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Selection of potato genotypes *Solanum tuberosum* group Andigena by their tolerance to *Phytophthora infestans* (Mont.) of Bary

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Selección de genotipos de papa *Solanum tuberosum* grupo Andigena según su tolerancia a *Phytophthora infestans* (Mont.) de Bary

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ABSTRACT

Phytophthora infestans is the most limiting biotic problem of potato crop in Colombia and the world. It is a pathogen that threatens the sustainability of the crop. Therefore, it is necessary to evaluate work collections of potato to identify genotypes that show disease tolerance. The objective of this work was to select genotypes of *Solanum tuberosum* group Andigena by their tolerance to *P. infestans*. This study was carried out under conditions of Pasto, in the South of Colombia at 2,820 masl. A total of 76 introductions of guata potatoes were evaluated under natural inoculum, including Capiro as a susceptible control, Betina as moderately tolerant and Pastusa Suprema as highly tolerant. The number of stems and stolons per plant was registered. Disease severity assessments and traits related to the area under the disease progress curve were made. At harvest stage, yield values per plant and its components were recorded. Principal Component and Classification analyses discriminated tolerant introductions of susceptible. Significant positive correlations were found between the yield with the number of stolons, tubers per plant and tuber weight, and negative correlations with severity and area under the relative disease progress curve. The selected introductions showed high yield per plant and mostly minor severities to the population, indicating an agronomic potential that must be evaluated in different environments to determine its adaptability and stability. UdenarStGua53, UdenarStGua61, UdenarStGua68, UdenarStGua73, UdenarStGua75, UdenarStGua77 y UdenarStGua78, coming from the International Potato Center (CIP) are confirmed as a source of tolerance to *P. infestans* and can be considered as parental within species improvement programs.

Palabras clave:
Tizón tardío
Susceptibilidad
Tolerancia

RESUMEN

Phytophthora infestans es uno de los problemas más limitantes de la papa en Colombia y en el mundo. Es un patógeno que amenaza la sostenibilidad del cultivo. Por lo tanto, es necesario evaluar colecciones de trabajo por su reacción ante el patógeno, con el fin de identificar genotipos que muestren tolerancia a la enfermedad. El objetivo de este trabajo fue seleccionar genotipos de *Solanum tuberosum* grupo Andigena acorde con su tolerancia a *P. infestans.* Esta investigación se realizó bajo condiciones del Altiplano de Pasto, Sur de Colombia a 2,820 msnm. Un total de 76 introducciones de papa guata fueron evaluadas bajo condiciones de inóculo natural, incluyendo Capiro como control susceptible, Betina como moderadamente tolerante y Pastusa Suprema como altamente tolerante. Se registró el número de tallos y estolones por planta y se hicieron evaluaciones de severidad y de variables relacionadas con el área bajo la curva de progreso de la enfermedad. En la cosecha, se consignaron los valores de rendimiento por planta y sus componentes. Los análisis de Componentes Principales y de Clasificación discriminaron introducciones tolerantes y susceptibles. Se encontraron correlaciones significativas positivas entre el rendimiento y el número de estolones, tubérculos por planta y peso de tubérculo y correlaciones negativas con severidad y área bajo la curva de progreso relativo de la enfermedad. Las introducciones seleccionadas mostraron alto rendimiento por planta y en su mayoría severidades menores a la población, indicando un potencial agronómico que debe ser evaluado en diferentes ambientes para determinar su adaptabilidad y estabilidad. UdenarStGua53, UdenarStGua61, UdenarStGua68, UdenarStGua73, UdenarStGua75, UdenarStGua77 y UdenarStGua78 provenientes del CIP se confirman como fuente de tolerancia a *P. infestans* y pueden ser considerados como parentales dentro de programas de mejoramiento de la especie.

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Potato cultivation is one of the most widespread agricultural activities in Colombia. Its production is distributed in 283 municipalities, mainly in the departments of Cundinamarca, Boyacá, Nariño, Antioquia, Santander, Norte de Santander, Cauca, Tolima, and Caldas, with a share of 3.3% in the national Gross Domestic Product. For the year 2017, 169,002 ha were reported with a production of 3,740,000 t. Its cultivation benefits 110,000 families and generates 75,000 direct jobs and 189,000 indirect jobs (Fedepapa, 2017). The 94% of the production is consumed mainly as a fresh product and 6% is used in industry (Agronet, 2019).

The potato is one of the most genetically diverse cultivated species, with diploid, triploid, tetraploid and pentaploid species, the vast majority is found in the Andean zone of South America. In the Andes, the genus is represented by eight cultivated species and about 200 wild ones. The rich diversity of the cultivated species is included in a polyploid series (2n=24, 36, 48, and 60 chromosomes), which includes 4,000 edible varieties, with high genetic potential for yield and broad adaptability to different climates, which has allowed it to become one of the most important crops of the world diet (Estrada, 2000).

However, the crop is subjected to different biotic and abiotic stresses that threaten its sustainable development. In this sense, one of the main biotic stress in the field, not only in Colombia but worldwide, is the late blight caused by *Phytophthora infestans* (Mont.) of Bary. It is a pathogen belonging to the Oomycete class, in the Chromista kingdom and phylogenetically related to Diatoms and brown algae. This fungus has a rapid development in high humidity conditions and can survive for days or even weeks, although its sporangia cannot withstand freezing temperatures. The main strategy adopted by farmers to control this pathogen is the application of fungicides, a practice that has represented between 10 and 29.9% of production costs (Juyó *et al*., 2011).

One of the alternatives for solving the biotic problems of crops is finding cultivars with genetic tolerance, which can be integrated into chemical control to reduce the use of fungicides, decrease the cost of production, and decline the damage to human health and the environment. Obtaining tolerant cultivars to late blight can provide additional protection to the crop over time, reducing the risk of losses from the disease and/or the costs of chemical control in each crop cycle (Muñoz *et al*., 2019).

In the case of *P. infestans*, researches have been carried out in various fields from conventional breeding, biotechnology, molecular marker assisted breeding to genetic transformation. Cristinzio and Testa (2019), used the technique of plant electrolyte exudation caused by the filtering of the pathogen culture to detect genetic tolerance under *in vitro* conditions of 10 potato cultivars to *P. infestans* with eight strains. Electrolyte leakage was used to screen leaf and tuber tissues with fungal culture filtrates. Under the leaf or tuber trials with almost all cultivars there were statistical differences in susceptibility, while leaf tolerance did not correlate with tuber tolerance. The Ajax variety was the least susceptible in the leaf and tuber tests, while Prima was the most susceptible in the tuber tests.

One of the indications of tolerance to *P. infestans* in potato cultivars is the presence of tolerant genes R1 and R2. Díaz *et al.* (2003) evaluated different genotypes of *S. tuberosum* group *Tuberosum* according to their tolerance to *P. infestans* and the molecular detection via PCR (Polymerase Chain Reaction) of R1 and R2 genes. The results showed a strong phenotypic and genotypic correspondence regarding the presence of R1 and R2 alleles in the different potato genetic materials containing one or another allele.

In the field of traditional breeding, in Southern and Central American countries, germplasm evaluation has been carried out and methods of inter- and intraspecific crosses, backcrossing and recurrent selection have been used to obtain more productive cultivars with tolerance to *P. infestans* (Gabriel *et al*., 2001; Barquero *et al*., 2005; Solano *et al.,* 2014). In Colombia, Rodríguez *et al.* (2009), obtained three new varieties of creole potato registered as Criolla Latina with yields between 18 to 20 t ha^{-1}, Criolla Paisa with yields of 22 to 25 t ha^{-1} and Criolla Colombia with yields of 13 to 15 t ha^{-1}. The first two were reported with moderate tolerance to *P. infestans*, while the latter was reported as sensitive to this pathogen.

According to the above mentioned authors, it is necessary to increase the probability of finding long-lasting tolerance and to do so, the genetic base of tolerance should be broadened, based on the evaluation of the available germplasm in breeding programs being developed by institutions such as the University of Nariño and the National University of Colombia; in addition, sources of tolerance should be sought in wild germplasm (Forbes and Huarte, 2014) in order to improve traditional varieties, which are generally susceptible to late blight. Therefore, the objective of this study was to select genotypes of guata potato *Solanum tuberosum* group Andigena by their tolerance to the natural inoculum of *Phytophthora infestans* (Mont.) of Bary, under conditions of Pasto, South of Colombia.

MATERIALS AND METHODS

Plant material

As genetic materials, 76 potatoes were used (Table 1), of which 43 were introduced from the CIP-Peru on July 18, 2016; 21 belong to the working collection of the University of Nariño (UDENAR), three were procured from the National University of Colombia, Bogotá (UNAL) and correspond to the improved varieties Betina, Única and Pastusa Suprema, and nine were obtained from the Central Colombian Collection under the responsibility of AGROSAVIA (Colombian Agricultural Research Corporation). Of these populations, the genetic material susceptible to late blight *P. infestans* was the variety Capiro (Monsalve-Fonnegra *et al.,* 2012), while Betina is moderately tolerant and Pastusa Suprema is highly tolerant (Ñustez, 2019). These varieties were used as controls of susceptibility and tolerance at field level.

Table 1. Population of 76 introductions of *Solanum tuberosum* group Andigena and their sources.

ID	Introduction	Source	ID	Introduction	Source
1	UdenarStGua07	UNAL-Col	39	UdenarStGua59	CIP-Peru
2	UdenarStGua12	Colombia	40	UdenarStGua60	CIP-Peru
3	UdenarStGua13	Colombia	41	UdenarStGua61	CIP-Peru
4	UdenarStGua20	UNAL-Col	42	UdenarStGua62	CIP-Peru
5	UdenarStGua21	Colombia	43	UdenarStGua63	CIP-Peru
6	UdenarStGua22	Colombia	44	UdenarStGua64	CIP-Peru
7	UdenarStGua23	Colombia	45	UdenarStGua65	CIP-Peru
8	UdenarStGua24	Colombia	46	UdenarStGua66	CIP-Peru
9	UdenarStGua25	Colombia	47	UdenarStGua67	CIP-Peru
10	UdenarStGua26	Colombia	48	UdenarStGua68	CIP-Peru
11	UdenarStGua27	Colombia	49	UdenarStGua69	CIP-Peru
12	UdenarStGua28	Colombia	50	UdenarStGua70	CIP-Peru
13	UdenarStGua29	Colombia	51	UdenarStGua71	CIP-Peru
14	UdenarStGua30	Colombia	52	UdenarStGua72	CIP-Peru
15	UdenarStGua31	UNAL-Col	53	UdenarStGua73	CIP-Peru
16	UdenarStGua33	Colombia	54	UdenarStGua74	CIP-Peru
17	UdenarStGua34	Colombia	55	UdenarStGua75	CIP-Peru
18	UdenarStGua35	Colombia	56	UdenarStGua76	CIP-Peru
19	UdenarStGua36	Colombia	57	UdenarStGua77	CIP-Peru
20	UdenarStGua38	Colombia	58	UdenarStGua78	CIP-Peru

Table 1. (continuation)

ID	Introduction	Source	ID	Introduction	Source
21	UdenarStGua39	Colombia	59	UdenarStGua79	CIP-Peru
22	UdenarStGua40	Colombia	60	UdenarStGua80	CIP-Peru
23	UdenarStGua41	Colombia	61	UdenarStGua82	CIP-Peru
24	UdenarStGua42	Corpoica	62	UdenarStGua83	CIP-Peru
25	UdenarStGua43	Corpoica	63	UdenarStGua84	CIP-Peru
26	UdenarStGua44	Corpoica	64	UdenarStGua85	CIP-Peru
27	UdenarStGua45	Corpoica	65	UdenarStGua86	CIP-Peru
28	UdenarStGua46	Corpoica	66	UdenarStGua87	CIP-Peru
29	UdenarStGua47	Corpoica	67	UdenarStGua89	CIP-Peru
30	UdenarStGua48	Corpoica	68	UdenarStGua90	CIP-Peru
31	UdenarStGua49	Corpoica	69	UdenarStGua91	CIP-Peru
32	UdenarStGua50	Corpoica	70	UdenarStGua93	CIP-Peru
33	UdenarStGua53	CIP-Peru	71	UdenarStGua94	CIP-Peru
34	UdenarStGua54	CIP-Peru	72	UdenarStGua95	CIP-Peru
35	UdenarStGua55	CIP-Peru	73	UdenarStGua97	CIP-Peru
36	UdenarStGua56	CIP-Peru	74	UdenarStGua99	CIP-Peru
37	UdenarStGua57	CIP-Peru	75	UdenarStGua100	CIP-Peru
38	UdenarStGua58	CIP-Peru	C	Control (C)	Colombia

Location

The experiment was carried out in Botana Experimental Farm of the University of Nariño, located at 2,820 masl, 1°09'28.3" NL and 77°16'29.5" WL, with a relative humidity of 82%, average temperature of 12 °C and a rainfall of 800 mm. The area is climatically classified as a low mountain rainforest, with sandy clayey Andisol soils (IDEAM, 2016).

Experimental arrangement

The evaluated genotypes were arranged in a total experimental area of 581 m^2, with a distance between furrows of 1.2 m and distance between plants of 0.4 m with previous application of lime and organic matter, for a planting density of 20,833 plants ha^{-1}. The area of the plot was 1.44 m^2. Each genotype was randomly located in each plot, which contained three plants. The Capiro introduction was established as a susceptible variety and it was the source of the inoculum. This variety was planted in each five plots. Every seven days, insecticides such as Tiametoxam+Lambdacihalotrina (2 $cm^3 L^{-1}$) and Profenofos+Cipermetrina (0.75 $cm^3 L^{-1}$) were applied. In addition, fungicides such as Carbendazim (1 $cm^3 L^{-1}$) and Difenoconazole (1 $cm^3 L^{-1}$) were applied, in order to protect plants from other pathogens and achieve uniformity.

The first edaphic fertilization was carried out at 20 days and the second one at 40 days after planting. It was applied 840 kg ha^{-1} of the formula 10-30-10 per plant. Additionally, periodic applications were made with foliar fertilizer in doses of 5 $cm^3 L^{-1}$.

Traits evaluated

In the vegetative phase, the number of stems and stolons per plant was recorded. Severity evaluations (SEV) of the disease caused by *P. infestans* were made every 14 days. At harvesting stage, yield values per plant and its components were recorded. The methodology for data collection of each of the traits is described below.

Number of stems per plant (NS). The number of stems per plant was counted and recorded for each plot.

Severity (SEV). SEV assessments were conducted from the first week of planting to 134 days of the crop cycle. In

each plant of the plot, a leaf from the middle third was randomly marked, in which the periodic SEV evaluations were made. The scale proposed by Clive (1971) was used for the qualification of the leaf area affected by the presence of the pathogen (Figure 1). The scale proposes values of 1, 10, 25, 50, 75 and 100%. The higher SEV values, the higher the susceptibility of the genotype evaluated.

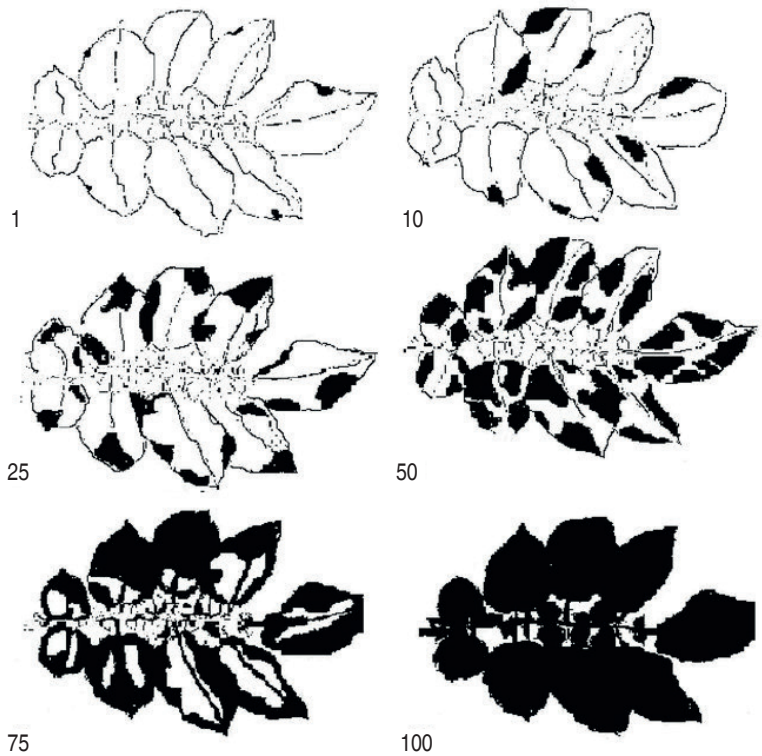

Figure 1. Clive's scale (1971) for the percentage of severity of *P. infestans* in *S. tuberosum* leaves, modified by Betancourth *et al.* (2008).

Area under the disease progress curve (AUDPC). The AUDPC is a variable that estimates the amount of disease throughout the crop cycle. It is calculated using Equation 1 proposed by Campbell and Madden (1990):

$$AUDPC = \sum_{i=1}^{n_i-1} \frac{(Y_i + Y_{i+1})}{2}(t_{i+1} - t_i) \qquad (1)$$

Where: t=time of each reading, Y_i=percentage of foliage affected in each reading and n=number of readings.

Relative area under disease progress curve (rAUDPC). The rAUDPC value indicates the proportion of infected tissue during the evaluation period, so that genotypes with severity values of 100% showed rAUDPC=1. Low rAUDPC values indicate a low percentage of infection during the evaluation period. These values correspond to the most tolerant genotypes (Pérez and Forbes, 2008). The rAUDPC was calculated using Equation 2:

$$rAUDPC = \frac{AUDPCX_i}{(t_f - t_i)} x100 \qquad (2)$$

Where: *rAUDPC*=relative area under disease progress curve, $AUDPCX_i$=area under the disease progress curve of the *i*-th genotype, t_f=time of the last evaluation and t_i=time of the first evaluation.

Rate of disease development (RD). The RD is a trait that measures the progress of the disease throughout the crop cycle. For its estimation, SEV reported in the first and last evaluation were taken as reference. The Equation 3 was used for the calculation of RD (Van Der Planck, 1963).

$$RD = \frac{1}{t_1 - t_0}\left(\log e\frac{X_0}{1-X_0} - \log e\frac{X_1}{1-X_1}\right) \quad (3)$$

Where: RD=rate of disease development, X_0=proportion of disease in the initial time, X_1=proportion of disease in the final time, t_0=initial time corresponding to the reading of X_0 and t_1=final time corresponding to the reading of X_1.

Decrease in disease (dAUDPC). For the calculation of dAUDPC in percentage, the Equation 4 proposed by Andrade *et al.* (2016) was applied.

$$dAUDPC = 1 - \frac{AUDPC_i}{AUDPC_t} x100 \quad (4)$$

Where: $AUDPC_i$=area under the disease progress curve of the *i*-th genotype and $AUDPC_t$=area under the disease progress curve of the control variety.

Genotype Susceptibility Scale (GSS). The GSS was calculated based on the resistance, tolerance and susceptibility to late blight scale proposed by Yuen and Forbes (2009) using the Equation 5, having a susceptible cultivar as reference.

$$GSS = \frac{rAUDPC_{Gn}}{rAUDPC_{GS}} x9 \quad (5)$$

Where: $rAUDPC_{Gn}$: relative area under disease progress curve of the potato genotype (Gn) and $rAUDPC_{Gs}$=area under the relative disease progress curve of the potato genotype with the highest susceptibility (Gs) and 9=value assigned to Gs.

Yield (Yld). Based on the weight of the plot harvested over the number of plants in the plot, the Yld was expressed in tuber weight (kg) per plant.

Number of tubers per plant (NTu). The average Ntu was obtained based on the plants in the plot.

Number of stolons per plant (NSt). The average NSt was determined based on the plants in the plot.

Tuber weight (TW). The TW corresponds to the ratio of Yld to NTu.

Data Analysis

The Path Analysis (PA) was performed, for which the correlations between the traits Yld, NTu, TW, NS, NSt, SEV, GSS, RD, dAUDPC, and rAUDPC were obtained. Based on the correlation coefficients, the traits were determined. Using the Excel program, the path coefficients were obtained to establish the direct and indirect effects on the association between the Yld and the other causal traits.

Likewise, the traits evaluated were subjected to Principal Component Analysis (PCA) and Hierarchical Classification, taking into account that only one of the two highly correlated traits was included in these analyses, in order to group the genotypes evaluated by discriminatory traits, such as yield and disease severity. To test the null hypothesis (Ho) that the group mean is equal to the original population mean, the *t-test,* proposed by Stiles (2000) was used (Equation 6):

$$t_c = \frac{\overline{Y}_i - \overline{Y}_j}{\sqrt{\frac{S_i^2 + S_j^2}{n_i + n_j - 2} x\left[\frac{n_i + n_j}{n_i \times n_j}\right]}} \quad (6)$$

Where: t_c=t calculated, $\overline{Y}_i$=average of the variable in the i-th group, $\overline{Y}_j$ =average of the variable in the j-th group, S_i^2 =variance of the i-th group, S_j^2=variance of the j-th group, n_i=number of individuals in the i-th group and n_j=number of individuals in the j-th group.

For the decision rule the t_c was compared with the t_t (t of the table with a α =0.05 and with degrees of freedom equal to $n_i + n_j$ -2). If $t_c < t_t$ Ho is accepted.

Subsequently, the best genotypes were selected based on a selection index (SI), whose weights were established according to the importance of the traits related to the Yld components and the disease. The first step was to standardize (S) the values of each of the traits that made up the SI (Lagos *et al*., 2015), using the Equation 7:

$$S = \frac{Y_{ij} - \overline{Y}}{SD} \quad (7)$$

Where: Y_{ij}=observation of the variable j-th in the introduction i-th, Y=overall average of variable j-th in the i-th

introductions and SD=standard deviation of variable j-th in the i-th introductions. Then, for each introduction (Y_{ij}) the SI was applied, given by the sum of the products of the standardized value of each variable by its weight (W), as follows: Yld(0.6), SEV(-0.3), rAUDPC(-0.1), dAUDPC(0.5), GSS(-0.05), RD(-0.05), NSt(0.08), NS(0.07), NTu(0.1) and TW(0.15).

RESULTS AND DISCUSSION

The Correlation Analysis for the 10 traits evaluated (Table 2), enabled to find a significant negative average association between Yld vs SEV (r=-0.50*) and Yld vs rAUDPC (r=-0.53*), indicating that the productive potential of the plants decreased due to the increase infection process caused by the pathogen. Yld vs NSt traits showed high positive association (r=0.70*) similar to Yld vs NTu (r=0.71*). This indicates that to improve Yld, it can be selected based on NSt and NTu.

For the Yld vs NS, the correlation was 0.46* (Table 2), however, the PA showed that the most of this dimension is explained by the indirect effect (outside the diagonal) through NTu with a value of 0.34 (Table 3). The association between Yld vs TW showed a value of association r= 0.70* (Table 2). Similarly, the PA showed that the direct effects (on the diagonal and in bold) explained the greater proportion of the dimensionality of the correlation, with a value of 0.62 (Table 3).

Table 2. Correlation analysis for traits related to yield and reaction components to disease caused by *P. infestans* in 76 introductions of *S. tuberosum* group Andigena.

Traits	SEV	rAUDPC	dAUDPC	GSS	RD	NSt	NS	NTu	TW
Yld	-0.50*	-0.53*	0.53*	-0.45*	0.07	0.70*	0.46*	0.71*	0.70*
SEV	1	0.59*	-0.59*	0.86*	-0.09	-0.50*	-0.41*	-0.49*	-0.18
rAUDPC		1	-1.00*	0.76*	-0.12	-0.59*	-0.36*	-0.53*	-0.24*
dAUDPC			1	-0.76*	0.12	0.50*	0.36*	0.53*	0.24*
GSS				1	-0.11	-0.43*	-0.34*	-0.45*	-0.18
RD					1	0.01	-0.07	0.04	0.05
NSt						1	0.66*	0.94*	0.15
NS							1	0.56*	0.13
NTu								1	0.10

*significant correlations (P<0.05)

Table 3. Path analysis (PA) for traits related to yield and disease response components caused by *P. infestans* in 76 introductions of *S. tuberosum* group Andigena.

Traits	SEV	rAUDPC	RD	NS	NTu	TW	rYld-y
SEV	**-0.08**	-0.01	0	0	-0.30	-0.10	**-0.50**
rAUDPC	-0.05	**-0.01**	0	0	-0.32	-0.20	**-0.53**
RD	0.01	0	**0.01**	0	0.02	0.03	**0.07**
NS	0.03	0.01	0	**0.01**	0.34	0.08	**0.46**
NTu	0.04	0.01	0	0	**0.60**	0.06	**0.71**
TW	0.01	0	0	0	0.06	**0.62**	**0.70**

SEV=severity (%), rYld-y=correlation between the Yld and the y variable

According to the PA in Table 3, the dimension of the correlations of Yld with SEV and rAUDPC is explained in greater proportion by the indirect effects through NTu (-0.30 and -0.32) than by the direct effects of SEV (-0.08) and rAUDPC (-0.01). These results differ from those found by Betancourth *et al.*(2008), who reported that the direct effect of SEV on Yld explains 50% of the magnitude of the correlation. Furthermore, the direct effect of the correlation between Yld and TW (0.70), is explained in greater proportion by the direct effect of TW (0.62) than by the indirect effects of the other variables of the PA. This result is useful to direct a selection by TW to achieve an increase in Yld.

Table 4 presents the PCA of the selected traits according to the correlation analysis related to the yield and reaction components to the disease caused by *P. infestans*. The first three components explain 82.70% of the total variance. Yld, NTu, TW, SEV, RD and rAUDPC were included in the PCA, generating six PCs (Núñez and Escobedo, 2014).

PCs accumulate a portion of the total variance and have greater importance and more accumulated variance the higher their eigenvalues. The PC1, whose eigenvalue is 2.90, has an accumulated variance (AV=48.4%). The first two PCs have an accumulated variance of 66.2% (Table 4). This procedure is used for quantitative data. The aim is to reduce the information, moving from one set of traits to another smaller set representing the former, without making any hypothesis about the meaning of the factors (David *et al.*, 2016).

Table 4. Principal Component Analysis (PCA) for traits related to yield and reaction to disease caused by *P. infestans* in 76 introductions of *S. tuberosum* group Andigena.

Traits	Principal Components (PC)		
	1	2	3
Yld	0.91	0.32	0.01
SEV	-0.74	0.34	-0.07
rAUDPC	-0.78	0.29	-0.03
RD	0.15	-0.26	-0.95
NTu	0.78	-0.27	0.22
TW	-0.55	0.79	-0.20
Eigenvalues	2.90	1.07	0.99
V	0.484	0.179	0.165
AV	0.484	0.662	0.827

V=proportion of the variance explained by the PC, AV=proportion of the cumulative variance explained by the PC.

For the selection of the PCs, the Kaiser Criterion was considered, which is based on the choice of PCs whose values or weights (Bernal *et al.*, 2019). Based on these considerations, the first three PCs that explain 82.7% were selected to explain the variance of the population studied (Table 4).

The traits Yld, SEV, rAUDPC and NTu define the PC1, with variable factor (rv-f) correlation values between -0.74 and 0.91. PC2 is related to the TW that generated the largest contribution to the total variance of the component with an rv-f of 0.79. Regarding PC3, the RD trait made the greatest contribution to the rv-f dimension with -0.95 (Table 4).

According to the Classification Analysis, four groups were identified (Figure 2 and Table 5). The first group (G1) consisted of 39 genotypes and the susceptible control Capiro identified by T1, T2, T3, T4, which corresponded to 49.37% of the population. This group is characterized by one of the highest percentages of SEV (86.90%) with respect to the general average of the population (A-Po) (53.96%). On the other hand, it showed a rAUDPC of 0.80, with 9.31 NTu and a TW of 54.11 g, which are

statistically lower than the average values of A-Po. The second group (G2) consisted of 33 genotypes, representing 36.71% of the total individuals studied (Figure 2). This group presented an Yld of 1.16 kg per plant which is higher than A-Po of 0.94 kg per plant. It also recorded a low SEV (19.33%), a RD of 0.06, values that differ statistically from population averages. Likewise, the RD (0.06) and the NTu (16.59) were higher than the A-Po (Table 5).

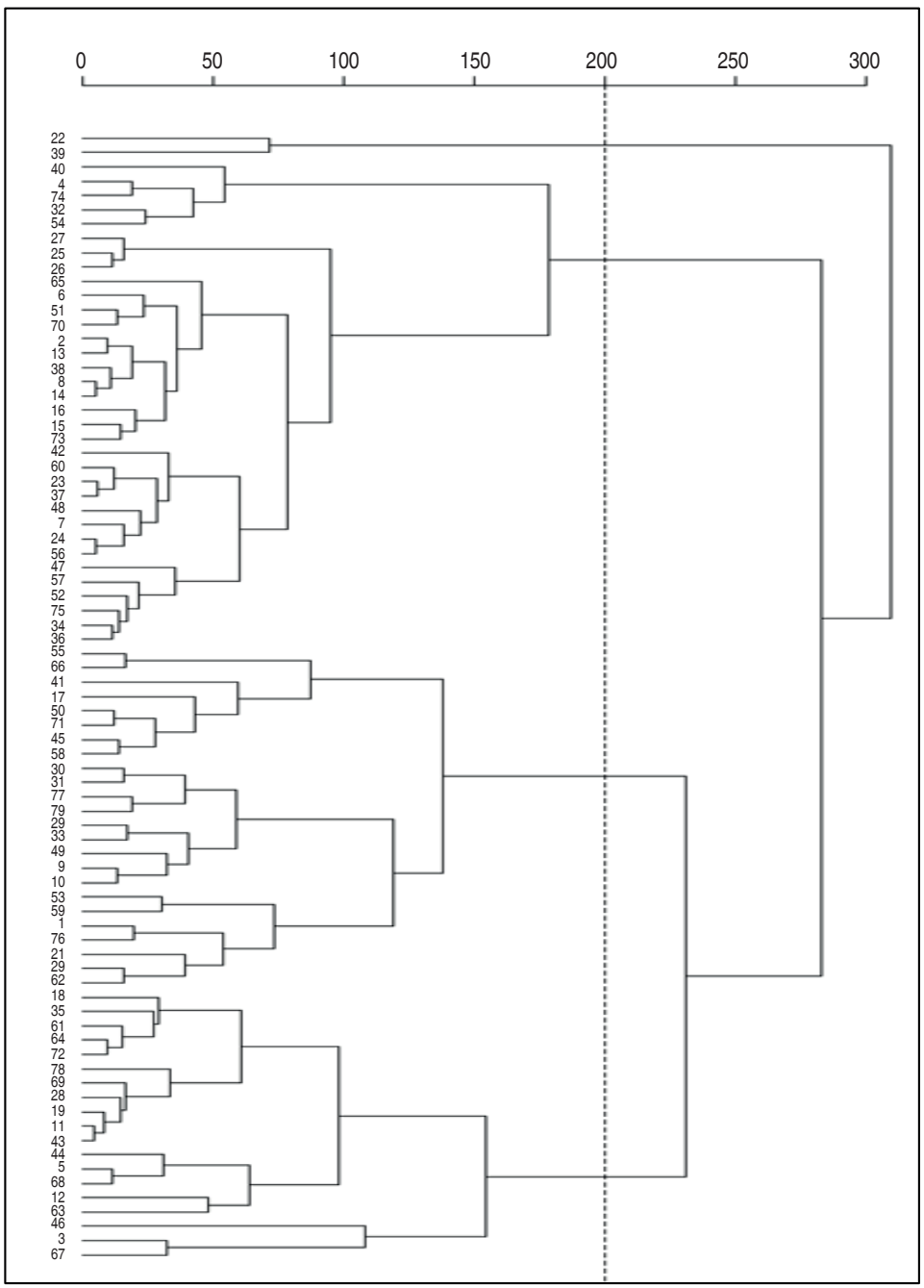

Figure 2. Dendrogram of Hierarchical classification analysis for 75 introductions of *S. tuberosum* group Andigena and one control sample evaluated for their reaction to disease caused by *P. infestans*.

Group three (G3) included five genotypes which are 6.33% of the total population. This group exhibited the highest Yld with 2.03 kg per plant higher than A-Po, a SEV (12.10%) lower than A-Po. The TW (164.84 g) recorded an average statistically higher than A-Po which showed an average of 72.40 g. Finally, group four (G4) included two genotypes, which presented the highest averages of TW and Yld with 272.29 g and 1.86 kg per plant, respectively, higher values than the overall average (Figure 2 and Table 5).

Table 5. Characteristics of four groups formed in the Classification Analysis according to six traits related to components of the disease *P. infestans* and yield in 76 genotypes of potato *Solanum tuberosum*.

Traits	A-Po N=76	SD-Po	A-G1 N=39	SD-G1	A-G2 N=33	SD-G2
SEV	53.96	36.84	86.90*	13.01	19.33*	13.28
rAUDPC	0.54	0.44	0.80*	0.32	0.29*	0.42
RD	0.03	0.17	0.01*	0.01	0.06*	0.26
NTu	12.47	6.79	9.31*	5.16	16.59*	6.86
TW	72.40	50.77	54.11*	32.49	67.89*	26.73
Yld	0.94	0.68	0.56	0.46	1.16*	0.59
Traits	**A-G3 N=5**	**SD-G3**	**A-G4 N=2**	**SD-G4**		
SEV	12.10*	11.72	87.50*	17.68		
rAUDPC	0.10*	0.10	0.74*	0.37		
RD	0.01*	0.00	0.02	0.01		
NTu	12.27	3.93	6.84*	1.18		
TW	164.84*	20.85	272.29*	3.84		
Yld	2.03*	0.71	1.86*	0.30		

*significant difference (P<0.05), A-Po=average of the population assessed, SD-Po=standard deviation of the population assessed, A-G=average group, SD-G=group standard deviation, N=number of individuals.

As it can be seen in the results described above, the introductions with the best behavior with regard to the disease are located in G3 with lower values of SEV and rAUDPC; However, in G4 are located the introductions of better behavior regarding the Yld, even under the pressure of the gradient of the disease, since in spite of reporting significant high values of SEV in comparison with the A-Po, they presented the highest values for the TW, for example, the genotype 40 that corresponds to the variety Red Huila M6 (UdenarStGua40) presented the greater TW with 275 g.

On the other hand, the selection index (SI) allowed the selection of 10 introductions that stood out from the original population, presenting a SI ranging from 1.90 to 3.63 with statistical differences regarding the population average (SI=0.00) (Table 6).

The introductions UdenarStGua53 (CIP 300046.22), UdenarStGua61 (CIP 391011.17), UdenarStGua68 (CIP 392557.171), UdenarStGua73 (CIP 393079.4), UdenarStGua75 (CIP 393280.82), UdenarStGua77 (CIP 393371.164) and UdenarStGua78 (CIP 393371.58) are from the CIP, where they are reported to be tolerant to attack by *P. infestans* (CIP, 2019). This behavior was similar in the present study, where they obtained values of SEV between 1.0 and 16.67% classified as tolerant and moderately tolerant, and with Ylds between 1.65 and 3.07 kg per plant, with significant differences with regard to the control varieties Capiro (0.05 kg per plant) and Betina (0.43 kg per plant).

Statistically, the Ylds of the 10 introductions surpassed the original population and the Betina and Capiro varieties, which are moderately tolerant and susceptible. With respect

Table 6. Selection index and mean traits of potato *S. tuberosum* group Andigena introductions chosen for high yield performance (Yld) and low severity levels (SEV) of *P. infestans* with susceptible and tolerant controls.

Genotype	Yld	SEV	rAUDPC	dAUDPC	GSS	RD	NSt	NS	NTu	TW	SI
UdenarStGua75	3.07	1.00	0.00	99.54	0.02	0.00	23.33	3.00	18.00	170.37	3.63
UdenarStGua61	2.24	5.33	0.06	92.76	0.32	0.01	12.00	4.00	11.33	197.94	2.71
UdenarStGua23	2.03	8.33	0.09	88.94	0.50	0.01	32.67	4.00	32.33	62.89	2.59
UdenarStGua73	2.15	10.00	0.11	86.31	0.61	0.01	22.00	1.67	20.67	104.03	2.33
UdenarStGua53	1.87	5.00	0.04	95.08	0.22	0.01	15.67	1.33	12.67	147.89	2.15
UdenarStGua77	1.65	10.00	0.05	93.12	0.31	0.01	25.00	4.00	22.33	73.88	2.09
UdenarStGua29	2.00	21.67	0.26	66.60	1.50	0.01	29.67	3.00	28.00	71.43	2.06
UdenarStGua12	1.90	16.67	0.20	74.28	1.15	0.01	26.67	2.33	25.67	74.03	2.00
UdenarStGua68	1.55	2.17	0.01	98.32	0.08	0.00	21.00	2.33	13.67	113.41	1.96
UdenarStGua78	1.78	15.00	0.17	78.56	0.96	0.01	24.67	2.33	20.33	87.70	1.90
Average (SG)	2.03	9.52	0.10	87.35	0.57	0.01	23.27	2.80	20.50	110.36	2.34
SD (SG)	0.42	6.63	0.09	10.92	0.49	0.00	6.12	0.97	6.87	46.74	0.53
Average Po (A)	0.94	53.96	0.54	30.76	2.77	0.03	15.08	2.03	12.47	72.40	0.00
SD Po (SD)	0.68	36.84	0.44	56.70	2.33	0.17	7.41	1.07	6.79	50.77	1.53
A+SD or A-SD	1.62	17.12	0·10	87.46	0.44	-0.14	22.49	3.11	19.26	123.17	1.53
SG-A	1.09	-44.44	-0.44	56.59	-2.20	-0.02	8.18	0.77	8.03	37.96	2.34
Capiro	0.05	95.00	0.78	0.25	4.47	0.02	2.83	1.25	2.58	22.02	-1.95
Betina	0.43	100.00	0.46	41.13	2.64	0.03	15.67	1.33	14.33	30.23	-0.84
P. Suprema	1.78	30.00	0.35	54.62	2.03	0.01	35.33	5.33	26.67	66.88	1.84

SG=selected genotypes. Po=population evaluated. SD = standard deviation. SI=selection index (estimated Yld). Underlined shows significant differences.

to the original population, these 10 selected introductions exceeded the population average by 1.09 kg per plant, which represents an increase in Yld of 53%. However, this gain is subject to factors, such as selection intensity, selection differential (SG-Po) and heritability, which define the true gain known as genetic gain (Nyquist, 1991).

CONCLUSIONS

Principal Components and Hierarchical Classification analyses allowed to discriminate between introductions of *Solanum tubersoum* group Andigena tolerant and moderately tolerant to the natural inoculum of *Phythopthora infestans*. As for the correlations of yield with severity and area under the relative disease progress curve, they showed a negative correlation.

The selected genotypes UdenarStGua75, UdenarStGua61, UdenarStGua23, UdenarStGua73, UdenarStGua53, UdenarStGua77, UdenarStGua12, UdenarStGua68 and UdenarStGua78 showed high yield values per plant and severity values below the population mean of 17.12%. Within the selected introductions, those from the International Potato Center-CIP (UdenarStGua75, UdenarStGua61, UdenarStGua73, UdenarStGua53, UdenarStGua77, UdenarStGua68 and UdenarStGua78) are considered as a potential source of tolerance to *P. infestans;* therefore they are recommended to be included in a breeding program that seeks to obtain tolerant varieties to the disease and should be considered for multi-environmental assessments to determine if there is differential behavior across contrasting conditions.

REFERENCES

Agronet. 2019. Estadísticas del cultivo de papa. En: Red de información y comunicación del sector Agropecuario Colombiano, https://www.agronet.gov.co/estadistica/Paginas/home.aspx?cod=1. 1 p. Retrieved: January 2019.

Andrade A, Capezio S y Huarte M. 2016. Caracterización de progenitores de papa en base a aptitud combinatoria y heterosis para la búsqueda de resistencia a *Phytophthora infestans*. Revista de la Facultad de Ciencias Agrarias 48(1): 9-20. http://revistas.uncu.edu.ar/ojs/index.php/RFCA/article/view/3216/2326

Barquero M, Gómez L y Brenes A. 2005. Resistencia al tizón tardío (*Phytophthora infestans*) en clones promisorios de papa en Costa Rica. Agronomía Costarricense 29(3): 31-45. https://www.mag.go.cr/rev_agr/v29n03_031.pdf

Bernal J, Martínez M y Sánchez J. 2019. Modelización de los factores más importantes que caracterizan un sitio en la red. pp. 1-13. En: Congreso XII jornadas de ASEPUMA. Asociación Española de Profesores de Matemáticas, Murcia. https://www.um.es/asepuma04/comunica/bernal_martinez_sanchez.pdf

Betancourth G, Portilla E y Salas P. 2008. Evaluación de la reacción de nueve genotipos de papa (*Solanum tuberosum* subsp. Andigena) al ataque de *Phytophthora infestans* (Mont.) de Bary. Agronomía Colombiana 26(3): 411-416. https://revistas.unal.edu.co/index.php/agrocol/article/view/11472

Campbell C and Madden L. 1990. Introduction to plant disease epidemiology. Sixth edition. John Wiley and Sons, Inc., New York. 532 p.

CIP. 2019. Catálogo de clones avanzados del CIP. En: Centro Internacional de la Papa. 1 p. https://research.cip.cgiar.org/cipcatlg_ac/Catalogue.php?cipnumber=CIP391002.6. Retrieved: November 2019.

Clive J. 1971. An illustrated series of assessment keys for plant diseases, their preparation and usage. Canadian Plant Disease Survey 51 (2): 39-65. https://phytopath.ca/wp-content/uploads/2014/10/cpds-archive/vol51/CPDS_Vol_51_No_2_(39-65)1971.pdf.

Cristinzio G and Testa A. 1999. *In vitro* evaluation of resistance of potato cultivars to *Phytophthora infestans*. Potato Research 41: 101-105. doi:10.1007/BF02358396

David R, Abdala G, Abdala M y Lescano J. 2016. Empleo del análisis multivariado en la evaluación de factores no genéticos de cabras Criollas. Archivos de Zootecnia 65 (250): 197-202. doi: 10.21071/az.v65i250.488

Díaz M, Fajardo D, Moreno J, García C y Nuñez V. 2003. Identificación de Genes R1 y R2 que confieren resistencia a *Phytophthora infestans* en genotipos colombianos de papa. Revista Colombiana de Biotecnología 5(2): 40-50. https://revistas.unal.edu.co/index.php/biotecnologia/article/view/574/1109.

Estrada N. 2000. La biodiversidad en el mejoramiento genético de la papa. PROINPA, CIP, CID. La Paz, 372 p.

Fedepapa. Federación Colombiana de la Papa. 2018. Boletín Mensual Regional No. 8 2(8): 2 p. https://fedepapa.com/wp-content/uploads/2017/01/NARI%C3%91O-2018.pdf. Retrieved: November 2019.

Forbes G y Huarte M. 2014. La resistencia al Tizón Tardío como herramienta de control en los países en desarrollo. Revista Latinoamericana de la Papa 18(2):36-58.

Gabriel J, Carrasco E, García W, Equise H, Navia O, Torres R, Ortuño N, Franco J, Thiele G y Estrada N. 2001. Experiencias y logros sobre mejoramiento convencional y selección participativa de papa en Bolivia. Revista Latinoamericana de la Papa 12: 169-192.

Huarte M y Capezio S. 2003. Niveles disponibles de resistencia al Tizón tardío. Revista de Información sobre Investigación y Desarrollo Agropecuario 3:101-107.

IDEAM. Instituto de Hidrología, Meteorología y Estudios Ambientales. 2016. Reporte Técnico estación meteorológica Botana. Pasto. Nariño.

Juyó D, Gerena H y Mosquera T. 2011. Evaluación de marcadores moleculares asociados con resistencia a gota (*Phytophthora infestans* L.) en papas diploides y tetraploides. Revista Colombiana de Biotecnología 13(2): 51-62. http://www.scielo.org.co/pdf/biote/v13n2/v13n2a05.pdf.

Lagos TC, Apráez J, Lagos LK y Duarte D. 2015. Comportamiento de 50 familias de medios hermanos de Solanum quitoense Lam. bajo selección recurrente. Revista Temas Agrarios. 20(2):19-29. doi: 10.21897/rta.v20i2.755

Monsalve-Fonnegra Z, Monsalve-Restrepo M, Urrea-Trujillo A, y Zapata J. 2012. Expresión diferencial durante la interacción *Solanum tuberosum* - *Phytophthora infestans*. Revista Colombiana De Biotecnología, 14(1), 77-92.

Muñoz M, Acuña I y Sagredo B. 2019. Resistencia varietal al tizón tardío de la papa. Capítulo 7. En: Tizón tardío de la papa: Estrategias de manejo integrado con alertas temprana. Boletín INIA. 18p.

Nyquist W. 1991. Estimation of heritability and prediction of selection response in plant populations. Critical Reviews in Plant Sciencies 10(3): 235-322. doi: 10.1080/07352689109382313

Núñez C y Escobedo D. 2014. Caracterización de germoplasma vegetal: la piedra angular en el estudio de los recursos fitogenéticos. Acta agrícola y pecuaria 1 (1): 1-6.

Ñustez C. 2019. Variedades liberadas por la Universidad Nacional de Colombia. Grupo de Investigación en papa. En: Grupo de Investigación en Papa, Universidad Nacional de Colombia. 1 p. http://papaunc.com/variedades-liberadas-por-la-universidad-nacional-de-colombia. Retrieved: November 2019.

Pérez W y Forbes G. 2008. Manual técnico. El tizón tardío de la papa. Centro Internacional de la Papa (CIP), Lima, Perú. 41p.

Rodríguez L, Ñustez C y Estrada N. 2009. Criolla Latina, Criolla Paisa y Criolla Colombia, nuevos cultivares de papa criolla para el departamento de Antioquia (Colombia). Agronomía Colombiana 27(3): 289-303.

Solano J, Acuña I, Esnault F and Brabant P. 2014. Resistance to *Phytophthora infestans* in *Solanum tubersosum* landraces in Southern Chile. Tropical Plant Pathology 39(4): 307-315. doi: 10.1590/S1982-56762014000400005

Stiles F. 2000. Curso de muestreo y análisis estadístico en investigaciones biológicas. Universidad de Nariño, Pasto. 153p.

Van Der Plank JE. 1963. Plant deseases: epidemics and control. Academic. New York. 349p.

Yuen, J.E and Forbes, G. 2009. Estimating the level of susceptibility to *Phytophthora infestans* in potato genotypes. Phytopathology 99: 783-786. doi:10.1094/PHYTO-99-6-0782