Neutrosophic Sets and Systems, {Special Issue: Advances in SuperHyperStructures and Applied Neutrosophic Theories)}, Vol. 74, 2024

University of New Mexico

Analysis of Genetic Components of Late Blight Resistance (Phytophthora infestans) in Potatoes (Solanum phureja) from Cutuglahua, Pichincha, Using Neutrosophic SuperHyperSoft Sets

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Abstract. Late blight (Phytophthora infestans) resistance in Solanum phureja has influenced potato genetic improvement due to the high incidence of this disease. This study analyzed key resistance attributes, such as lesion growth rate, lesion size, latency period, and sporulation intensity, through field and laboratory tests. To integrate these attributes and optimize the selection of resistant genotypes, Neutrosophic SuperHyperSoft Sets modeling was used. Among the results, genotypes such as Chaucha Amarilla (with high general combining ability) and progenies such as 11 (Ch. Negra x Ch. Amarilla), 1 (Ch. Negra x Ch. Negra), and 9 (Ch. Negra x Yema de Huevo) were identified, exhibiting high specific combining ability values. In conclusion, lesion size was identified as a crucial indicator, emphasizing the priority of integrating key attributes in genetic improvement programs for the development of more resistant and sustainable varieties.

Keywords: potato, infectious agent, potato rot, genetic resistance, Neutrosophic SuperHyperSoft Sets.

1 Introduction

Potato is a key crop globally, known for its high protein and energy yield per unit of land area [1]. In Ecuador, its economic and nutritional importance is reflected in the cultivated hectares and the yields achieved [2]. However, the crop faces critical challenges due to late blight [3], caused by Phytophthora infestans, a devastating disease that destroys plantations in just a few days, worsened by the constant emergence of new strains of the pathogen that overcome existing genetic resistances [4].

Therefore, the success in developing resistant varieties lies in the selection of parents with high general combining ability (GCA) and specific combining ability (SCA) [5][6][7]. This process is complex due to the tetra-allelic inheritance of potatoes, the polygenic nature of resistance, and the environmental influence on phenotypic expression [8][9]. To address these limitations, diallel methods, such as the one proposed by Griffing, are employed, which allow the evaluation of genetic interactions and the selection of promising hybrid combinations [10].

Therefore, this study analyzes key resistance parameters, such as lesion growth rate, lesion size, latency period, and sporulation intensity, through field and laboratory tests [11]. Additionally, Neutrosophic SuperHyperSoft Sets modeling is incorporated to facilitate the integration of multiple attributes, optimizing decision-making in the selection of genotypes. In fact, the goal is to identify progenitors and crosses with the potential to develop potato varieties resistant to late blight, contributing to the sustainability of the crop [12][13][14].

2 Preliminaries

2.1 Neutrosophic SuperHyperSoft Sets.

This section serves the purpose of remembering the basic notions of Fuzzy Extension SuperHyperSoft Sets and neutrosophic theory [10].

Definition 1 ([1, 9, 10]). Given U is the initial universe set and E is the set of parameters. A pair (F, E) is called a *soft set* (over U) if and only if F is a mapping of E into the set of all subsets of U.

That is to say, having a set E of parameters and fixing a parameter $\varepsilon \in \mathrm{E}$, then $\mathrm{F}(\varepsilon) \in \mathcal{P}(\mathrm{U})$, where $\mathcal{P}(\mathrm{U})$ denotes the power set of U and $\mathrm{F}(\varepsilon)$ is considered the set of ε-elements of the Soft Set (F, E) or the set of ε-approximate elements of the Soft Set [11] [12].

It is not difficult to realize that fuzzy sets are soft sets, this is a consequence of the α-levels definition of a membership function μ_A using the following formula:

$\mathrm{F}(\alpha) = \{x \in \mathrm{U} \mid \mu_A(x) \geq \alpha\}$, $\alpha \in [0, 1]$. Thus, if the family F is known, the function μ_A can be reconstructed using the following formula:

$$\mu_A(x) = \sup_{\substack{\alpha \in [0,1] \\ x \in F(\alpha)}} \alpha$$

Thus, a fuzzy set is a $(\mathrm{F}, [0, 1])$ soft set.

Given a binary operation * for subsets of the set U, where (F, A) and (G, B) are soft sets over U. Then, the operation * for soft sets is defined as follows:

$(\mathrm{F}, \mathrm{A}) * (\mathrm{G}, \mathrm{B}) = (\mathrm{J}, \mathrm{A} \times \mathrm{B})$, where $\mathrm{J}(\alpha, \beta) = \mathrm{F}(\alpha) * \mathrm{G}(\beta)$; $\alpha \in \mathrm{A}$, $\beta \in \mathrm{B}$, and $\mathrm{A} \times \mathrm{B}$ is the Cartesian product of the sets A and B.

Definition 2 ([2, 3, 11, 12])**.** Let U be a universe set, $\mathcal{P}(\mathrm{U})$ the power set of U. Let $a_1, a_2, \ldots, a_n$, for $n \geq 1$, be n distinct attributes, whose corresponding attribute values are respectively the sets $A_1, A_2, \ldots, A_n$, with $A_i \cap A_j = \emptyset$, for $i \neq j$, and $i, j \in \{1, 2, \ldots, n\}$. Then the pair $(F, A_1 \times A_2 \times \ldots \times A_n)$, where: $F: A_1 \times A_2 \times \ldots \times A_n \rightarrow \mathcal{P}(\mathrm{U})$ is called a *HyperSoft Set* over U.

Definition 3 ([2, 3, 11, 12])**.** Let U be a universe set, $\mathcal{P}(\mathrm{U})$ the power set of U. Let $a_1, a_2, \ldots, a_n$, for $n \geq 1$, be n distinct attributes, whose corresponding attribute values are respectively the sets $A_1, A_2, \ldots, A_n$, with $A_i \cap A_j = \emptyset$, for $i \neq j$, and $i, j \in \{1, 2, \ldots, n\}$. Then the pair $\left(F, \mathcal{P}(A_1) \times \mathcal{P}(A_2) \times \ldots \times \mathcal{P}(A_n)\right)$, where:

$F: \mathcal{P}(A_1) \times \mathcal{P}(A_2) \times \ldots \times \mathcal{P}(A_n) \rightarrow \mathcal{P}(\mathrm{U})$ is called a *SuperHyperSoft Set* over U.

Definition 4 ([4, 5, 13-15])**.** Let U be a universe set, $\mathcal{P}(\mathrm{U})$ the power set of U. Let $a_1, a_2, \ldots, a_n$, for $n \geq 1$, be n distinct attributes, whose corresponding attribute values are respectively the sets $A_1, A_2, \ldots, A_n$, with $A_i \cap A_j = \emptyset$, for $i \neq j$, and $i, j \in \{1, 2, \ldots, n\}$. Then the pair $\left(F, \mathcal{P}(A_1) \times \mathcal{P}(A_2) \times \ldots \times \mathcal{P}(A_n)\right)$, where:

$F: \mathcal{P}(A_1) \times \mathcal{P}(A_2) \times \ldots \times \mathcal{P}(A_n) \rightarrow \mathcal{P}\left(\mathrm{U}\left(x(d^0)\right)\right)$ is called a *Fuzzy_Extension SuperHyperSoft Set* over U.

Where $x(d^0)$ is the fuzzy or any fuzzy extension degree of appurtenance of the element x to the set U. Fuzzy extension means Fuzzy Set or Intuitionistic Fuzzy Set, Pythagorean Fuzzy Set, Fermatean Fuzzy Set, Neutrosophic Fuzzy Set, Plithogenic Fuzzy Set, etc [13].

Before concluding, let us recall some fundamental definitions of neutrosophic sets:

Definition 5 ([8]). The *Neutrosophic set* N is characterized by three membership functions [14], which are the truth-membership function T_A, indeterminacy-membership function I_A, and falsity-membership function F_A, where U is the Universe of Discourse and $\forall x \in \mathrm{U}$, $T_A(x), I_A(x), F_A(x) \subseteq]^{-}0, 1^{+}[$, and $^{-}0 \leq \inf T_A(x) + \inf I_A(x) + \inf F_A(x) \leq \sup T_A(x) + \sup I_A(x) + \sup F_A(x) \leq 3^{+}$ [15].

See that according to the definition, $T_A(x), I_A(x)$, and $F_A(x)$ are real standard or non-standard subsets of $]^{-}0, 1^{+}[$ and hence, $T_A(x), I_A(x)$ and $F_A(x)$ can be sub-intervals of $[0, 1]$. $^{-}0$ and 1^{+} belong to the set of hyperreal numbers.

Definition 6 ([8, 16, 17]). The *Single-Valued Neutrosophic Set* (SVNS) A over U is $A = \{< x, T_A(x), I_A(x), F_A(x) > : x \in U\}$, where $T_A: U \rightarrow [0, 1]$, $I_A: U \rightarrow [0, 1]$ and $F_A: U \rightarrow [0, 1]$. $0 \leq T_A(x) + I_A(x) + F_A(x) \leq 3$.

Single-Valued Neutrosophic Sets (SVNS) were introduced with the idea of applying neutrosophic sets for practical purposes. Some operations between SVNSs are expressed below [18, 9,20]:

Given $A_1 = (a_1, b_1, c_1)$ and $A_2 = (a_2, b_2, c_2)$, two SVNNs, the sum of A_1 and A_2 is defined as:

$$A_1 \ A_2 = (a_1 + a_2 - a_1 a_2, b_1 b_2, c_1 c_2) \tag{1}$$

Given $A_1 = (a_1, b_1, c_1)$ and $A_2 = (a_2, b_2, c_2)$, two SVNNs, the multiplication of A_1 and A_2 is defined as:

$$A_1 \ A_2 = (a_1 a_2, b_1 + b_2 - b_1 b_2, c_1 + c_2 - c_1 c_2) \tag{2}$$

The product of a positive scalar SVNN, A = (a, b, c) is defined as:

$$A = (1 - (1 - a), b, c) \tag{3}$$

The *Single-Valued Neutrosophic Number* (SVNN) is symbolized by $N = (t, i, f)$, such that $0 \leq t, i, f \leq 1$ and $0 \leq t + i + f \leq 3$.

3 Results

3.1 Case study

This research was carried out in the greenhouse of the Santa Catalina Experimental Station, located at 3050 meters above sea level, with controlled conditions of temperature (21 °C) and relative humidity (70%). Three native potato progenitors (Chaucha Negra, Chaucha Amarilla, and Yema de Huevo) were selected for their resistance to late blight and good agronomic quality, attributes that make them suitable for the genetic improvement of potatoes.

For the experimental design, a diallel design according to Model I, Method 2 of Griffing, combined with a completely randomized block design with four repetitions, was used. The crossings between the selected progenitors generated progenies that were evaluated in relation to the key genetic components (identified as attributes a_i in section 3.2). These parameters were analyzed using the Pearson correlation coefficient at 5%. This allowed for the establishment of the relationship between the late blight resistance components.

The crossings were carried out under controlled conditions, both in the field and using the bottle method. In the case of field crossings, five plants per progenitor were planted, while in the bottle method, branches with inflorescences were kept in water with water-soluble fertilizers. Subsequently, the flowers were emasculated and pollinated under optimal temperature and humidity conditions.

The seeds obtained from the crosses were germinated after being treated with gibberellic acid (1500 ppm) to standardize germination. The seedlings were grown in disinfected substrate and transplanted into plastic pots. The isolation and inoculation of Phytophthora infestans were carried out using a standard inoculum (40,000 sporangia/ml), which was applied to leaflets under controlled temperature conditions (18 °C) and a 14-hour light photoperiod.

3.2 Modeling with Neutrosophic SuperHyperSoft Sets

To improve the accuracy in the evaluation of the genetic resistance of the genotypes, the modeling of Neutrosophic SuperHyperSoft Sets was incorporated. This tool allows for the integration of the multiple relationships associated with the study attributes, as well as the neutrosophic mebership degrees in the evaluation of both progenitors and progenies (see Tables 1 and 2), in the resistance to the pathogen Phytophthora infestans.

Table 1: Progenitors for the analysis of the genetic components of late blight resistance. Source: Own elaboration.

Code	Progenitors
P1	Chaucha Negra
P2	Chaucha Amarilla
P3	Yema de Huevo

Table 2: Crosses derived from the combination of progenies. Source: Own elaboration.

Treatment	Cross	Progeny	Genealogy
T1	1x1	1	Ch. Negra x Ch. Negra
T2	1x2	11	Ch. Negra x Ch. Amarilla
T3	1x3	9	Ch. Negra x Yema de Huevo
T4	2x2	2	Ch. Amarilla x Ch. Amarilla
T5	2x3	15	Ch. Amarilla x Yema de Huevo
T6	3x3	5	Yema de Huevo x Yema de Huevo

On the other hand, the measurement attributes, as well as the combinatory aptitude attributes directed towards genetic improvement programs, are presented (see Tables 3 and 4). In fact, they help in selecting both the best progenitors individually and the best crosses between them to obtain the best possible varieties in terms of desired characteristics, such as disease resistance.

Table 3: Genetic attributes of progenitors and progenies. Source: Own elaboration.

Attribute	Name
a_1	General Combining Ability (GCA)
a_2	Specific Combining Ability (SCA)

Table 4: Measurement attributes for each progenitor and progeny. Source: Own elaboration.

Attribute	Genetic components of late blight resistance
b_1	Lesion growth rate (LGR)
b_2	Lesion size (LS)
b_3	Latency period (LP)
b_4	Sporulation intensity (SI)

Each group of determined attributes forms a Neutrosophic SuperHyperSoft, which is formed by $(F, \mathcal{P}(A_1) \times \mathcal{P}(A_2))$, as well as $(G, \mathcal{P}(B_1) \times \mathcal{P}(B_2) \times \ldots \times \mathcal{P}(B_4))$. Thus, both functions return neutrosophic $\mathcal{P}\left(\mathrm{U}\left(x(d^0)\right)\right)$ for each progenitor and progeny. Therefore, the following Neutrosophic SuperHyperSoft $(H, \left(\mathcal{P}(A_1) \times \mathcal{P}(A_2)\right) \times \left(\mathcal{P}(B_1) \times \mathcal{P}(B_2) \times \ldots \times \mathcal{P}(B_4)\right))$ is proposed, as well as a new neutrosophic degree of membership $x(d^0)$, obtained from the intersection of the attributes $a_i \cap b_i$. The following functions are proposed to determine which treatment shows greater resistance to *late blight*, as well as their values in the estimation of progenitors and progenies of potatoes (see Tables 5 and 6).

- $F\,(a_1 \cap b_i) = \{P_i\}, \left\{\left(x_{a_1}(d^0)\right) \cap (x_{b_i}(d^0))\right\}$
- $F\,(a_2 \cap b_i) = \{T_i\}, \left\{\left(x_{a_2}(d^0)\right) \cap (x_{b_i}(d^0))\right\}$

Table 5: Values in the estimation of the attributes $(a_1 \cap b_i)$ for potato progenitors (Solanum phureja). Source: Own elaboration.

Progenitor	$\boldsymbol{a_1 \cap b_1}$		$\boldsymbol{a_1 \cap b_2}$		$\boldsymbol{a_1 \cap b_3}$		$\boldsymbol{a_1 \cap b_4}$
	LGR averages (mm2)	Effects of GCA	LS averages (mm2)	Effects of GCA	LP averages (days)	Effects of GCA	Average.
P1	14.54	-4.49	69.30	-2.58	3.75	-2.67	1.00
P2	11.28	14.68	55.49	20.99	4.25	21.22	1.00
P3	18.60	-10.19	77.48	-18.41	3.25	-18.55	2.00

Table 6: Values in the estimation of the attributes $(a_2 \cap b_i)$ for potato progenies (Solanum phureja). Source: Own elaboration.

Progeny	$\boldsymbol{a_2 \cap b_1}$		$\boldsymbol{a_2 \cap b_2}$		$\boldsymbol{a_2 \cap b_3}$		$\boldsymbol{a_2 \cap b_4}$
	LGR averages (mm2)	Effects of SCA	LS averages (mm2)	Effects of SCA	LP averages (days)	Effects of SCA	Average.
T1	23.85	42.40	83.62	50.91	3.13	44.49	1.89
T2	9.27	-54.09	75.88	-65.58	3.85	-60.28	1.27
T3	13.53	-30.71	82.65	-36.25	3.60	-28.69	1.54
T4	21.08	15.37	77.51	20.74	3.44	21.51	1.34
T5	29.27	23.35	88.82	24.09	3.16	17.26	1.80
T6	29.05	3.68	99.92	6.08	3.00	5.71	2.00

Comparative analysis:

- $a_1 \cap b_1$: In Table 5, it is observed that Chaucha Amarilla (P2) is the progenitor with the lowest lesion growth rate, followed by Chaucha Negra, and finally, Yema de Huevo shows the highest values in lesion growth rate. On the other hand, the knowledge of general combining ability (GCA) and the estimation of the effect in all crosses show that the progenitor Chaucha Amarilla achieved a positive value of 14.68 in its GCA effects, indicating its superiority over the other progenitors. This parent originated more resistant progenies to late blight, presenting a high probability of using this progenitor in the INIAP Potato Program's genetic improvement programs, as it possesses the ability to transmit resistance to late blight to its descendants.
- $a_2 \cap b_1$: The progenies from crosses 11 (Ch. Negra x Ch. Amarilla), 1 (Ch. Negra x Ch. Negra), and 9 (Ch. Negra x Yema de Huevo) showed high absolute values for Specific Combining Ability (SCA). This indicates that the progenies performed better than the average GCA of their progenitors.
- $a_1 \cap b_2$: The high GCA value of 20.99 for Chaucha Amarilla recognizes this progenitor, indicating a high probability of being employed in genetic improvement programs. According to the reviewed literature, it is possible to select four times more potato clones from a progenitor with high GCA than from one with low GCA.
- $a_2 \cap b_2$: High absolute values in the effects of SCA were observed in progenies 11 (Ch. Negra x Ch. Amarilla), 1 (Ch. Negra x Ch. Negra), and 9 (Ch. Negra x Yema de Huevo), indicating that the offspring showed a better or superior performance compared to the average GCA of their parents.
- $a_1 \cap b_3$: When considering the number of days in the development of symptoms (LP) of Phytophthora infestans (P. infestans), progenitors with high resistance levels were identified, with Chaucha Amarilla standing out, followed by Yema de Huevo and Chaucha Negra, respectively. Therefore, Chaucha Amarilla was chosen as the progenitor with a high GCA effect of 21.22, indicating that it is the best parent capable of transmitting resistance to late blight to its offspring.
- $a_2 \cap b_3$: By accounting for a higher number of days in the appearance of symptoms, progenies 11 (Ch. Negra x Ch. Amarilla), 1 (Ch. Negra x Ch. Negra), and 9 (Ch. Negra x Yema de Huevo) showed high absolute values for SCA. This indicates that the progenies performed better or

superior to the average GCA of their parents, showing a degree of heterosis for resistance to P. infestans.

- $a_1 \cap b_4$: The averages obtained for the progenitors, based on the visual scale of sporulation intensity, determined that Chaucha Amarilla and Chaucha Negra exhibited the lowest sporulation intensity with 1.00 (low sporulation). Meanwhile, the progenitor Yema de Huevo showed the highest sporulation intensity with 2.00 (medium sporulation), and the overall average for the progenitors was 1.33, considered as low sporulation.
- $a_2 \cap b_4$: The averages obtained for the offspring in terms of sporulation intensity established that the progenies from cross 11 (Ch. Negra x Ch. Amarilla) showed the lowest sporulation intensity with 1.27 (low sporulation). Meanwhile, the progenies from family 5 (Yema de Huevo x Yema de Huevo) showed the highest sporulation intensity with 2.00 (medium sporulation).

Correlation analysis: The genetic components of resistance to late blight in Solanum phureja showed significant relationships between the variables LGR, LS, and SI, with positive correlations at 1% between LGR - LS and LGR - SI, and a moderate relationship between LS - SI at 5%. These correlations indicate that an increase in one variable is associated with an increase in the others (see Table 7). In contrast, the negative correlations between LGR - LP, LP - SI, and LS - LP suggest that a higher value in one variable reduces the other, such as a shorter latency period (LP) with an increase in LGR and LS.

Table 7: Correlation analysis of components a_i. Source: Own elaboration.

	LGR	LS	LP	SI
LGR	-----			
LS	0.58**	-----		
LP	-0.54**	-0.45*	-----	
SI	0.54**	0.51*	-0.64**	-----

** Significant at 1% probability

* Significant at 5% probability

LGR was identified as the most relevant component in the resistance to P. infestans, and its relationship with other resistance variables (LS, LP, SI) suggests that these components are useful for evaluating and selecting resistant germplasm. The results reinforce the need to consider both additive and non-additive effects in the inheritance of resistance. It suggests that both the progenitors and the progenies show significant differences in the expression of this resistance. Therefore, the study highlights the value of phenotypic evaluations for genetic improvement in late blight resistance programs.

Neutrosophic membership degree: The neutrosophic degree of membership for each intersection of the sets of $P(T_i)$ is determined, as shown in Tables 8 and 9. Each neutrosophic degree of membership belongs to the set P(A_i) and P(B_i).

Table 8: Values of $x(d^0)$ in the estimation of the attributes (a_1) and (b_i). Source: Own elaboration.

	a_1	b_1	a_1	b_2	a_1	b_3	$a_1 \cap b_4$
P1	(0.6,0.35,0.4)	(0.8,0.15,0.2)	(0.6,0.35,0.4)	(0.8,0.15,0.2)	(0.2,0.75,0.8)	(0,0.95,1)	(0.7,0.25,0.3)
P2	(0.7,0.25,0.3)	(0.4,0.55,0.6)	(0.6,0.35,0.4)	(0.4,0.55,0.6)	(0.3,0.65,0.7)	(0.4,0.55,0.6)	(0.7,0.25,0.3)
P3	(0.5,0.45,0.5)	(0.6,0.35,0.4)	(0.5,0.45,0.5)	(0.5,0.45,0.5)	(0.2,0.75,0.8)	(0.3,0.65,0.7)	(0.4,0.55,0.6)

Table 9: Values of $x(d^0)$ in the estimation of the attributes (a_2) and (b_i). Source: Own elaboration.

	a_2	b_1	a_2	b_2	a_2	b_3	$a_1 \cap b_4$
T1	(0.8,0.15,0.2)	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0.1,0.85,0.9)	(0.2,0.75,0.8)	(0.7,0.25,0.3)
T2	(0.8,0.15,0.2)	(0.6,0.35,0.4)	(0.8,0.15,0.2)	(0.6,0.35,0.4)	(0.2,0.75,0.8)	(0.3,0.65,0.7)	(0.8,0.15,0.2)
T3	(0.8,0.15,0.2)	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0.2,0.75,0.8)	(0.1,0.85,0.9)	(0.7,0.25,0.3)

	a_2	b_1	a_2	b_2	a_2	b_3	$a_1 \cap b_4$
T4	(0.7,0.25,0.3)	(0.8,0.15,0.2)	(0.8,0.15,0.2)	(0.8,0.15,0.2)	(0.1,0.85,0.9)	(0.1,0.85,0.9)	(0.8,0.15,0.2)
T5	(0.7,0.25,0.3)	(0.8,0.15,0.2)	(0.7,0.25,0.3)	(0.8,0.15,0.2)	(0.1,0.85,0.9)	(0.1,0.85,0.9)	(0.7,0.25,0.3)
T6	(0.7,0.25,0.3)	(0.9,0.05,0.1)	(0.7,0.25,0.3)	(0.9,0.05,0.1)	(0.1,0.85,0.9)	(0,0.95,1)	(0.7,0.25,0.3)

To determine the new neutrosophic membership degree of $(H, (\mathcal{P}(A_i)) \times (\mathcal{P}(B_i)))$ P(A,B), the t_{norm} and t_{conorm} were used to determine the intersection between the functions defined in the study (see Tables 10 and 11). For this, the aggregation operation $\left(min_j\{\mathrm{T}_{ij}\}, max_j\{\mathrm{I}_{ij}\}, max_j\{\mathrm{F}_{ij}\}\right)$ Was used.

Table 10: Values of $x(d^0)$ in the estimation of the attributes $(a_1 \cap b_i)$ in $\mathcal{P}\left(\mathrm{U}(x(d^0))\right)$. Source: Own elaboration.

	$a_1 \cap b_1$	$a_1 \cap b_2$	$a_1 \cap b_3$	$a_1 \cap b_4$
P1	(0.6,0.35,0.4)	(0.6,0.35,0.4)	(0,0.95,1)	(0.7,0.25,0.3)
P2	(0.4,0.55,0.6)	(0.4,0.55,0.6)	(0.3,0.65,0.7)	(0.7,0.25,0.3)
P3	(0.5,0.45,0.5)	(0.5,0.45,0.5)	(0.2,0.75,0.8)	(0.4,0.55,0.6)

The results in Table 10 define the progenitor Chaucha Amarilla (P2), which demonstrated greater resistance to late blight. It has a degree of membership of (0.3, 0.65, 0.7) in the intersection of the analyzed function for this treatment $F\ (a_1 \cap b_i) = \{P_i\}, \left\{\left(x_{a_1}(d^0)\right) \cap (x_{b_i}(d^0))\right\}$. In contrast, Chaucha Negra showed a lower degree of neutrosophic membership, although it contributed resistance through its progenies.

Table 11: Values of $x(d^0)$ in the estimation of the attributes $(a_2 \cap b_i)$ in $\mathcal{P}\left(\mathrm{U}(x(d^0))\right)$. Source: Own elaboration.

	$a_1 \cap b_1$	$a_1 \cap b_2$	$a_1 \cap b_3$	$a_1 \cap b_4$
T1	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0.1,0.85,0.9)	(0.7,0.25,0.3)
T2	(0.6,0.35,0.4)	(0.6,0.35,0.4)	(0.2,0.75,0.8)	(0.8,0.15,0.2)
T3	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0.1,0.85,0.9)	(0.7,0.25,0.3)
T4	(0.7,0.25,0.3)	(0.8,0.15,0.2)	(0.1,0.85,0.9)	(0.8,0.15,0.2)
T5	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0.1,0.85,0.9)	(0.7,0.25,0.3)
T6	(0.7,0.25,0.3)	(0.7,0.25,0.3)	(0,0.95,1)	(0.7,0.25,0.3)

In contrast, in Table 11, according to the specific combining ability (SCA) effects, the genotype exhibiting the best absolute value in its effects is the progeny Ch. Negra x Ch. Amarilla (T2). It obtained a neutrosophic degree of membership of (0.2, 0.75, 0.8) over the other treatments, according to the following function $F\ (a_2 \cap b_i) = \{T_i\}, \left\{\left(x_{a_2}(d^0)\right) \cap (x_{b_i}(d^0))\right\}$.

Based on the results obtained, it was projected that the integration of genotypes with high general combining ability (GCA) and specific combining ability (SCA) is essential for optimizing genetic improvement programs for Solanum phureja with resistance to late blight. The identification of outstanding genotypes, such as Chaucha Amarilla (high GCA), along with progenies such as 11 (Ch. Negra x Ch. Amarilla), 1 (Ch. Negra x Ch. Negra), and 9 (Ch. Negra x Yema de Huevo), which demonstrated high values in SCA, suggested that the inheritance of resistance is regulated by both additive and non-additive effects. This observation allowed the identification that a more precise selection, considering the genetic variability of progenies and the specific influence of progenitors, would facilitate the development of genotypes with greater resistance.

Furthermore, the relevance of lesion growth rate (LGR) constitutes a critical indicator of resistance to the pathogen and, therefore, one of the main criteria for future selection programs. As the understanding of interactions between additive and non-additive genetic effects deepens, breeding strategies will be developed in potato crops. These strategies would focus on optimizing specific resistance traits against late blight in different agroecological zones, contributing to the creation of more resistant potato varieties and the sustainability of production against emerging diseases like Phytophthora infestans.

4 Conclusion

The genetic evaluation of late blight resistance (Phytophthora infestans) in Solanum phureja allowed the identification of genotypes with significant variability in their resistance, highlighting both positive and negative correlations between the attributes a_i. On the other hand, the additive and non-additive genetic effects showed a greater influence of specific combining ability (b_2) over general combining ability (b_1). This emphasized the relevance of non-additive effects in late blight resistance. In fact, the variance and neutrosophic degree of membership analysis reflected that for b_i in the intersection with the attributes a_i, the progenitor Chaucha Amarilla was the most resistant. Meanwhile, Chaucha Negra, with a lower neutrosophic degree of membership, contributed resistance through its progenies. Additionally, progenies 11 (Ch. Negra x Ch. Amarilla), 1 (Ch. Negra x Ch. Negra), and 9 (Ch. Negra x Yema de Huevo) showed the highest b_2 values, while the self-fertilization 5 (Yema de Huevo x Yema de Huevo) exhibited greater susceptibility. Consequently, these results open new lines of research in understanding and leveraging non-additive effects in genetic resistance improvement.

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Received: July 24, 2024. Accepted: September 22, 2024