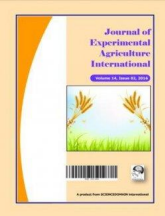

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Selection in Base Population of Ornamental Peppers (*Capsicum annuum* L.)

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Authors' contributions

This work was carried out in collaboration between all authors Author JAML wrote most of the work and made all the corrections, the study elaborated. Author ERR performed a statistical analysis. Author MMP did made the fungus identification. Author GHNS suggested the study analyzes. Authors MMR and MGC managed as a bibliographic research. Author AMSP helped in writing the work. All authors read and approved the final manuscript.

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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

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peppers (*Capsicum annuum L*), belonging to the Germplasm Bank 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: Genotypes were characterized according to the descriptors for *Capsicum* 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 Solanaceae family 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 accessions that can be used in the genetic improvement aiming to develop new cultivars [5]. The ornamental pepper offers countless opportunities to develop unique cultivars, which can be marketed in three ways: potted plant, garden plants and bouquets [6,7].

Peppers agribusiness (*Capsicum* spp.) is among the best examples of integration among all those that work in the vegetable production chain [8]. According to Finger et al. [9] family farming has been the main responsible, in Brazil, for the expansion of the growing area of peppers. Rêgo et al. [10] 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. 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 [11,12].

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. [13] and lines with greater resistance to ethylene SANTOS et al. [14], 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. MATERIALS AND METHODS

2.1 Location of the Experiment

The experiment was conducted in a greenhouse of the Plant Biotechnology Laboratory of the Center of Agrarian Sciences (CCA) of the Federal University of Paraiba (UFPB) in the city of Areia - PB, an altitude of 618 m, latitude 06°57'48'.

2.2 Plant Material

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 [11]) and obtained from the cross between the UFPB390 x UFPB137 parents. The plants were grown in 900 mL pots filled with commercial substrate.

2.3 Morphological Characterization

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 [15].

2.4 Plant Descriptors

For the morphoagronomic characterization, 20 quantitative traits were considered: corolla length, flower width, petal diameter, anther length, style length, plant height, canopy width , first bifurcation height, stem diameter, leaf length, leaf width, pedicel length, fruit weight, fruit length, larger fruit diameter, lower fruit diameter, pericarp thickness, placenta length, number of seeds per fruit and fresh matter according to the list of descriptors suggested by the IPGRI [15]. The qualitative characteristics were used: incidence = 1 and 0 = no incidence.

2.5 Description and Analysis of Plant Material

To analyze the presence of pathogens, five leaves were randomly collected from each plant, then placed in trays disinfected with 70% alcohol. These were lined with paper towel added to 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® 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 an optical microscopy using the illustrated descriptor generates of imperfect fungi.

2.6 Statistical Analysis

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 [16].

All analyzes were performed using the Genes Computational Program [17].

3. RESULTS AND DISCUSSION

According to Tocher 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. [5] analyzing qualitative traits obtained the formation of six groups in *Capsicum spp*. Bento et al. [18], 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

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	(%)
Corolla length	9,092(%)
Flower width	6.385(%)
Petal diameter	4.985(%)
Anther length	4.631(%)
Style length	5.323(%)
Plant height	4.983(%)
Canopy width	9,725(%)
First bifurcation height	3,879(%)
Stem diameter	0.544(%)
Leaf length	4.074(%)
Leaf width	2.060(%)
Pedicel length	5.753(%)
Fruit weight	9,784(%)
Fruit length	8,713(%)
Larger fruit diameter	0.540(%)
Lower fruit diameter	5.521(%)
Pericarp thickness	1.981(%)
Placenta length	3.444(%)
Number of seeds per fruit	7.875(%)
Fresh matter	0.699(%)

Table 3. Grouping of 354 individuals according to four qualitative traits 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

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

The characters that contributed less were the fresh matter (0.699%), stem diameter (0.540%), and the larger fruit diameter (0.544%) (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. [19].

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 04 qualitative characteristics. CCA-UFPB, Areia, 2018

Variables	(%)
Fusarium sp	43.191(%)
Colletotrichum sp.	13.7389(%)
Cladosporium sp.	36.2611(%)
Puccinia pampas	6.809(%)

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

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 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	(%)
Corolla length	4.889(%)
Flower width	3.433(%)
Petal diameter	2.680(%)
Anther length	2.490(%)
Style length	2.862(%)
Plant height	2.679(%)
Canopy width	5.229(%)
First bifurcation height	2.086(%)
Stem diameter	0.292(%)
Leaf length	2.190(%)
Leaf width	1.108(%)
Pedicel length	3.094(%)
Fruit weight	5.261(%)
Fruit length	4.685(%)
Larger fruit diameter	0.290(%)
Lower fruit diameter	2.969(%)
Pericarp thickness	1.065(%)
Placenta length	1.852(%)
Number of seeds per fruit	4.235(%)
Fresh matter	0.376(%)
Fusarium sp	19.965(%)
Colletotrichum sp.	6.351(%)
Cladosporium sp.	16.762(%)
Puccinia pampas	3.147(%)

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.

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).

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%), canopy width (5.229%),corolla length (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 (0.292%), larger fruit diameter (0. 290%) and fresh matter (0.376%) for genetic diversity (Table 6). Barroso et al. [20]) working with *C. annuum* species separated 50 genotypes of a segregating generation into eight groups.

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

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.	LI 26; 59; 156; 158; 167; 296; 297; 298; 303; 307; 321; 341; 353
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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