

General and specific combining abilities and partial diallel analysis of hop genotypes for traits of agronomic interest in the highlands of Santa Catarina

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ABSTRACT: Hops (*Humulus lupulus* L.) are of particular economic importance in the highlands of the state of Santa Catarina, Brazil, by virtue of the number of breweries in the region. However, since the cultivars currently available in the country present poor qualitative attributes and low cone productivity, there is considerable demand for improved genotypes. The results of diallel crossing experiments help to increase our understanding of inheritance processes and the mechanisms controlling the transfer of alleles with additive or non-additive action, thereby allowing breeders to explore the benefits of heterosis. The present study evaluated the general and specific combining abilities (GCA and SCA, respectively) of four hop genotypes and to obtain F1 hybrids with agronomic traits superior to those of the parents and the ability to adapt to the environmental conditions in the Santa Catarina highlands. Partial diallel crosses were performed using a randomized complete block design involving 14 treatments, namely two male parents (Cascade and Hallertauer), four female parents (Columbus, Chinook, Cascade and Hallertauer) and eight hybrid combinations, with three repetitions each. The results showed that SCA was the predominant controlling mechanism for the manifestation in hybrids of the traits length of the lateral branch, height of insertion of the first cone, plant green mass and cone productivity. Some parental combinations also exhibited high GCA, indicating the presence of favorable alleles with additive action. The best combination was Hallertauer × Cascade, a finding that highlights the importance of choosing parents from different gene pools (American × European) to obtain genetically enhanced hybrids.

Key words: *Humulus lupulus*, new cultivars, low latitude.

Capacidades de combinação geral e específica e análise dialélica parcial de genótipos de lúpulo para caracteres de interesse agrônomo na região do Planalto Catarinense

RESUMO: O lúpulo (*Humulus lupulus* L.) possui grande importância econômica no planalto serrano do estado de Santa Catarina, uma vez que existem inúmeras cervejarias nesta região do Brasil. Como as cultivares disponíveis no país carecem de bons atributos qualitativos e apresentam baixa produtividade de cones, existe grande demanda por genótipos melhorados. Os resultados de experimentos de cruzamento dialélico aumentam a compreensão dos processos de herança e dos mecanismos de controle associados à transferência de alelos com ação aditiva ou não aditiva, permitindo assim que os geneticistas explorem os benefícios da heterose. Os objetivos deste estudo foram avaliar as capacidades de combinação geral e específica (CGC e CEC, respectivamente) de quatro genótipos de lúpulo e obter híbridos F1 com características agrônomicas superiores às dos genitores e habilidade para se adaptar às condições ambientais do planalto catarinense. Os cruzamentos dialélicos parciais foram realizados em delineamento de blocos casualizados envolvendo 14 tratamentos, i.e. dois genitores masculinos (Cascade e Hallertauer), quatro genitores femininos (Columbus, Chinook, Cascade e Hallertauer) e oito combinações híbridas, com três repetições cada. Os resultados mostraram que a CEC dos genitores foi o mecanismo de controle predominante para a manifestação nos híbridos das características comprimento do ramo lateral, altura de inserção do primeiro cone, massa verde da planta e produtividade de cones. Algumas combinações entre genitores também manifestaram CGC elevada, indicando a presença de alelos favoráveis com ação aditiva. A melhor combinação foi Hallertauer × Cascade e essa descoberta demonstra a importância da escolha de genitores originários de diferentes grupos genéticos (Americano × Europeu) para obter híbridos geneticamente melhorados.

Palavras-chave: *Humulus lupulus*, novas cultivares, baixa latitude.

INTRODUCTION

The common hop (*Humulus lupulus* L.; Cannabaceae), known in Brazil as lúpulo, is a dioecious perennial species that probably originates from temperate regions. The hop is of great importance for its cone-shaped flowers because contain lupulin glands that produce bioactive compounds, such as

bitter alpha- and beta-acids, as well as essential oils and other chemicals used in the production of beer (DURELLO et al., 2019).

The Brazilian state of Santa Catarina has the highest number of breweries per capita with around one brewery per 34 thousand inhabitants but hop production in the existing plantations in the area is not sufficient to supply the regional market. Although,

there are various initiatives encouraging the culture of hops in the highlands of Santa Catarina (the Planalto Serrano), several key issues need to be addressed, specifically low production efficiency and the lack of suitable cultivars adapted to the local climate (SANTOS et al., 2022). Hence, genetic improvement of the crop and the establishment of productive genotypes with superior brewing characteristics are of fundamental importance to consolidate and expand hop cultivation in the region.

Knowledge regarding the principles of genetic inheritance is fundamental for hop improvement and, in this context, diallel crosses are recognized as the safest and most efficient method for estimating genetic parameters such as general and specific combining abilities (GCA and SCA, respectively) and heterosis (CRUZ et al., 2012; GRIFFING, 1956). These parameters allow breeders and geneticists to make assumptions regarding the genetic control of the characters of interest and to develop new genotypes. GCA is a measure of the average performance of an individual or line with respect to a trait in a series of crosses and is used to estimate the effects of additive genetic action. SCA is defined as the positive or negative deviations from the average performance (GCA values) of two individuals or lines (parents) and is used to estimate the effects of non-additive dominance (effects of favorable dominant genes at different loci) or overdominance (interaction of different alleles at the same locus) (ORTON, 2019; GRIFFING, 1956; HENNING et al., 2005). SCA is particularly important for heterosis or hybrid vigor, the phenomenon whereby hybrids present phenotypic superiority over their parents, and knowledge of this parameter makes it possible to predict potential gains from the selection and fixation of desirable alleles through asexual reproduction (SHULL, 1948; 1952; ALLARD, 1999).

According to HENNING & TOWNSEND (2005), the genetic improvement of hops has thus far been based primarily on the selection of traits with additive action, while the role of dominant genes has been little explored by breeders and geneticists. Studies on heterosis allow the establishment of pure male and female lines, the production of crossing blocks and the selection of promising hybrids for subtropical regions. In view of the above, the present study aimed to evaluate GCA and SCA for the hop genotypes Columbus, Chinook, Cascade and Hallertauer and to obtain hybrids with superior agronomic traits appropriate for the climatic conditions in the highlands of Santa Catarina.

MATERIALS AND METHODS

Study site

All experiments were carried out in the research area of the Institute of Molecular and Genetic Improvement (IMEGEM) at the Science Center of the Universidade do Estado de Santa Catarina (UDESC, Lages, SC, Brazil). According to the Köppen classification, the climate in the region is classified as temperate (Cfb) with cool summers and mild winters. The average annual temperature is 15 °C and the average rainfall was 1,500 mm during the months of October to June in the years 2020/2022.

Plant material

The parent plants comprised two male genotypes (Cascade and Hallertauer; group 1) and four female genotypes (Cascade, Columbus, Chinook and Hallertauer; group 2). These genotypes were selected because they had no patents attached, information about their history could be obtained directly from farmers, their performance and qualitative traits (flavor and aroma) are appropriate for the brewing industry, and the parents were genetically divergent according to preliminary tests (data not shown).

The F1 hybrid progenies resulted from crosses between group 1 and group 2 genotypes, totalizing eight combinations. Forty female plants (> 2.5 m height) of each genotype were selected and 10 young and receptive inflorescences on each plant were protected with pollination bags to avoid contamination with extraneous pollen or unwanted material. Pollen from male plants of the two genotypes was collected, dried at room temperature and stored in glass vials in the fridge. Artificial pollination of the inflorescences was carried out in the morning using a syringe containing pollen suspended in water. Pollinated cones were identified, isolated using pollination bags and the seeds subsequently harvested to give rise to the F1 progenies (families of half-siblings). Seeds obtained in 2019/2020 and 2020/2021 from 1600 crossings, along with clones of the parent plants obtained by asexual propagation, were placed in Styrofoam trays containing commercial substrate and grown on in a greenhouse. At around 90 days after sowing, seedlings bearing two definitive leaves were transferred to plastic pots where they remained for approximately two years, following which the adult plants were relocated to the field.

Partial diallel experiment

The partial diallel cross experiment was performed according to a randomized complete

block design involving 14 treatments (2 male parents, 4 female parents and 8 hybridizations) with three repetitions of each. The experimental unit comprised five plants of the clone parents and the F1 hybrid progenies. Cultural treatments were performed in accordance with the technical recommendations for the crop. Pruning was carried out regularly so that only two main stems were maintained per plant, and the basal leaves located around 1 to 1.5 m from the soil were removed to avoid potential sources of disease. The following production parameters of the parent plants and the F1 hybrid progenies were determined: length of the lateral branch (LLB, cm), height of insertion of the first cone (HFC, cm), total plant height (TPH, m), plant green mass (PGM, g plant⁻¹) and cone productivity (PROD, g plant⁻¹).

Data analysis

Normality of distribution and homogeneity of variance of the data were verified using the Shapiro-Wilk and Levene statistical tests, respectively. Data were submitted to analysis of variance (ANOVA) according to equation 1:

$$Y_{ijl} = \mu + \text{Treatment}_i + e_{ijl} \quad (1)$$

where Y_{ijl} is the observed value, μ is the overall mean, Treatment_i is the population effect and e_{ijl} is the effect of the experimental error.

The mean squares and estimates of GCA and SCA were obtained from diallel analyses performed using Method II as described by GRIFFING (1956). The statistical model describing the experimental observations is shown in equation 2:

$$Y_{ij} = \mu + \frac{1}{2}(d1+d2) + g_i + g_j + s_{ij} + \epsilon_{ij} \quad (2)$$

where, μ is the overall mean of the diallel cross, $d1$ and

$d2$ are the differences between the means of groups 1 and 2, respectively, and the overall mean, g_i is the effect of the GCA of the i^{th} parent of group 1, g_j is the effect of the GCA of the j^{th} parent of group 2, s_{ij} is the effect of SCA, and ϵ_{ij} is the mean experimental error. The statistical significances of the effects of GCA and SCA were determined using the F test.

Heterosis (HET) and heterobeltiosis or contribution to the heterosis of each parent (HBT) with respect to a specific character were calculated using equations 3 and 4, respectively:

$$\text{HET} = [(F1 - MVP)/MVP] \times 100 \quad (3)$$

$$\text{HBT} = [(F1 - VBP)/VBP] \times 100 \quad (4)$$

where $F1$ is the value of the trait for the hybrid, MVP is the mean value for the parents involved in the cross, and VBP is the value of the better parent.

All statistical analyzes were performed using Genes (<http://www.ufv.br/dbg/genes/genes.htm>) and SAS 14.2 software (SAS, Cary, NC, USA).

RESULTS

The results of ANOVA (mean squares) for each of the production traits analyzed, namely LLB, HFC, TPH, PGM and PROD (Table 1), revealed significant differences ($P < 0.05$) between treatments. Although there were no significant effects for any of the characteristics among members of the F1 hybrid group, there were statistically significant differences for all traits within the parent group ($P < 0.05$) and in the interactions between parents and hybrids ($P < 0.001$). The overall mean values of the traits (Table 1) demonstrated that the performances of the F1 hybrids were statistically superior ($P < 0.05$) to those of the parents with the single exception of HFC. In

Table 1 - Summary of the analysis of variance of production traits describing the within- and between-group differences in hops in the second year of cultivation (2023) at Lages, SC, Brazil.

Sources of variation	Degrees of freedom	LLB cm	HFC cm	TPH m	PGM g plant ⁻¹	PROD g plant ⁻¹
Mean squares						
Treatments	13	3541*	5224*	2.159*	136289*	133271*
F1 hybrids	7	1878	661	4.678	64579	45685
Parents	5	2643*	11512*	4.540*	82948*	80662*
Hybrids vs. Parents	1	11345**	4166**	4.678**	436910**	198984**
Residue	28	794	1079	0.167	33474	27923
Overall mean values						
F1 hybrids		100.31	137.98	4.90	600.90	358.00
Parents		67.10	162.38	4.22	394.80	163.78
CV (%)		37.78	22.33	8.87	32.29	59.94

LLB - length of the lateral branch, HFC - height of insertion of the first cone, TPH - total plant height, PGM - plant green mass, PROD - cone productivity, CV - coefficient of variation. Significant at $P < 0.05$ (*) or $P < 0.001$ (**) according to F test.

particular, the overall mean values of PGM and PROD for the F1 hybrids were, respectively, 52 and 118% higher than those of the parents. The coefficients of variance can be considered low for HFC and TPH, medium for LLB and PGM, and high for PROD.

In the diallel analysis (Table 2), the mean squares of treatments showed significant differences between parents and the hybrid combinations of groups 1 and 2. It is notable that SCA displayed significant differences ($P < 0.05$) for the traits LLB, ATT, PGM and PROD. However, the GCA mean squares in the parent groups were significantly higher ($P < 0.05$) than those of SCA only for the variables HFC (86%) and PROD (5%) within group 2 (female parents), indicating a predominance of additive genes for these characteristics. The mean values of all traits analyzed (Table 2) were considerably higher in group 2 in comparison with those of group 1 (male parents).

The effects of SCA on the productivity traits of parent groups 1 and 2 and F1 hybrids (Table 3) showed both positive and negative deviations from the mean GCA values. Within the male parent group, all traits bar HFC were affected in a negative manner, but with Cascade presenting the higher value for PROD, indicating that it is more favorable for this character. The male parent Hallertauer presented desirable positive characteristics for HFC. Within the female parent group, Hallertauer exhibited the best performance with LLB and PROD being influenced in a positive manner, indicating that it could contribute to improve these phenotypes in

the progenies. Cascade showed the worse performance with negative deviations for all the traits, hence the contribution of this genotype in hybridization processes would be insignificant. Interestingly, Cascade presented the biggest negative deviation for HFC (-6.23 cm), which represents an advantage over the other genotypes with respect to the improvement of plant architecture.

Analyses of the effects of SCA on the productivity traits of the hybrids suggest that many desirable characteristics were not transmitted from parents to progenies (Table 3). The best parental combination was Hallertauer $\times$ Cascade, since the traits of the progeny were improved in relation to those of the parents with positive deviations for all characteristics and most particularly for PROD. This cross presented a specific PROD capacity of 75.09 with a mean productivity of 641 ± 987 g plant⁻¹. The next best combination was Cascade $\times$ Cascade because the progenies presented positive deviations for LLB, TPH, PGM and, especially, PROD indicating that they had inherited favorable alleles from the parents. Furthermore, the negative value of HFC (-6.66 cm) for this combination represents an improvement in phenotype regarding plant architecture. The other combinations were of less interest since they displayed either negative deviations or positive deviations with intermediate values.

Table 4 presents the effects of heterosis on cone productivity (PROD) in the F1 hybrids. The best cross was Hallertauer $\times$ Cascade, the

Table 2 - Summary of the diallel analysis of production traits describing the within- and between-group differences in hops in the second year of cultivation (2023) at Lages, SC, Brazil.

Sources of variation	Degrees of freedom	LLB cm	HFC cm	TPH m	PGM g plant ⁻¹	PROD g plant ⁻¹
Mean squares						
Treatments	13	3541*	5224*	2.159*	136289*	133272*
GCA group 1	1	641	2528	0.201	28482	62872
GCA group 2	3	1086	3037*	0.1947	61127	153337*
SCA	8	4534*	420	1.563*	184891*	146419*
Group 1 vs. Group 2	1	5855*	52896*	15.480*	80757*	38291
Residue	28	1058	1079	0.167	33474	27924
Overall mean values						
Group 1		40.45	82.06	2.67	208.00	81.84
Group 2		80.44	196.83	4.99	486.75	195.25
h ² (%)		71.64	67.0	92.3	74.65	57.26

LLB - length of the lateral branch, HFC - height of insertion of the first cone, TPH - total plant height, PGM - plant green mass, PROD - cone productivity, GCA - general combining ability, SCA - specific combining ability. h² - broad-sense heritability.

Group 1 (male parents): Cascade and Hallertauer genotypes.

Group 2 (female parents): Cascade, Columbus, Chinook and Hallertauer genotypes.

*Significant at $P < 0.05$ (F test).

Table 3 - Effect of the specific combining ability (SCA) on the productivity traits of the parents (groups 1 and 2) and their F1 hybrid progenies in the second year of cultivation (2023) at Lages, SC, Brazil.

Group 1 (male parents)	Group 2 (female parents)	LLB cm	HFC cm	TPH m	PGM g plant-1	PROD g plant-1
Cascade	-	-29.5	0.73	-0.86	-240.2	-73.0
Hallertauer	-	-47.1	6.01	-0.84	-314.1	-212.8
-	Cascade	-28.7	-6.23	-0.62	-155.6	-245.0
-	Chinook	-32.9	9.51	-0.46	-125.7	-83.6
-	Columbus	-25.5	0.43	-0.32	-104.2	-82.6
-	Hallertauer	10.8	3.03	-0.36	-168.8	125.3
Cascade × Cascade		20.00	-6.66	0.4	1.1	242.2
Cascade × Chinook		33.24	-0.44	0.52	108.9	31.1
Cascade × Columbus		33.97	-0.62	0.3	51.9	-80.7
Cascade × Hallertauer		-28.1	6.27	0.5	318.6	-46.5
Hallertauer × Cascade		38.13	19.12	0.81	310.4	247.7
Hallertauer × Chinook		32.58	-18.57	0.41	143.3	136.0
Hallertauer × Columbus		17.06	-0.25	0.29	156.3	245.9
Hallertauer × Hallertauer		6.49	-12.33	0.17	18.9	-204.1
Standard deviation (Sii)		10.91	12.72	0.16	70.9	64.7
Standard deviation (Sjj)		8.91	10.39	0.13	57.9	52.8
Standard deviation (Sij)		13.93	16.29	0.2	81.8	82.9

LLB - length of the lateral branch, HFC - height of insertion of the first cone, TPH - total plant height, PGM - plant green mass, PROD - cone productivity, Sii - standard deviation of the effect of the SCA of the i^{th} parent of group 1 and the j^{th} parent of group 2 with the same female parent, Sjj - standard deviation of the effect of the SCA of the i^{th} parent of group 1 and the j^{th} parent of group 2 with the same male parent, Sij - standard deviation of the effect of the SCA of the i^{th} parent of group 1 and the j^{th} parent of group 2.

progenies of which showed a mean heterosis of 476.57 g plant⁻¹ with both male and female parents contributing dominant favorable alleles for this phenotype. However, the reverse cross (Cascade × Hallertauer) was disadvantageous regarding PROD since the mean heterosis was -72.67 g plant⁻¹. In this case, while the male parent contributed in a positive manner with favorable alleles, the contribution of the female parent was negative. The next best cross for

productivity was Cascade × Cascade, which showed a mean heterosis of 401.25 g plant⁻¹ with positive contributions from both male and female parents.

DISCUSSION

This study was evaluated the GCA and SCA of four hop genotypes and obtained F1 hybrids with superior agronomic traits appropriate for the climatic

Table 4 - Effects of heterosis on cone productivity (g plant⁻¹) of F1 hybrid progenies in the second year of cultivation (2023) at Lages, SC, Brazil.

F1 hybrids (group 1 × group 2)	Mean heterosis (hybrids)	-----Contribution to heterosis-----	
		group 1 (male parent)	group 2 (female parent)
Cascade × Cascade	401.25	423.17	379.33
Cascade × Chinook	109.40	104.77	114.03
Cascade × Columbus	-2.93	14.40	-20.27
Cascade × Hallertauer	-72.67	229.70	-375.03
Hallertauer × Cascade	476.57	495.97	457.17
Hallertauer × Chinook	284.22	277.07	291.37
Hallertauer × Columbus	393.58	408.40	378.77
Hallertauer × Hallertauer	-160.38	139.47	-460.23

conditions of the highlands of Santa Catarina. Our results demonstrated that the genotypes Columbus, Chinook, Cascade and Hallertauer carry favorable alleles for both general and specific abilities, and that certain combinations of parents show promise for the selection of the desired characteristics.

In this sense, GCA was significant in the transmission of alleles associated with HFC and PROD, indicating the predominance of additive effects involved in the genetic control of the evaluated traits. According to NASS et al. (2000), GCA is important at the beginning of the breeding program since it facilitates the genetic improvement of species. On this basis, the combinations Cascade $\times$ Cascade and Hallertauer $\times$ Chinook can be employed in the genetic improvement of hops because of their superior performance regarding the traits HFC and PROD. These genotypes are not only can transmit favorable alleles to their progenies but also present high SCA. CRUZ et al. (2004) stated that these attributes are essential for obtaining gains in traits in intra-population improvement programs.

However, our study showed that the Hallertauer $\times$ Cascade cross was the most advantageous combination since both genotypes, but particularly the female parent, presented a high frequency of favorable genes for GCA and good complementation with dominant alleles for SCA in the progenies, demonstrating strong hybrid vigor (CRUZ & VENCOVSKY, 1989). According to WHITE et al. (2007), the superiority of heterozygous individuals (hybrids) in relation to their parents is associated with the capacity to adapt to new environments or stress conditions as, for example, the low availability of light. Such adaptation can be explained by the manifestation of heterosis, which confers beneficial advantages to hybrids cultivated under adverse conditions. The better performance of hybrids can be attributed to intralocus variability, or dominance reversal, in which the presence of two different gene pairs at the same locus can result either in the preservation of homeostasis during plant development or useful behavioral changes in relation to homozygous individuals (PROHENS et al., 2004).

The crosses that expressed SCA and heterosis were those involving contrasting genotypes such as Cascade $\times$ Hallertauer (American $\times$ European groups), Cascade $\times$ Columbus (American $\times$ American groups) and Hallertauer $\times$ Cascade (European $\times$ American groups). The results relating to the traits LLB, HFC and PGM demonstrated the greater importance of SCA and the possibility of performing interpopulation selection for the purpose of capturing

the effects of heterosis and achieving phenotypic gains. For example, the progeny from parents presenting negative HFC values may have improved architecture whereby the hop vines have lower lateral branches, this being a feature that facilitates the mechanized harvesting of cones and enhances productivity. Indeed, the exploration of SCA is essential for maximizing the effects of heterosis and improving the performance of hybrids with respect to plant architecture and productivity. Our experiments revealed that hybrids derived from the combinations Hallertauer $\times$ Cascade and Hallertauer $\times$ Columbus were up to three times more productive (1000 and 1450 g plant⁻¹, respectively) than the mean national productivity (500 g plant⁻¹), even though the plants were only in their second year of cultivation.

The critical criterion for maximizing the manifestation of heterosis is the divergence between the parents as, for example, in the crosses between Hallertauer males and Cascade/Columbus/Chinook females, although the average gene frequency of the diallel also influences heterosis. Hence, a more comprehensive analysis of contrasting groups and their intercrosses will increase the likelihood of obtaining transgressive segregation and novel superior genotypes and phenotypes in future generations (CRUZ et al., 2004).

It is known that crosses between highly divergent genotypes that also present complementary agronomic characteristics can result in superior hybrids because of the accumulation of favorable dominant alleles (heterosis). In this context, the use of inbred lines originating from distinct gene pools has been widely employed (REIF et al., 2005). In addition, some researchers (HENNING et al., 2004; HENNING & TOWNSEND, 2005) have reported positive correlations between parental diversity and the occurrence of heterosis in the progeny, thereby confirming that heterosis is inversely proportional to the degree of kinship between the parents involved in the cross (NESVADBA et al., 2013).

Despite the lack of diversity and the limited availability of male parents in Brazil, the parent genotypes employed in the present study presented distinct phenotypic characteristics. According to HENNING et al. (2004), the main difficulty encountered in the genetic improvement of hops is the restricted genetic basis. The gene pools of European hops and their American hybrids used in the crosses are descendants of few related lineages that have a common grandparent or great-grandparent, and such crosses result in few genetic gains or in inbreeding depression (LEMMENS, 1998;

SKOMRA et al., 2013; PATZAK & HENYCHOVÁ, 2018). Genotypes that are native to regions of low latitude, such as the Neomexican ecotypes, constitute a more contrasting group that could be introduced in Brazil. However, the introduction of such genotypes would require pre-improvement of the male parents since they may transmit undesirable characteristics or may not adapt to the local climate (HENNING, 2006; DARBY, 2005; FRANCKE et al., 1982). Moreover, the importation or introduction of new male genotypes can be costly in both the time span involved and the investment required (SANTOS et al., 2022). Therefore, new populations are important to increase the variability available to hop breeders in Brazil and to provide new sources of germplasm for the development of elite male parents.

SANTOS et al. (2022) stated that breeding programs should focus on the development of germplasm of female cultivars with qualities that are superior to those currently cultivated in Brazil, and most especially genotypes with unique and long-lasting aromatic properties. Our study revealed that hybridizations involving the Hallertauer male genotype are promising since the hybrids displayed better performances compared with their parents. Furthermore, Hallertauer hybrids present good potential for passing tests of distinctness, homogeneity and stability or value for cultivation and use, and could be employed as experimental brewery lines (HIERONYMUS, 2012). Genetically improved hybrids may be registered or used as parents in future breeding cycles to select new hop cultivars that are suitable for the highlands of Santa Catarina. A particular advantage of developing hop hybrids is that they can be propagated vegetatively such that the characteristics of interest can be easily fixed, and the cultivars released after a single selection cycle (HENNING, 2006).

CONCLUSION

There were phenotypic differences between the groups of parents studied and some parental combinations gave rise to F1 hybrids bearing favorable alleles for the traits evaluated. The effects of SCA were superior to those of GCA as demonstrated by the manifestation of dominant genes with non-additive action for the evaluated characteristics. The transmission of dominant alleles from the parent genotypes employed in this study made possible the creation of hybrids with desirable traits. The best combination was Hallertauer × Cascade, a finding that highlights the importance of choosing parents

from different gene pools (American × European) in order to obtain hybrids with superior traits.

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DECLARATION OF CONFLICT OF INTEREST

The authors declare no conflict of interest.

AUTHORS' CONTRIBUTIONS

All authors contributed equally to the manuscript.

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