Original Research Article

SELECTION IN BASE POPULATION OF ORNAMENTAL PEPPERS (*Capsicum annuum* L.)1

.

ABSTRACT

Aims: The aim of this study was to characterize and select plants with ornamental potential and resistant to pathogens in generation F2.

Study Design: For genetic divergence analysis, Tocher's grouping method was used, based on the standardized Euclidean distance. Analyses were carried out for the quantitative and qualitative data separately and also for the data together. In addition, the relative importance of the characteristics evaluated for genetic divergence was calculated using SINGH's Methodology (1981). All analyses were performed using the computational Genes program.

Place and Duration of Study: The experiment was conducted in a greenhouse of the Plant Biotechnology Laboratory of the Center of Agrarian Sciences (CCA) of the Federal University of Paraíba (UFPB). The treatments consisted of 354 progenies, an F2 generation of ornamental peppers (*Capsicum annuum L*), belonging to the Bank of germplasm of UFPB, derived from the controlled self-fertilization of F1 and obtained from the crossing between the parents UFPB390 X UFPB137, plants grown in vessels of 900 mL filled with commercial substrate. There was variability among genotypes for the evaluated characters.

Methodology: As they reached adulthood, genotypes were characterized according to the descriptors for *Capscicum* suggested by IPGRI. 20 quantitative characters and 4 qualitative in ornamental peppers were evaluated. Leaves identified from an optical microscope using the illustrated descriptor of imperfect fungus.

Results: The variability between genotypes was higher for qualitative characters related to disease resistance. It is possible to select individual plants for opening lines in Generation F3. 7 plants; 7; 15; 50;

69; 120; 155; 157; 196; 314; 326; 331; 347 should be selected for not presenting symptoms of fungi diseases.

Conclusion: Greater diversity among genotypes was detected when the incidence of diseases in the plants was evaluated. The plants 7 ; 15; 50; 69; 120; 155; 157; 196; 314; 326; 331; 347 should be selected because they do not present symptoms of fungal diseases.

Keywords: diversity, ornamental pepper, segregating.

1. INTRODUCTION

The genus Capsicum, belongs to the family Solanaceae and comprises five domesticated species of peppers that are marketed around the world: Capsicum annuum L.., Capsicum chinense Jacq., Capsicum frutescens L., Capsicum baccatum L. e Capsicum pubescens [1; 2]

The peppers of the genus Capsicum are part of the heritage of Brazilian biodiversity, which differs as to the type, color, size, flavor, and poignancy in several marketed cultivars [3;4]

There are few varieties destined for trade in peppers to ornamentation. Although, the germplasm banks of Capsicum in the country possess in their collection accesses that can be used in the genetic improvement aiming to develop new cultivars [6].The ornamental pepper offers countless opportunities to develop unique cultivars, which can be marketed in three ways: plant vases, garden plants and bouquets [7; 8].

Peppers agribusiness (Capsicum spp.) is among the best examples of integration among all those that work in the vegetable production chain [9]. According to Finger et al. [10] family farming has been the main responsible, in Brazil, for the expansion of the growing area of peppers. Rêgo et al. [11] demonstrated that the production of new varieties of ornamental peppers allowed the increase in the income of woman family farmers of the state of Paraíba, providing the generation of new jobs and the fixation of these rural farmers and their families, in the countryside.

All information regarding the variability of a collection of germplasm, serves to increase the efficiency of the works of improvement of the species [12; 13]. According to Silva Filho et al [14] lacks information on pepper of the wild and semi-domesticated species.

Genetic improvement acts as an important link in the agribusiness chain of ornamental plants, in search of selecting cultivars resistant to pest, diseases, biotic and abiotic stresses [15]

The Federal University of Paraíba in twelve years develops a program of improvement of ornamental peppers, by hybridization and selection [11]. In that program was possible to select lines with longer life post-production Rêgo et al. [16] and lines with greater resistance to ethylene SANTOS et al. [17], as well as develop 30 intraspecific hybrids (C. annuum) [11]), which generated several F2 families, which are in the evaluation phase.

This study aimed to characterize and select plants with ornamental potential and resistant to pathogens in generation F2.

2. MATERIAL AND METHODS

The experiment was conducted in a greenhouse of the Plant Biotechnology Laboratory of the Center of Agrarian Sciences (CCA) of the Federal University of Paraíba (UFPB) in the city of Areia - PB, at na altitude of 618 m, latitude 06 ° 57 '48'. The treatments consisted of 354 progenies from a F2 generation of ornamental pepper plants (Capsicum annuum L) , belonging to the Germplasm Bank of the UFPB, from the controlled self-fertilization of F1 (Rêgo et al., 2012b [11]) and obtained from the cross between the UFPB390 x UFPB137 parents , and the plants were grown in 900 mL pots filled with commercial substrate.

When the seedlings had four pairs of definitive leaves, they were transplanted into 900 ml pots using the same substrate. When necessary, the cultural practices recommended for culture have been carried out. When they had at least one mature fruit were characterized according to the descriptors for Capsicum suggested by IPGRI[18]). For the morphoagronomic characterization, 20 quantitative traits were considered: plant height (PH), crown diameter (CD), height of first bifurcation (HFB), stem diameter (SD), leaf length (LL), leaf width (LW), length of the anther (LA), length of the stiletto (LS), width of the petal (WP), weight of the fruit (WF), length of pedicel (LP), larger diameter (LaD), lower diameter (LoD), fruit Length (CL), pericarp thickness (PT), placenta length (PL), number of seeds per fruit (NSF), fresh matter (FM) according to the list of descriptors suggested by the IPGRI (1995 [18]). 4 qualitative characteristics were used: = 1, 0 = no incidence.

To analyze the presence of pathogens, five leaves were randomly collected from each plant, then placed in trays disinfested with 70% alcohol. These were lined with paper towel added with distilled water, autoclaved, deionized and

covered with plastic. The leaves were maintained for 72 hours on cement benches at room temperature. After this period the spores were collected. Durex tape was used to collect them. After being collected the spores were placed on a glass slide and stained with methylene blue. After staining the cells were identified under optical microscopy using the illustrated descriptor generates of imperfect fungi

For the analysis of genetic divergence, the Tocher grouping method was used, based on the standardized mean Euclidean distance. Analyzes were performed for the quantitative and qualitative data separately and also for the data together. In addition, the relative importance of the characteristics evaluated for the genetic divergence was calculated using the methodology of SINGH [19].

All analyzes were performed using the Genes computational program [20].

3. RESULTS AND DISCUSSION

According to Tocher's methodology , using the quantitative data, the highest variation was found in group 1 , composed of 352 genotypes, group 2 and 3 with only one plant per group 188 and 324 respectively (Table 1). Neitzke et al.[21], also using the Tocher method, obtained the formation of only four groups, when reporting the variability of 8 plant and fruit characters in *Capsicum spp*. Also corroborated by Bento et al.[22], found two groups based on 15 quantitative characters, in 29 accessions of *Capsicum spp.*

Table 1. Grouping of 354 individuals, according to 20 characteristics of base population of ornamental pepper (*Capsicum annuum* L.) according to the Tocher method. CCA-UFPB, Areia, 2018.

Groups	People
1	Other genotypes

2	188
3	324

The characteristic corolla length, fruit weight and canopy width were the main contributors to the divergence with (9,092%), (9,784%) and (9,725%), respectively.

The characters that contributed less were the weight of the fresh matter, the diameter of the stem, and the larger diameter of the fruit with (0.699), (0.540%), (0.544%), respectively (table 2). Variables that contributed a very low percentage or did not contribute to the detected variability, can be discarded in later studies of genetic diversity of the analyzed population, as described by Rêgo et al. [23].

Table 2. Estimates of the relative contribution of each variable to the genetic divergence among individuals of a base population of ornamental pepper (*Capsicum annuum* L.), for 20 characteristics. CCA-UFPB, Areia, 2018.

Variables	Values (%)
Length of corolla	9,092
Flower Width	6.385
Petal diameter	4.985
Length of anther	4.631
Length of fillet	5.323
Plant Height	4.983
Cup width	9,725
First Bifurcation Height	3,879
Stem diameter	0.544
Sheet length	4.074

Width of sheet	2.060
Pedicle length	5.753
Weight of the fruit	9,784
Length of fruit	8,713
Larger fruit diameter	0.540
Lower fruit diameter	5.521
Diameter of pericarp	1981
Length of placenta	3,444
Number of seeds	7.875
Weight of fresh matter	0.699

For the grouping of individuals by the Tocher method for the qualitative characteristics, it was possible to observe the formation of 7 groups, forming more groups than the grouping using the quantitative characteristics. Group 1 had the largest number of individuals, 278 of the total. Group 2 gathered 13 genotypes, group 3 gathered 46 subjects followed by groups 4, 5, 6 collected 11, 10, 9 respectively for each group. Group 7 gathered only two plants (Table 3).

Table 3. Grouping of 354 individuals according to four features for base population of ornamental pepper plant (*Capsicum annuum* L.) according to the Tocher method. CCA-UFPB, Areia, 2018.

Groups	People
1	Other genotypes
2	4, 28, 30, 34, 41, 51, 123, 234, 239, 350, 44, 188, 226
3	7.10, 12, 14, 15, 33, 42, 45, 50, 69, 82, 83, 84, 104, 120, 157, 173, 196, 198, 201, 213, 217, 233, 240, 281, 283, 293, 294, 295, 298, 310, 314, 315, 316,

	317, 318, 320, 331, 333, 347, 351, 354
4	8, 52, 54, 179, 290, 291, 292, 311, 312, 313, 352
5	9, 18, 105, 140, 145, 197, 210, 244, 256, 148
6	26, 158, 167, 296, 303, 307, 321, 341, 59
7	297, 353

It was possible to identify based on the criterion of Singh, greater contribution for the genetic divergence was the presence of Fusarium sp (43.191%), the others contributed, Cladosporium sp with (36.2611%), Colletotrichum sp. (13.7389%) and Puccinia pampas (6.809%) (Table 4). Added the percentages of Fusarium variables sp and Cladosporium sp corresponds to 79.472% of the contribution of the genetic variability of the study population. Results for these characteristics were important for pointing out the genetic diversity presented in the base population in relation to the tolerance to the analyzed fungal diseases.

Table 4. Estimates of the relative contribution of each variable to the genetic divergence among individuals from a base population of ornamental pepper (*Capsicum annuum* L.), for 24 characteristics. CCA-UFPB, Areia, 2018.

Variables	Values (%)
Fusarium sp	43,191
Colletotrichum sp .	13.7389
Cladosporium sp .	36.2611
Puccinia pampas	6.809

For the Tocher grouping, using the quantitative and qualitative characteristics, it was possible to separate the genotypes into three divergent groups. Being in group 1 it gathered 354 individuals. Groups 2 and 3 gathered only one plant (188) and (324) respectively (Table 5). Results similar to those found for the 20 quantitative characteristics (Table 1).

Table 5. Grouping of 354 individuals, according to 24 characteristics of the base population of ornamental pepper plant (*Capsicum annuum* L.) according to the Tocher method. CCA-UFPB, Areia, 2018.

Groups	People
1	Other genotypes
2	324
3	188

The variables that contributed most to the relative importance of the characters were the Fusarium sp (19.965 %), followed by Cladosporium sp. (16.762 %), Colletotrichum sp. (6.351%), fruit weight (5.269%), crown width (5.229%), length of the corolla (4.889%) and fruit length (4.685%). Added to these characteristics obtained an estimated value of 55.86% of the detected variability. The characteristics of stem diameter, larger fruit diameter and fresh matter weight contributed only with (0.292%), (0. 290%) and (0.376%), respectively, for genetic diversity (Table 6). Barroso et al. [24]) working with 23 quantitative ornamental pepper characters, it was observed that only one characteristic, the diameter of the stem (SD), contributed with approximately 79% of the genetic divergence. In this study, the effect of the capsicum was similar to that observed in the control group [22;23].

Table 6. Estimates of the relative contribution of each variable to the genetic divergence among individuals from a base population of ornamental pepper (Capsicum annuum L.), for 24 characteristics. CCA-UFPB, Areia, 2018.

Variables	Values (%)
Length of corolla	4.889

Flower Width	3.433
Petal diameter	2.680
Length of anther	2.490
Length of fillet	2,862
Plant Height	2.679
Cup width	5.229
First Bifurcation Height	2.086
Stem diameter	0.292
Sheet length	2.190
Width of sheet	1,108
Pedicle length	3.094
Weight of the fruit	5.261
Length of fruit	4.685
Larger fruit diameter	0.290
Lower fruit diameter	2,969
Diameter of pericarp	1.065
Length of placenta	1,852
Number of seeds	4.235
Weight of fresh matter	0.376
Fusarium sp	19,965
Colletotrichum sp .	6.351

Cladosporium sp .	16,762
Puccinia pampas	3.147

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137 It is important to point out that there were asymptomatic plants for all pathogens (Table 7). It is necessary to carry out a
138 resistance study with specific isolates to confirm the non-susceptibility of these plants to the detected pathogens.

139

140 Table 7. Plants F_2 of ornamental pepper with and without pathogen incidence.

Pathogens	Infested plants
Fusarium sp.	2; 5;8; 16; 17; 19; 22; 23; 24; 25; 44; 52; 54; 59; 60; 64; 73; 80; 81; 85; 86; 87; 88; 89; 91; 92; 94; 95; 96; 101; 103; 107; 113; 115; 121; 125; 126; 127; 128; 130;133;134; 135; 146; 147; 148; 149;150; 152; 169; 179; 183; 188; 192; 194; 202; 203; 204; 205;214; 224; 226; 231; 234; 242; 243; 253;257; 258; 263; 264; 267; 270; 278; 282; 284; 286; 289; 290;291; 292; 302; 306; 308; 311; 312; 313; 332;336;345;352
Colletotrichum sp.	26; 59; 156; 158; 167; 296; 297; 298; 303; 307; 321;
Cladosporium sp.	2; 3; 5; 6; 8; 10; 12; 13; 16; 17; 18; 19; 20; 21; 22; 23; 24; 25; 26; 27; 31; 35; 38; 39; 40; 43; 45; 46; 47; 53; 55; 56; 57; 59; 60; 61; 62; 63; 64; 65; 66; 67; 68; 71; 72; 73; 74; 75; 76; 77; 78; 79; 80; 81; 85; 86; 87; 88; 89; 90; 91; 92; 93; 94; 95; 96; 97; 98; 99; 100; 101; 102; 104; 106; 107; 108; 109; 110; 111; 112; 113; 114; 115; 116; 117; 118; 119; 121; 122; 124; 125; 126; 127; 128; 129; 130; 131; 132; 133; 134; 135; 136; 137; 138; 139; 140; 141; 142; 143; 144; 145; 146; 147; 148; 149; 150; 151; 152; 153; 154; 156; 158; 159; 160; 161; 162; 163; 164; 165; 166; 167;

	168; 169; 170; 171; 172; 174; 175; 176; 177; 178; 180; 182; 183; 184; 185; 186; 187; 189; 190; 191; 192; 193; 194; 195; 199; 200; 203; 204; 205; 206; 207; 208; 209; 210; 211; 212; 214; 215; 218; 219; 220; 221; 222; 223; 224; 225; 228; 231; 232; 236; 237; 238; 211; 242; 243; 244; 245; 246; 247; 248; 249; 250; 251; 252; 253; 254; 255; 256; 257; 258; 259; 260; 262; 264; 266; 267; 268; 269; 270; 271; 272; 273; 274; 275; 276; 278; 279; 282; 289; 291; 296; 299; 300; 301; 302; 303; 304; 305; 306; 307; 308; 310; 311; 312; 313; 314; 315; 316; 317; 318; 320; 321; 322; 323; 324; 325; 327; 328; 329 330; 332; 334; 335; 336; 337; 338; 339; 340; 341; 342; 343; 344; 345; 346; 348; 349; 351; 352; 353; 354
Puccinia pampeana	4; 9; 18; 28; 30; 34; 41; 44; 51; 103; 123; 140; 145; 148; 188; 197; 210; 226; 234; 239; 244; 256; 350
No infested plants	7; 15; 50; 69; 120; 155; 157; 196; 314; 326; 331; 347

4. CONCLUSION

The morphoagronomic characters were efficient for evaluation and determination of genetic diversity;

Greater diversity among genotypes was detected when the incidence of diseases in the plants was evaluated. The plants 7 ; 15; 50; 69; 120; 155; 157; 196; 314; 326; 331; 347 should be selected because they do not present symptoms of fungal diseases.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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