fourth in the world after Brazil, Colombia and Honduras by producing about 423300.0 kg (7.4% of world production) in the 2017/18 cropping year (Service Foreign Agriculture, 2018). Despite the abundance of coffee genetic diversity and centre of origin for *Coffea arabica*, the productivity per unit area remained very low in Ethiopia compared with average national clean coffee yield of 670 kg ha^{-1} (Cochrane and Bekele, 2018). Numerous biotic and abiotic constraints have been affecting the production and productivity of the crop in the country. Among biotic constraints, diseases are attacking fruits, leaves, stems and roots and reducing the yield, quality and marketability of the crop. According to Cavalcante and Sales (2001), coffee thread blight (CTB), caused by the phytopathogenic fungus *Corticium koleroga*, is an important disease of coffee in India, Tobago and Trinidad. In Ethiopia, the disease was first recorded at Gera and Mettu areas in 1978 (Derso, 1997).

Coffee thread blight disease has been known on Ethiopian coffee for more than 42 years and has been considered as minor coffee disease. Currently, it is increasingly

becoming an important disease and has been observed as an economically important disease in many coffee growing regions of Ethiopia (Belachew *et al*., 2015; Dechassa *et al*., 2020a). Southwestern parts of Ethiopia are the major coffee producing belts where the damage by CTB is frequently reported with increasing disease pressure from year to year (Belachew *et al*., 2015; Dechassa *et al*., 2020a). The study conducted at 12 districts of the region indicated that CTB was prevalent and seriously devastated all above ground parts of coffee trees with disease incidence and severity ranged from 0 to 46% and 0 to 44.04%, respectively. The highest mean CTB disease incidence of 46% and severity of 44% were recorded in Masha district, followed by Mettu, Andaracha, Alle, Gera and Gomma (Dechassa *et al*., 2020a). Besides, disease intensity was the highest at midland and highland altitudes, plantation coffee production systems, open shade level and local coffee varieties (Dechassa *et al*., 2020b).

Temperature, rainfall and relative humidity decisively determine the occurrence, prevalence and severity of coffee fungal diseases (Belachew and Teferi, 2015). According to Belachew *et al*. (2015), heavy, long and continuous rainfall as well as higher relative humidity from the month of June to September triggered thread blight disease outbreak in 2014 at most coffee growing areas of Ethiopia. Susceptible coffee genotypes, heavy shade and buildup of diseases causing pathogens are also factors contributing to the occurrence and outbreaks of CTB. Similar report by López-Bravo *et al*. (2012) also indicated that the development of thread blight was favored by continuous and heavy rainfall, high atmospheric humidity, shade and overhanging branches.

Disease dispersal has occurred through human activities and by the introduction of infected plants in disease free areas. *Corticium koleroga* is an aerial pathogen transmitted by free water and splashing over short distances. Lines of expansion over longer distances follow roads or are due to accidental transportation of infected planting material over long distances. The spread of the disease is assisted by wind, water, insects as well as mechanical means (Whitfield, 1939). The disease spreads mainly by the fungus threads (hyphae) growing from leaf to leaf or along branches within a tree and from tree to tree through infected fallen branches from tall shade trees. It also spreads through airborne basidiospores released from basidia formed during wet weather. Moreover, the disease might be spread by Antestia bug (*Antetsopsis antiricata*) and *Usingeria mirabilis* (Dechassa, 2019).

Moreover, human involvement to expand coffee production from location to location plays a great role in transmission of the disease across regions over years (Dechassa *et al*., 2020b). For instance, the outbreak of the disease at Southwestern on coffee estate farms (Limmu, Bebeka and AgriCeft), Western coffee farms (Mugi) and Southern coffee farms (Awada) reported to result in considerable damages (Belachew *et al*., 2015). The disease is still recurring every year and spreading to the neighboring zones of coffee producing areas of the country, implying for comprehensive intervention to sustain production and productivity of coffee.

The management of coffee diseases largely depends on the deployment of resistant varieties, and significant variations in the reactions of Arabica coffee genotypes to diseases have been documented (Derso *et al*., 1999). As Ethiopia is rich in Arabica coffee genetic resources, resistant varieties can play an undeniable role in combating diseases (Benti *et al*., 2021). For centuries, Ethiopian coffee selections proved to be resistant against many diseases and pests (van der

Graaff, 1981). However, little information is available in the literature to support varietal reaction against thread blight disease and the causative pathogen on *Coffea arabica* in Ethiopia. Therefore, this study was carried out with the objective to evaluate the resistance reactions of coffee (*Coffea arabica*) genotypes to thread blight (*C. koleroga*) disease and their yield performance at Mettu district in Ilubabor zone, Ethiopia.

Materials and Methods

Experimental materials and site

A field experiment was conducted at Mettu Agricultural Research Sub-Centre in the 2017 cropping year to evaluate the reactions of 124 *Coffea arabica* genotypes and two commercial coffee varieties (74110 and 74112) against CTB. These *C. arabica* genotypes were collected from Yayu forest and its surroundings, and the genotypes and the released varieties were evaluated by dividing them into two sets (Set-I and Set-II) to keep the homogeneity of the experimental field. Each set consisted of 64 genotypes including two released coffee varieties. Mettu is located between 8°30'N latitude and 36°00'E longitude and at an altitude of 1550 meter above sea level (m.a.s.l.). The area is characterized by high rainfall (>1900 mm per annum) and moderate temperature (19.50 °C) based on 11 years meteorological data. The area is reported to be hotspot and conducive for CTB disease establishment and development (Derso *et al.*, 1999; Belachew *et al.*, 2015).

Source of *C. koleroga* inoculum

The experimental field was planted with Arabica coffee genotypes and two standard checks during the 2013 cropping season. Plant debris of infected twigs' bark, leaves, berries and berry stalks were left in the field during the 2016 cropping season to serve as sources of inoculum for the actual experimental year of 2017.

Experimental design, field management and evaluation procedures

The coffee seedlings were planted in the 2013 cropping year. Two sets of coffee genotypes, based on their ecological closeness, were arranged in 8x8 simple lattice designs with two replications each. Each genotype was planted in a single row of six trees using a spacing of 2 m x 2 m. The genotypes were established under uniform *Sesbania sesban* temporary shade trees and all other management practices were uniformly applied as per the coffee agronomic production practices in the areas.

Disease assessment

During the experiment, three plants per plot were randomly tagged and physically numbered from 1-3. Data were collected on thread blight severity as percentage of coffee parts covered by the symptoms at 15 days interval for five consecutive times starting from the onset of clear symptoms on some coffee genotypes. The data were recorded starting from July to September 2017. Three pairs of branches, i.e., each pair from upper, middle and lower canopy layers of the coffee plants were considered and marked with label to assess the disease incidence and severity. Number of total leaves, number of diseased leaves, number of total berries, number of diseased berries, number of total twigs and number of diseased twigs per pairs of tagged branches were noted and converted into per plant basis. Data on disease incidence (DI) was calculated at fifteen days interval by the following formula:

$$\text{Disease incidence (\%)} = \frac{\text{Number of infected plant parts}}{\text{Total number of plant parts assessed}} \times 100$$

The severity of thread blight was recorded with a slight modification of 0-5 scoring scale as used by Verma (1991) and described in Table 1. Disease severity data were converted into percentage severity index (PSI) for analysis (Sahile *et al.*, 2008) as follows:

$$\text{PSI} = \frac{\text{Sum of all numerical ratings}}{\text{Number of plant parts observed x maximum score on scale}} \times 100$$

On the basis of disease severity, area under disease progress curve (AUDPC) as well as apparent infection rate were calculated and coffee genotypes were categorized into different reaction classes (highly resistant, resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible). The area under disease progress curve was calculated using the formula employed by Jeger and Viljanen-Rollinson (2001).

$$\text{AUDPC} = \sum_{i=1}^{n-1} \left(\frac{y_i + y_{i+1}}{2}\right)(t_i + 1 - t_i)$$

Where, y_i is an assessment of disease severity (percentage) at the i^{th} observation, t_i is time (in days) for the i^{th} observation, and is the total number of observations in the disease severity assessment.

Apparent infection rate was calculated by using the following formula as mentioned below (Madden et al., 2007):

$$r = \frac{2.3}{(ti + 1 - ti)}\left\{\frac{\log(xi + 1)}{1 - xi + 1} - \log\frac{xi}{1 - xi}\right\}$$

Where, r = apparent rate of infection at log phase of epidemic development and t_i and t_{i+1} for time intervals when disease severities are x_i and x_{i+1}.

Table 1. Coffee thread blight category based on lesion size scoring scale (0-5 grade) devised by (Verma, 1991) with the slight modification.

Rating	Area covered with lesions (%)	Category	Description of rating scales
0	0	Highly resistant	No infection
1	0.01–1.0	Resistant	Very few lesions on tree parts
2	1.1–10.0	Moderately resistant	Few lesions on twigs, leaves and/or berries up to 10% necrotic area covered
3	10.1–25.0	Moderately susceptible	Lesions covering up to 25% of twigs, leaves and/or berries area covered
4	25.1–50.0	Susceptible	More than 30 % of twigs, branches and berries covered under necrotic lesions
5	>50	Highly Susceptible	More than 50% of twigs, branches and/or berries covered under necrotic lesions

Yield assessment

Total fresh cherries were harvested from all tees and weighed in grams per plot basis and converted into clean coffee of kg ha^{-1}.

Data analyses

Data that included disease incidence, severity, AUDPC and apparent infection rate were subjected to analysis of variance (ANOVA) using the SAS Statistical Software Version 9.3 Packages (Westfall *et al.*, 2011). Mean separation was performed with Tukey's Test. Correlation and regression analyses were performed by Pearson correlation and regression analyses using SPSS 20.0 Software Package (Green and Salkind, 2013).

Results and Discussion

Evaluation of coffee genotypes for their reaction to thread blight

Set-I

Based on disease severity, AUDPC and apparent infection rate, the tested genotypes were categorized into five groups (Table 2). These categories included highly resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible. Seven genotypes (Y36, Y47, Y48, Y52, Y53, Y58 and Y62) were highly resistant, 10 genotypes (Y5, Y26, Y27, Y29, Y31, Y32, Y44, Y49, Y50, Y59) and one released variety (74112) were moderately resistant, 16 genotypes (Y1, Y3, Y4, Y7, Y8, Y9, Y11, Y12, Y17, Y24, Y40, Y41, Y42, Y45, Y56 and Y60) were moderately susceptible, 20 genotypes (Y2, Y10, Y13, Y14, Y15, Y19, Y20, Y21, Y22, Y23, Y28, Y30, Y33, Y35, Y37, Y39, Y46, Y51, Y57, Y61) and one released variety (74110) were susceptible and nine genotypes (Y6, Y16, Y18, Y25, Y34, Y38, Y43, Y54 and Y55) had a highly susceptible reaction to the target disease.

The highly susceptible coffee genotypes had a disease severity that ranged from 50 to 55%, AUDPC values of 29 to 32%-days and apparent infection rate of 0.05 to 0.07 units day^{-1}. On the other hand, the highly resistant genotypes had recorded no disease. The other groups (susceptible, moderately susceptible and moderately resistant genotypes) recorded intermediate severity (4 to 48%), with AUDPC values of 2 to 28%-days and apparent infection rates of 0.02 to 0.12 units day^{-1}. These findings are in agreement with the findings of Meles *et al.* (2004) who indicated that AUDPC is more informative than apparent infection rate when assessing the level of resistance of various diseases in the field. As the rate of disease increase is jointly proportional to the level of diseased and healthy tissue, differential leaf growth of various genotypes may be responsible for less variation in apparent infection rate (Pandey *et al.*, 2003).

Table 2. Evaluation of coffee genotypes against thread disease (*C. koleroga*) under field conditions for set-I at Mettu Agricultural Research Sub-Centre, Ethiopia in the 2017 cropping season.

Coffee genotype	Disease components [1]					
	DI	DS	AUDPC	r	Yield (Kg ha^{-1})	DR
Y25	61.76^{a}	54.93^{a}	3249^{a}	0.07^{a-d}	1655.80^{a-e}	HS
Y34	60.43^{ab}	54.36^{a}	3223^{a}	0.05^{b-e}	1098.10^{e-f}	HS
Y18	58.24^{ab}	52.32^{a}	3099^{a}	0.06^{b-e}	1426.40^{b-f}	HS
Y6	57.77^{abc}	51.84^{a}	3081^{a}	0.05^{c-f}	997.60^{df}	HS
Y16	57.76^{abc}	51.52^{a}	3043^{a}	0.05^{b-e}	1095.30^{e-f}	HS
Y54	57.08^{abc}	50.52^{a}	3002^{a}	0.06^{b-e}	1206.20^{b-f}	HS
Y55	56.83^{abc}	50.44^{a}	2993^{a}	0.05^{b-e}	1561.50^{a-f}	HS
Y43	55.85^{bc}	50.34^{a}	2988^{a}	0.05^{b-e}	1564.70^{a-f}	HS
Y38	55.38^{bc}	50.17^{a}	2969^{a}	0.05^{b-e}	2018.20^{abc}	HS
Y2	53.20^{c}	48.24^{a}	2882^{a}	0.05^{d-f}	1363.50^{b-f}	S
Y57	46.33^{d}	41.31^{b}	2429^{b}	0.06^{d-f}	940.60^{e-f}	S
Y22	45.20^{d}	41.00^{b}	2410^{b}	0.07^{b-e}	1451.00^{b-f}	S
Y33	44.51d^{e}	40.36^{bc}	2402^{bc}	0.08^{a-d}	1770.30^{a-e}	S
Y37	44.47^{de}	40.11^{bc}	2400^{bc}	0.08^{a-d}	1300.80^{b-f}	S
Y19	44.19^{de}	39.49^{bcd}	2355^{b-d}	0.07^{b-e}	1759.50^{a-e}	S
74110	43.70^{def}	39.44^{b}	2317^{b-e}	0.06^{c-f}	1476.50^{b-f}	S
Y21	42.64^{d-g}	38.72^{bcd}	2285^{b-e}	0.08^{a-d}	1926.50^{a-e}	S
Y23	41.22^{d-h}	38.25^{b-e}	2268^{b-e}	0.07^{b-e}	1822.80^{a-e}	S
Y14	38.78^{e-i}	35.11^{b-f}	2084^{b-f}	0.06^{c-f}	1535.30^{a-f}	S
Y30	38.10^{f-i}	33.93^{c-g}	2035^{b-g}	0.11^{ab}	1623.40^{a-e}	S
Y51	37.99^{ghi}	33.49^{c-g}	1955^{c-g}	0.08^{a-d}	1572.70^{a-f}	S
Y39	37.01^{g-j}	32.99^{d-g}	1930^{d-e}	0.07^{b-c}	1566.00^{a-f}	S

Table 2. Continued.

Y20	36.28^{hij}	31.89^{e-g}	1886^{e-g}	0.10^{a-c}	1282.90^{b-f}	S
Y46	35.56^{h-k}	31.70^{e-g}	1799^{f-h}	0.08^{a-d}	1675.90^{a-e}	S
Y35	34.79^{ijk}	30.19^{f-h}	1793^{f-h}	0.07^{b-e}	1611.00^{a-e}	S
Y28	34.30^{ijk}	29.61^{f-i}	1754^{f-i}	0.08^{a-d}	2128.00^{ab}	S
Y13	34.26^{ijk}	29.15^{f-j}	1748^{f-i}	0.08^{a-d}	1699.30^{a-e}	S
Y61	33.77^{i-l}	28.95^{f-j}	1698^{f-i}	0.10^{b-c}	1914.30^{a-e}	S
Y10	31.70^{j-m}	27.40^{g-j}	1615^{g-j}	0.07^{b-e}	1802.00^{a-e}	S
Y15	30.18^{klm}	25.33^{h-k}	1443^{h-k}	0.08^{a-d}	1063.30^{c-f}	S
Y12	28.57^{lmn}	24.51^{h-k}	1434^{h-k}	0.07^{b-e}	1288.70^{b-f}	MS
Y7	27.70^{mn}	24.03^{h-k}	1384^{i-l}	0.10^{a-c}	1134.70^{b-f}	MS
Y40	27.54^{mn}	23.61^{i-l}	1369^{i-l}	0.10^{a-c}	1089.90^{c-f}	MS
Y9	27.01^{mno}	23.26^{j-l}	1332^{j-m}	0.10^{a-c}	1881.10^{a-e}	MS
Y24	23.76^{nop}	19.71^{k-m}	1127^{k-n}	0.05^{d-f}	1607.30^{a-e}	MS
Y41	22.02^{opq}	18.29^{l-n}	1066^{l-o}	0.08^{a-d}	1817.60^{a-e}	MS
Y60	21.15^{pqr}	17.61^{m-o}	1015^{m-p}	0.10^{a-c}	1908.80^{a-e}	MS
Y11	20.70^{pqr}	17.49^{m-o}	1006^{m-p}	0.07^{b-e}	1338.60^{b-f}	MS
Y45	20.62^{pqr}	17.23^{m-o}	987^{n-p}	0.10^{a-c}	1937.60^{a-e}	MS
Y4	18.96^{p-s}	15.46^{m-p}	890^{n-q}	0.05^{a}	1666.50^{a-e}	MS
Y17	17.60^{q-t}	14.92^{m-q}	853^{n-r}	0.08^{a-d}	2034.10^{abc}	MS
Y8	17.08^{q-u}	13.98^{m-r}	806^{o-s}	0.08^{a-d}	1486.30^{b-f}	MS
Y3	15.72^{r-v}	13.09^{o-s}	778^{o-t}	0.08^{a-d}	1128.70^{b-f}	MS
Y56	15.66^{r-v}	12.86^{o-t}	766^{o-t}	0.08^{a-d}	1483.70^{b-f}	MS
Y42	14.30^{s-w}	12.27^{p-u}	719^{p-u}	0.02^{fg}	2501.00^{a}	MS
Y1	13.97^{s-w}	11.76^{p-u}	675^{q-v}	0.08^{a-d}	1854.30^{a-e}	MS
Y32	13.2^{s-w}	9.93^{q-v}	598^{r-w}	0.06^{c-f}	1581.40^{a-e}	MR
Y27	12.88^{t-w}	9.75^{r-v}	548^{s-w}	0.12^{a}	1784.10^{a-e}	MR
Y26	12.29^{t-w}	9.56^{r-v}	536^{t-w}	0.12^{b-e}	1434.20^{b-f}	MR

Table 2. Continued.

Y50	11.97^{t-w}	9.38^{s-v}	525^{t-w}	0.12^{a-c}	1947.50^{a-d}	MR
Y44	11.52^{uvw}	9.08^{s-v}	515^{t-w}	0.10^{a-d}	1713.40^{a-e}	MR
Y29	11.09^{vw}	8.620^{s-v}	487^{u-v}	0.08^{a-d}	1934.10^{a-e}	MR
Y59	10.26^{vwx}	8.470^{t-v}	469^{u-w}	0.08^{a-d}	1743.10^{a-e}	MR
Y49	9.89^{vwx}	7.85^{uv}	455^{u-w}	0.06^{c-f}	1880.90^{a-e}	MR
Y5	9.53^{wx}	7.84^{uv}	401^{w}	0.11^{ab}	1933.90^{a-e}	MR
Y31	8.36^{wx}	6.67^{v}	393^{w}	0.06^{c-f}	1257.30^{b-f}	MR
74112	4.94^{xy}	3.66^{w}	217^{x}	0.04^{g}	569.20^{f}	MR
Y36	0.00^{y}	0.00^{x}	0.00^{y}	0.00^{g}	1305.50^{b-f}	HR
Y47	0.00^{y}	0.00^{x}	0.00^{y}	0.00^{g}	1414.60^{b-f}	HR
Y48	0.00^{y}	0.00^{x}	0.00^{y}	0.00^{g}	1943.60^{a-e}	HR
Y52	0.00^{y}	0.00^{x}	0.00^{y}	0.00^{g}	1512.30^{a-f}	HR
Y53	0.00^{y}	0.00^{x}	0.00^{y}	0.00^{g}	1098.70^{c-f}	HR
Y58	0.00^{y}	0.00^{x}	0.00^{y}	0.00^{g}	1655.00^{a-e}	HR
Y62	0.00^{y}	0.00^{x}	0.00^{y}	0.00^{g}	1782.10^{a-e}	HR

[1] *DI = disease incidence (mean of five times); DS = disease severity (mean of five times); AUDPC = area under disease progress curve; r = apparent infection rate; HS = highly susceptible; S = susceptible; MS = moderately susceptible; MR = moderately resistant; and HR = highly resistant. Means in a column followed by the same letter(s) are not significantly different from each other at p = 0.05.*

Set-II

Similar to the coffee genotypes tested in Set-I, the genotypes included in this set of experiment were also categorized into five disease reaction groups (highly resistant, moderately resistant, moderately susceptible, susceptible and highly susceptible) (Table 3). Seven coffee genotypes (Y73, Y77, Y93, Y97, Y99, Y100 and Y106) were highly resistant, 17 coffee genotypes (Y76, Y63, Y69, Y72, Y74, Y78, Y79, Y80, Y81, Y82, Y89, Y98, Y100, Y103, Y105, Y110 and Y117) and one released variety (74112) were moderately resistant, 17 genotypes (Y65, Y67, Y70, Y71, Y83, Y84, Y86, Y88, Y90, Y92, Y96, Y102, Y107, Y111, Y112, Y116 and Y124) were moderately susceptible, 15 genotypes (Y64, Y68, Y75, Y85, Y87, Y91, Y95, Y104, Y108, Y109, Y113, Y115, Y119, Y120 and Y123) and one released variety (74110) were susceptible and six genotypes (Y66, Y94, Y114, Y118, Y121 and Y122) were found highly susceptible to thread blight under field conditions.

The highly susceptible *C. arabica* genotypes had CTB severity that ranged from 50 to 56%, AUDPC values of 2969 to 3346%-days and apparent infection rate of 0.05 to 0.08 units day^{-1}. On the contrary, the highly resistant genotypes did not get infected and results in zero disease components. The remaining groups had moderate disease reaction levels across the evaluation criteria. Results from this set of experiment are in line with those from Set-I in revealing the resistance classes. This suggests the potential Ethiopian coffee genotypes may have in combating against this economically important disease.

The current study showed considerable variations in the response of 124 *C. arabica* genotypes to coffee thread blight disease. Out of the 126 *C. arabica* genotypes evaluated, 14 genotypes were highly resistant, 28 moderately resistant, 32 moderately susceptible, 37 susceptible and 15 genotypes were highly susceptible to the disease. From a plant breeding perspective, it has been suggested that the use of moderate resistance may be more durable than complete resistance (Stuthman et al., 2007). Most of the evaluated *C. arabica* genotypes showed at least some levels of thread blight by mid-July to mid-September and the disease progressed at an average rate of 0.07 units day^{-1} (Tables 2 and 3).

Table 3. Evaluation of coffee genotypes against *C. koleroga* at field conditions for set-II at Mettu Agricultural Research Sub-Centre in 2017 cropping season.

Coffee genotype	Disease components [1]					
	DI	DS	AUDPC	r	Yield (kg ha^{-1})	DR
Y118	64.67^{a}	56.09^{a}	3346^{a}	0.08^{c-f}	663.90^{d-i}	HS
Y122	63.24^{ab}	55.83^{a}	3291^{a}	0.05^{e-i}	1308.70^{a-h}	HS
Y66	61.91^{ab}	54.66^{a}	3237^{ab}	0.05^{e-i}	1186.00^{a-i}	HS
Y114	59.65^{abc}	52.41^{a}	3117^{ab}	0.05^{e-i}	836.50^{c-i}	HS
Y121	58.42^{abc}	51.52^{ab}	3084^{a-c}	0.05^{e-i}	1395.00^{a-h}	HS
Y94	56.33^{a-e}	50.09^{abc}	2984^{a-c}	0.05^{e-i}	673.50^{d-i}	HS
Y113	54.49^{a-e}	47.32^{bcd}	2738^{b-d}	0.05^{e-i}	836.50^{c-i}	S
Y109	52.74^{a-f}	43.14^{b-d}	2608^{c-d}	0.12^{bc}	1137.50^{a-i}	S
Y64	49.94^{a-g}	41.47^{cd}	2469de	0.10^{c-e}	1370.70^{a-i}	S
Y68	49.36^{a-g}	40.76^{d-f}	2456de	0.11^{b-d}	1236.40^{a-i}	S
Y119	45.67^{a-h}	40.08^{d-g}	2398^{d-f}	0.11^{b-d}	1331.80^{a-h}	S
Y120	45.10^{a-h}	39.06^{d-g}	2324^{d-f}	0.08^{c-f}	1320.10^{a-h}	S
Y85	44.86^{a-i}	37.37^{e-h}	2261^{d-g}	0.16^{ab}	1090.60^{a-i}	S
Y123	43.34^{b-i}	36.77^{e-h}	2229^{e-h}	0.16^{ab}	1168.90^{a-i}	S
74110	40.73^{c-j}	34.70^{e-i}	2059^{e-i}	0.10^{c-e}	1575.10^{a-d}	S
Y87	38.71^{c-k}	31.00^{f-i}	1893^{f-j}	0.11^{b-d}	1097.70^{a-i}	S
Y95	36.57^{d-k}	31.04^{g-i}	1826^{g-k}	0.10^{c-e}	1192.60^{a-i}	S
Y91	36.28^{d-k}	29.96^{hi}	1779^{h-k}	0.10^{c-e}	987.60^{b-i}	S
Y104	35.32^{d-m}	28.83^{hi}	1719^{i-k}	0.08^{c-f}	1243.60^{a-i}	S
Y115	34.78^{e-m}	28.77 ^{hi}	1704^{i-k}	0.07^{c-g}	1275.00^{a-h}	S
Y75	32.42^{f-o}	26.57^{i-k}	1571^{j-l}	0.18^{a}	1497.10^{a-f}	S
Y108	30.24^{g-p}	25.56^{i-l}	1539^{j-l}	0.10^{c-e}	543.80^{f-i}	S
Y111	29.44^{g-p}	24.65 $^{j-l}$	1474^{k-m}	0.02^{g-i}	1091.90^{a-i}	MS
Y92	28.98^{g-q}	24.48 $^{j-l}$	1432^{k-m}	0.11^{b-d}	1177.60^{a-i}	MS

Table 3. Continued.

Y90	27.14^{h-q}	23.21^{j-m}	1390^{k-m}	0.12^{bc}	1054.00^{a-i}	MS
Y107	23.83^{i-r}	18.96^{k-n}	1119^{l-o}	0.05^{e-i}	1546.40^{a-e}	MS
Y65	22.09^{j-t}	16.72^{l-o}	1004^{m-p}	0.11^{b-d}	1392.50^{a-h}	MS
Y71	22.07^{j-t}	16.68^{l-o}	993^{m-q}	0.07^{c-g}	1138.30^{a-i}	MS
Y124	20.67^{j-u}	16.43^{l-p}	974^{m-r}	0.06^{d-h}	586.30^{e-i}	MS
Y102	19.38^{k-u}	16.31^{l-p}	963^{m-r}	0.06^{d-h}	947.70^{b-i}	MS
Y96	18.46^{k-u}	15.12^{m-q}	946^{m-s}	0.04^{f-i}	1891.50^{ab}	MS
Y112	18.03^{k-u}	15.03^{m-q}	885^{n-t}	0.07^{c-g}	1505.20^{a-f}	MS
Y88	17.41^{l-u}	14.79^{m-q}	884^{n-t}	0.06^{d-h}	809.70^{e-i}	MS
Y116	17.16^{l-u}	13.50^{n-r}	794^{o-t}	0.02^{g-i}	891.00^{e-i}	MS
Y70	16.84^{l-u}	12.96^{n-s}	755^{o-u}	0.02^{g-i}	1267.00^{a-h}	MS
Y84	15.54^{l-u}	12.53^{n-s}	740^{o-v}	0.06^{d-h}	295.00^{i}	MS
Y67	14.99^{m-u}	12.30^{n-t}	731^{o-w}	0.01^{hi}	1688.20^{abc}	MS
Y86	14.69^{m-u}	12.26^{n-t}	720^{o-w}	0.07^{c-g}	1492.60^{a-f}	MS
Y83	13.97^{n-u}	10.69^{n-t}	654^{o-w}	0.06^{e-i}	1575.10^{a-d}	MS
Y89	13.66^{n-u}	9.95^{n-t}	596^{o-w}	0.05^{e-i}	1311.10^{a-h}	MR
Y76	12.11^{o-u}	9.86^{n-t}	593^{o-w}	0.07^{c-g}	1476.90^{a-f}	MR
Y110	13.66^{n-u}	9.56^{n-t}	596^{o-w}	0.05^{e-i}	1610.90^{a-d}	MR
Y79	12.11^{o-u}	8.02^{o-u}	593^{o-w}	0.07^{c-g}	1695.00^{abc}	MR
Y98	10.93^{p-u}	8.01^{o-u}	475^{p-x}	0.01^{hi}	1439.20^{a-g}	MR
Y105	10.78^{p-u}	7.53^{o-u}	468^{p-x}	0.04^{f-i}	1686.80^{abc}	MR
Y101	9.73^{p-u}	7.05^{o-u}	426^{q-x}	0.02^{g-i}	1524.30^{a-e}	MR
Y69	9.24^{p-u}	7.02^{o-u}	425^{q-x}	0.02^{g-i}	1169.50^{a-i}	MR
Y81	9.19^{p-u}	6.85^{p-u}	410^{r-x}	0.02^{g-i}	1482.90^{a-e}	MR
Y117	8.18^{q-u}	6.50^{q-u}	394^{s-x}	0.02^{g-i}	1037.80^{b-i}	MR
Y74	7.50^{r-u}	5.95^{q-u}	352^{t-x}	0.00^{i}	1378.20^{a-h}	MR
74112	7.31^{r-u}	5.64^{q-u}	352^{t-x}	0.04^{f-i}	1100.50^{a-i}	MR

Table 3. Continued.

Y80	7.07^{r-u}	5.42^{q-u}	340^{t-x}	0.04^{f-i}	1458.90^{a-f}	MR
Y82	6.61^{r-u}	4.84^{r-u}	292^{u-x}	0.05^{d-h}	607.20^{e-i}	MR
Y78	5.91^{stu}	4.33^{r-u}	271^{u-x}	0.01^{hi}	885.80^{c-i}	MR
Y103	4.70^{stu}	3.73^{s-u}	225^{u-x}	0.02^{g-i}	477.50^{ghi}	MR
Y63	3.49^{stu}	3.51^{s-u}	210^{v-x}	0.02^{i}	1323.60^{a-h}	MR
Y72	3.21^{stu}	2.72^{tu}	162^{wx}	0.01^{hi}	1864.00^{ab}	MR
Y77	0.00^{u}	0.00^{u}	0.00^{x}	0.00^{i}	1267.50^{a-h}	HR
Y93	0.00^{u}	0.00^{u}	0.00^{x}	0.00^{i}	1664.50^{abc}	HR
Y73	0.00^{u}	0.00^{u}	0.00^{x}	0.00^{i}	1328.10^{a-h}	HR
Y100	0.00^{u}	0.00^{u}	0.00^{x}	0.00^{i}	660.40^{d-i}	HR
Y97	0.00^{u}	0.00^{u}	0.00^{x}	0.00^{i}	1959.00^{a}	HR
Y106	0.00^{u}	0.00^{u}	0.00^{x}	0.00^{i}	1211.30^{a-i}	HR
Y99	0.00^{u}	0.00^{u}	0.00^{x}	0.00^{i}	1290.00^{a-h}	HR

[1] *DI = disease incidence (mean of five times); DS = disease severity (mean of five times); AUDPC = area under disease progress curve; r = apparent infection rate; HS = highly susceptible; S = susceptible; MS = moderately susceptible; MR = moderately resistant; and HR = highly resistant. Means in a column followed by the same letter(s) are not significantly different from each other at p = 0.05.*

Yield performance of evaluated coffee genotypes

The current study showed that there were considerable yield variations among *C. arabica* genotypes (Tables 2 and 3). The highest (2501 kg ha^{-1}) yield of coffee was obtained from genotype Y42 with disease severity of 12.27%, followed by Y28 with the mean yield of 2128 kg ha^{-1} with disease severity of 29.61% in set-I of the experiments. Whereas, the lowest yield was obtained from Yayu coffee genotype Y6, followed by Y16 with mean yield of 998 and 1095 kg ha^{-1} with disease severity of 51.84 and 51.52%, respectively in set-I of the experiments. Similarly, the highest yield of coffee was obtained from genotype Y97 (1959 kg ha^{-1}), followed by Y72 with the mean yield of 1864 kg ha^{-1}. Of course, Y97 and Y72 noted mean disease severity of 0.00 and 2.72%, respectively in set-II. Whereas, the lowest yield of coffee was obtained from Yayu coffee genotype Y118, followed by Y94 with the mean yield of 664 and 674 kg ha^{-1}, respectively, with corresponding disease severity of 51.84 and 51.52% in that order in set-II.

Relationship between disease parameters and coffee yield

Moderate to strongly positive correlation coefficients were computed between CTB parameters (disease incidence, severity, AUDPC and apparent infection rate) and yield of coffee (Table 4). Results of the correlation analysis revealed weak and negative relationship between disease parameters and coffee yield. The correlation analysis obtained similar trends between the two sets of experiments. A highly positive correlation of disease severity was observed with disease incidence (range: r = 0.98 to 0.99, $p \leq 0.01$), AUDPC (range: r = 0.92 to 0.99, $p \leq 0.01$) and apparent infection rate (range: r = 0.53 to 0.60, $p \leq 0.01$) (Table 4). However, the associations of disease severity with coffee yield were non-significant, negative and weak (range: r = -0.18 to -0.31; $p > 0.05$). This might be because the yield of coffee (a perennial plant) is affected by many more factors than a single season disease pressure.

Table 4. Correlation coefficients between disease parameters and coffee yield for set-I (below diagonal) and set-II (above diagonal) at Mettu Agricultural Research Sub-Centre in the 2017 cropping season.

Parameter [a]	DI	DS	r	AUDPC	Yield
DI	1	0.99^{**}	0.62^{**}	0.99^{**}	-0.17^{ns}
DS	0.98^{**}	1	0.60^{**}	0.92^{**}	-0.18^{ns}
r	0.58^{**}	0.53^{**}	1	0.61^{**}	-0.11^{ns}
AUDPC	0.98^{**}	0.99^{**}	0.54^{**}	1	-0.18^{ns}
Yield	-0.24^{ns}	-0.31^{ns}	-0.28^{ns}	-0.18^{ns}	1

[a]DI = disease incidence; DS = disease severity; r = apparent infection rate; and AUDPC = area under disease progress curve. ** = correlation is highly significant at $p \leq 0.01$, ns = not significant at $p > 0.05$.

The identification of highly resistant to moderately resistant *C. arabica* genotypes through different disease parameters indicates the potential use of these accessions in *C. arabica* resistance breeding program against thread blight. A combination of disease parameters (DS, DI, AUDPC and r) are widely used for

assessment of foliar fungal disease reactions. The current results indicated that there was substantial genetic variability across the different disease parameters assessed, where 14 *C. arabica* genotypes were categorized as highly resistant and asymptomatic to CTB, while 28 genotypes were grouped under moderately resistant genotypes, which had the lowest disease ratings, indicating a potential source of resistance for further study. In plant breeding, the use of moderate resistance may be more durable than complete resistance. Although significant genetic differences were manifested by r (12-fold), the difference was not as distinct as that of AUDPC (20-fold).

Conclusion and Recommendation

In conclusion thread blight disease (*C. koleroga*) is becoming an important disease in coffee producing areas of southwestern Ethiopia. Different *C. arabica* genotypes had different reaction against the disease. Out of 126 *C. arabica* genotypes evaluated, 42 were highly resistant to moderately resistant, whereas 84 genotypes were moderately susceptible to highly susceptible disease reaction against the disease under field conditions. Therefore, it is recommendable to promote the genotypes categorized under highly resistant to moderately resistant reaction groups to varietal trial levels to test both under greenhouse and across different field conditions, and plant highly resistant to moderately resistant genotypes along with other management options in the study areas and other related agro-ecologies. However, future research should be directed towards studying resistance mechanisms to transfer resistance genes to released coffee varieties and study the economic importance of the disease regarding coffee yield losses.

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