

Survey on Nigerian Castor Germplasm for Potential Resistant Genotypes to *Cercospora* Leaf Spot

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Abstract

Fungal diseases cause a lot of economic damage in castor and in some instances; it is a limiting factor to commercial cultivation of the crop. In the present study, survey on castor germplasm for sources of resistant genes to *Cercospora* leaf spot was carried out at National Cereals Research Institute Badeggi, Nigeria. The genotypes were grown in a resolvable incomplete block design with three replications. The results obtained revealed high variability of host resistance among the genotypes. Percentage disease incidence ranged between 16.67% and 100%. A range between 1.43 score and 4.17 scores with average score of 2.89 were recorded for disease severity among the genotypes. Highest (95.92%) and lowest (13.03%) damage index were observed in the genotypes Acc. 059 and Acc. 022 respectively. The Principal component (PC) 1 to 4 explained 100% of the variability in the germplasm. PC1 explained 69.72% of the variability with the major contributory parameters being the disease incidence, severity and damage index. Significant negative correlations were recorded between the seed yield and all the three disease indices. The result of cluster analysis revealed six cluster groups among the germplasm with cluster membership ranging between 4 and 40 members. The cluster I contained members (Acc. 002, Acc. 017, Acc. 022, Acc. 026, Acc. 027, Acc. 048 and Acc. 061) with low average disease incidence, severity and damage index. The results reported here could serve as a basis for further screening of the potential resistant genotypes under controlled condition to develop resistant lines.

Keywords: castor; *Cercospora*; disease; germplasm; lines; resistance

Introduction

Castor (*Ricinus communis* L.) is a non-edible oil crop with high economic values around the world (Gana *et al.*, 2013). It is widely cultivated in the tropics, subtropics and warm regions for its seed from which oil is extracted (Purseglove, 1968; Weiss, 1971). The oil, also known as castor oil, is very critical to many industrial applications because of its ability to form many important derivatives (Ogunniyi, 2006). The oil is used in pharmaceutical, rubber/plastic and lubricants/biodiesel industries (Mutlu and Meier, 2010). In Southern part of Nigeria, a food condiment (*Ogiri*) among the Igbo tribe is produced from castor seeds (Gana, 2015). The residual meal of castor seed,

after detoxified by boiling, could be used as supplement feed in preparation of broiler finishing diets without any harmful effect (Ani and Okorie, 2009). Also, the meal (autoclaved) could be used in place of the soybean meal in sheep rations. Organic fertilizer produced from castor meal was reported to have advantage of high nitrogen content, fast mineralization and anti-nematode effects (Lima *et al.*, 2011). The leaves, seeds and capsules of castor are used for traditional medicines (Gana, 2015).

Castor plant suffers from many diseases caused by fungi and bacteria (Salihu *et al.*, 2014). There are many causal pathogens known to cause infections in castor. Some of these pathogens are seed-borne. Fungal diseases cause a lot of economic damage in castor and in some areas it is a limiting factor to commercial castor cultivation (Anjani *et al.*, 2004). The fungal disease incidences often appear in

castor farms and if not managed, cause severe economic loss to the farmers. Some fungal diseases commonly infect castor include leaf spot caused by *Cercospora ricinella*, wilt cause by *Fusarium oxysporum* f *spricini*, root rot cause by *Macrophomina phaseolina*, gray rot cause by *Botrytis ricini*, and leaf spot caused by *Alternari aricini* (Anjani et al., 2004; Salihu et al., 2014). In the present study, on-field observation of fungal infection caused by *Cercospora ricinella* in castor was carried out, in an effort to identify potential resistant genotypes in the Nigerian castor germplasm evaluated.

Materials and Methods

On-field observations on fungal leaf spot disease caused by *Cercospora ricinella* were made on 86 castor genotypes at Castor Research Field of the National Cereals Research Institute (NCRI) Badeggi during 2016 growing season. The genotypes were grown on a resolvable incomplete block design with three replications. The plot size was 3 m by 1.5 m with Inter-row and intra-row spacing of 75 cm. Two seeds per hole were planted and later thinned to one seedling per hole at three to four weeks after planting. Fertilizers were applied at one month after planting and weeding was done three times during the experiment. Disease incidence was determined by counting diseased plant and expressed as percentage of total plant per plot. Disease severity was carried out by scoring diseased plants using a 1 - 5 scale as described by Mamza (2008). Damage index (DI) was determined according to Manandhar et al. (2016). Data were taken on 10 plant samples in each plot, amounting to 30 plant samples per genotypes. The disease observations were made at first spike flowering and maturity. The scoring and estimation of damage index was done as follows;

Score scale for the leaf spot:

1 = All leaves without symptom

2 = 1 - 25% of total leaf number with symptoms

3 = 26 - 50% of total leaf number with symptoms

4 = 51 - 75% of total leaf number with symptoms

5 = 76% and above of total leaf number with symptoms

Damage index (DI) = (Incidence X Severity) / Highest severity × 100

Analysis of variance was done according to Muhammad et al. (2015). Multivariate analysis was done according to the procedure of Statistical Tool for Agricultural Research (STAR 2.0.1).

Results and Discussion

The results showed significant differences among the germplasm for all the parameters considered (Tables 1, 2). Average mean values for disease incidence, disease severity and damage index are presented in Table 1. Disease incidence varied between 16.67% (Acc. 017) and 100% (Acc. 059), with average of 65.91%. A range between 1.43 score (Acc. 022) and 4.17 score (Acc. 056 and Acc. 094), and average of 2.89 score were recorded for disease severity among the genotypes. Highest (95.92%) and lowest

(13.03%) damage index was observed in Acc. 059 and Acc. 022 respectively. The values obtained here are similar to those described by Mamza et al. (2008) who reported fungal leaf blight incidence and severity on castor seedling at different stages. Yield loss of 80% to 100% has been attributed to fungal disease in India (Mamza et al., 2008). Lakshmi et al. (2010) reported that damage to castor leaves caused reduction in seed yield and any 1 m² loss of leaf area resulted in production loss of 37.83 g and 24.4 g seed yield and seed oil yield per hectare respectively.

Seed yield among the genotypes varied from 334.75 kg/ha (Acc. 067) to 1349.84 kg/ha (Acc. 001) with population mean of 645.66 kg/ha (Table 2). The predicted genotype means showed similar pattern among the genotypes with a range of 540.76 kg/ha to 1083.24 kg/ha and average of 646.91 kg/ha. Thirty-six out of the eighty-six genotypes evaluated recorded higher mean than the population mean. Table 3 depicts the contributions of the seed yield and the disease indices to the total variability observed in the germplasm. The principal component (PC) 1 to 4 explained 100% of the variability in the germplasm. PC1 explained 69.72% of the variability with the major contributory parameters being the disease incidence, severity and damage index. The PC2 accounted for 19.47% of the variation with seed yield being the major contributor. Disease severity is the major contributor in PC3 which accounted for 10.47% of the total variability. Correlation coefficients between the seed yield and the disease indices recorded are presented in Table 4. Significant negative correlations at P < 0.01 were recorded between the seed yield and all the three disease indices. Disease severity showed the highest negative correlation (-0.407) with the seed yield, followed by damage index (-0.404) and then disease incidence (-0.308).

Dendrogram which showed the grouping of the genotypes into different clusters based on their reactions to the disease studied is presented in the Fig. 1. At cophenetic correlation coefficient of 0.58, six groups were identified with cluster membership ranging between 4 and 40 members. The cluster VI had the highest (40) cluster members and the least cluster members was observed for cluster II (Table 5). The cluster I contained members with low average disease incidence, severity and damage index (Table 5). Thus, this group made up of potential genotypes for resistance to *Cercospora* leaf spot among the genotypes evaluated. This group also had average seed yield (669.41 kg/ha) greater than population mean (645.67 kg/ha). Cluster IV comprised genotypes with high average disease incidence, severity and damage index and also low average yield, indicating susceptibility to the leaf spot. The results obtained revealed high variability of host reaction to the disease among the genotypes. This may be an indication for presence of different gene recombinants for the leaf spot resistance among the genotypes from which resistant lines could be developed. In this sense, the genotypes with low disease severity and low damage index could serve as relevant sources for the resistance genes. Adequate genetic diversity in castor has also been reported by Allan et al. (2008); Milani et al. (2009) and Foster et al. (2010).

Table 1. Mean values of disease incidence, severity and damage index (DI) of 86 castor genotypes at NCRI Badeggi

S/N	Genotypes	Incidence	Severity	DI
1	Acc.001	44.33	2.33	24.77
2	Acc.002	39.00	1.83	17.12
3	Acc.003	75.00	3.67	66.01
4	Acc.004	64.33	1.93	29.77
5	Acc.005	74.67	1.67	29.90
6	Acc.006	60.33	2.77	40.08
7	Acc.007	51.67	2.67	33.08
8	Acc.008	67.00	2.77	44.51
9	Acc.009	61.00	2.93	42.86
10	Acc.010	70.67	2.77	46.94
11	Acc.012	53.67	2.77	35.65
12	Acc.015	71.33	3.10	53.03
13	Acc.016	75.00	3.33	59.89
14	Acc.017	16.67	2.15	18.60
15	Acc.018	50.67	2.43	29.53
16	Acc.019	42.00	2.30	23.17
17	Acc.022	38.00	1.43	13.03
18	Acc.024	58.00	2.60	36.16
19	Acc.026	37.33	2.00	17.90
20	Acc.027	43.67	2.00	20.95
21	Acc.028	80.00	2.77	53.14
22	Acc.029	39.00	2.27	21.23
23	Acc.031	57.00	3.50	47.84
24	Acc.032	59.67	3.00	42.93
25	Acc.033	72.33	2.67	46.31
26	Acc.034	71.00	3.00	51.08
27	Acc.035	39.00	2.50	23.38
28	Acc.036M1	64.00	2.27	34.84
29	Acc.036	67.00	3.00	48.20
30	Acc.039	71.33	2.67	45.67
31	Acc.040	77.00	3.33	61.49
32	Acc.041	53.67	2.67	34.36
33	Acc.042	89.00	2.33	49.73
34	Acc.043	87.00	3.33	69.48
35	Acc.044	71.33	2.17	37.12
36	Acc.045	56.00	2.50	33.57
37	Acc.046	40.67	2.50	24.38
38	Acc.047	85.00	2.43	49.53
39	Acc.048	38.67	1.83	16.97
40	Acc.050	77.67	3.17	59.04
41	Acc.051	82.00	2.30	45.23
42	Acc.052	74.67	3.43	61.42
43	Acc.053	61.75	2.88	42.65
44	Acc.054	43.67	3.33	34.87
45	Acc.055	79.00	3.00	56.84
46	Acc.056	86.67	4.17	86.67
47	Acc.057	80.60	2.92	56.44
48	Acc.058	74.67	3.17	56.76
49	Acc.059	100.00	4.00	95.92
50	Acc.060	73.33	2.27	39.92
51	Acc.061	38.67	1.93	17.90
52	Acc.062	63.33	3.10	47.08
53	Acc.063	89.00	3.00	64.03
54	Acc.064	70.00	2.83	47.51
55	Acc.065	75.67	3.60	65.33
56	Acc.066	58.67	2.77	38.97
57	Acc.067	65.00	3.50	54.56
58	Acc.068	71.00	3.60	61.30
59	Acc.069	79.67	3.10	59.23
60	Acc.070	54.33	3.17	41.30
61	Acc.071	70.33	2.77	46.72
62	Acc.072	51.67	2.50	30.98
63	Acc.073	67.33	3.17	51.18
64	Acc.075	78.33	3.83	71.94
65	Acc.076	66.50	2.50	39.87
66	Acc.077	61.67	2.43	35.94
67	Acc.080	96.00	4.10	94.39
68	Acc.081	92.67	4.00	88.89
69	Acc.083	68.00	3.67	59.85
70	Acc.085	80.00	2.00	38.37
71	Acc.087	59.00	2.93	41.46
72	Acc.088	74.00	3.43	60.87
73	Acc.089	43.00	3.60	37.12
74	Acc.090	75.50	3.58	64.82
75	Acc.091	58.67	2.83	39.82
76	Acc.093	70.00	3.00	50.36
77	Acc.094	87.00	4.17	87.00
78	Acc.095	92.67	3.60	80.00
79	Acc.096	83.67	3.50	70.23
80	Acc.097	67.33	3.43	55.38
81	Acc.098	64.33	3.27	50.45
82	Acc.099	61.67	2.17	32.09
83	Acc.100	69.67	3.27	54.63
84	Acc.101	67.00	3.50	56.24
85	Acc.102	60.33	2.17	31.40
86	Acc.103	48.00	2.50	28.78
	Minimum	16.67	1.43	13.03
	Maximum	100.00	4.17	95.92
	Mean	65.43	2.88	46.58
	SE-Mean	1.74	0.07	1.97
	Mean Square	777.38*	1.14*	1005.35**
	HSD	7.31	0.43	3.68

Note: HSD = Test Statistic for Tukey's's Honest Significant Difference

Table 2. Mean values for seed yield (SY) and predicted genotype seed yield (PGSY) among eighty-six castor genotypes

S/N	Genotypes	SY	PGSY
1	Acc.001	1349.84	1083.24
2	Acc.036M1	1191.04	936.64
3	Acc.036	918.86	829.74
4	Acc.010	995.96	762.26
5	Acc.045	985.32	760.04
6	Acc.005	971.66	755.82
7	Acc.026	688.82	751.06
8	Acc.053	941.70	734.96
9	Acc.099	884.92	725.90
10	Acc.040	844.94	711.88
11	Acc.048	840.88	709.16
12	Acc.003	609.42	704.48
13	Acc.046	811.90	700.80
14	Acc.009	995.02	696.78
15	Acc.022	593.14	695.08
16	Acc.019	799.44	685.78
17	Acc.042	741.62	676.46
18	Acc.012	642.62	676.12
19	Acc.002	721.72	669.08
20	Acc.091	717.92	668.68
21	Acc.072	715.98	666.64
22	Acc.016	514.36	664.24
23	Acc.006	538.88	662.86
24	Acc.044	656.12	661.40
25	Acc.027	562.74	660.44
26	Acc.097	682.64	659.12
27	Acc.103	682.06	656.92
28	Acc.073	676.66	654.96
29	Acc.061	677.46	654.76
30	Acc.062	666.02	651.98
31	Acc.047	665.44	650.16
32	Acc.051	681.90	649.44
33	Acc.100	656.68	648.62
34	Acc.095	658.10	647.82
35	Acc.070	699.22	647.10
36	Acc.035	1002.88	646.58
37	Acc.039	642.40	643.06
38	Acc.015	706.54	642.56
39	Acc.031	559.30	642.48
40	Acc.056	633.74	640.50
41	Acc.096	631.76	639.88
42	Acc.050	619.66	634.70
43	Acc.089	612.14	631.82
44	Acc.004	971.44	631.00
45	Acc.018	718.32	629.04
46	Acc.033	542.10	628.92
S/N	Genotypes	SY	PGSY
47	Acc.093	597.86	627.96
48	Acc.063	608.84	627.92
49	Acc.024	961.16	625.54
50	Acc.057	565.32	623.08
51	Acc.098	583.24	622.36
52	Acc.090	565.08	620.14
53	Acc.054	569.38	620.00
54	Acc.064	566.98	618.70
55	Acc.081	565.60	616.78
56	Acc.028	531.44	616.12
57	Acc.032	597.26	613.42
58	Acc.007	541.34	608.76
59	Acc.034	654.30	608.72
60	Acc.008	797.60	608.34
61	Acc.043	536.60	606.14

62	Acc.041	533.94	605.24
63	Acc.029	646.96	604.76
64	Acc.066	526.10	604.32
65	Acc.065	505.86	604.00
66	Acc.087	519.58	601.38
67	Acc.017	601.08	600.26
68	Acc.080	516.30	599.68
69	Acc.077	511.12	592.44
70	Acc.068	496.28	592.14
71	Acc.052	489.64	591.28
72	Acc.102	488.46	590.50
73	Acc.058	455.36	582.30
74	Acc.094	450.42	577.68
75	Acc.085	450.54	577.08
76	Acc.060	442.70	575.30
77	Acc.071	443.70	574.16
78	Acc.075	441.60	571.72
79	Acc.088	423.82	568.06
80	Acc.059	430.26	567.26
81	Acc.076	414.30	567.14
82	Acc.055	412.52	565.40
83	Acc.069	397.58	560.16
84	Acc.101	367.30	553.66
85	Acc.083	363.92	548.20
86	Acc.067	334.76	540.76
	Minimum	334.76	646.66
	Maximum	1349.84	
	Mean	645.67	
	SE-Mean	20.50	
	Mean Square	10845.42**	
	HSD	51.25	

Note: HSD = Test Statistic for Tukey's Honest Significant Difference

Table 3. Principal components for the disease index and yield among eighty-six castor genotypes

Variables	PC1	PC2	PC3	PC4
SY	-0.3403	-0.9230	0.1793	-0.0021
I	0.5131	-0.3189	-0.6624	0.4429
S	0.5268	-0.0541	0.7267	0.4375
DI	0.5860	-0.2082	0.0309	-0.7825
Standard deviation	1.6700	0.8825	0.6472	0.1166
Proportion of Variance	0.6972	0.1947	0.1047	0.0034
Cumulative Proportion	0.6972	0.8919	0.9966	1.0000
Eigen Values	2.7888	0.7788	0.4189	0.0136

Table 4. Correlation coefficients between seed yield and disease indices of *Cercospora* leaf spots among eighty-six castor genotypes

Parameters		Seed yield (kg/ha)	Predicted seed yield mean (kg/ha)	Disease incidence (%)	Disease severity	Disease damage index (%)
SY	coef	1.000	0.842	-0.308	-0.407	-0.404
	p-value		0.000	0.004	0.000	0.000
PSY	coef		1.000	-0.265	-0.341	-0.335
	p-value			0.014	0.001	0.002
Incidence	coef			1.000	0.568	0.877
	p-value				0.000	0.000
Severity	coef				1.000	0.874
	p-value					0.000
DI	coef					1.000
	p-value					

Table 5. Cluster membership performances of eighty-six castor genotypes evaluated for disease indices

Parameters		Cluster I	Cluster II	Cluster III	Cluster IV	Cluster V	Cluster VI
Disease Incidence	Min	16.67	43.00	39.00	75.00	60.33	58.67
	Max	43.67	57.00	58.00	100.00	80.00	89.00
	Mean	36.00	49.50	48.33	85.85	67.78	71.01
Disease Severity	Min	1.43	3.17	2.27	3.33	1.67	2.30
	Max	2.15	3.60	2.77	4.17	2.50	3.67
	Mean	1.88	3.40	2.50	3.80	2.16	3.02
Disease Damage Index	Min	8.60	34.87	21.23	64.82	29.77	38.97
	Max	20.95	47.84	36.16	95.92	39.92	64.03
	Mean	16.07	40.28	29.16	78.39	34.92	51.34
Seed Yield	Min	562.74	559.30	533.94	430.26	414.30	334.76
	Max	840.88	699.22	1349.84	658.10	1191.04	995.96
	Mean	669.41	610.01	799.37	545.39	698.23	612.07
Number of Members		7	4	13	12	10	40
Cluster Members		Acc.002 Acc.017 Acc.022 Acc.026 Acc.027 Acc.048 Acc.061	Acc.031 Acc.054 Acc.070 Acc.089	Acc.001, Acc.007 Acc.012, Acc.018 Acc.019, Acc.024 Acc.029, Acc.035 Acc.041, Acc.045 Acc.046, Acc.072 Acc.103	Acc.003, Acc.043 Acc.056, Acc.059 Acc.065, Acc.075 Acc.080, Acc.081 Acc.090, Acc.094 Acc.095, Acc.096	Acc.004, Acc.005 Acc.036M1, Acc.044 Acc.060, Acc.076 Acc.077, Acc.085 Acc.099, Acc.102	Acc.006, Acc.008, Acc.009 Acc.010, Acc.015, Acc.016 Acc.028, Acc.032, Acc.033 Acc.034, Acc.036, Acc.039 Acc.040, Acc.042, Acc.047 Acc.050, Acc.051, Acc.052 Acc.053, Acc.055, Acc.057 Acc.058, Acc.062, Acc.063 Acc.064, Acc.066, Acc.067 Acc.068, Acc.069, Acc.071 Acc.073, Acc.083, Acc.087 Acc.088, Acc.091, Acc.093 Acc.097, Acc.098, Acc.100 Acc.101

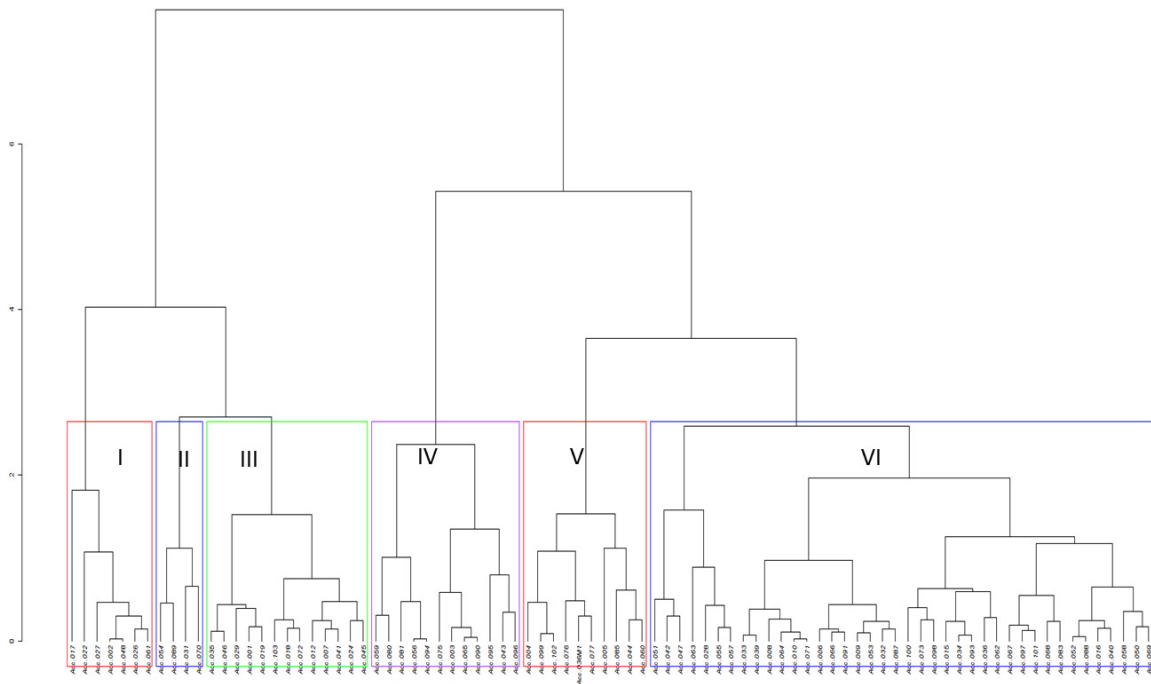


Fig. 1. Dendrogram from agglomerative cluster analysis of eighty-six castor genotypes for *Cercospora* disease indices

Conclusions

The results of the study revealed variation in disease incidence, disease severity and damage index among the germplasm evaluated. Highly significant negative correlations were observed between the seed yield and all the three disease indices under consideration. Seven genotypes (Acc. 002, Acc. 017, Acc. 022, Acc. 026, Acc. 027, Acc. 048 and Acc. 061) were identified as potential sources of resistance genes to the *Cercospora* leaf spots disease examined.

Conflict of Interest

The authors declare that there are no conflicts of interest related to this article.

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