

## INHERITANCE OF PUNGENCY IN *Capsicum chinense* JACQ. (SOLANACEAE)

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### ABSTRACT

The inheritance of capsaicin content in *Capsicum chinense* Jacq. was studied from two crosses between the accessions 157 (pungent) x 261 (non pungent) and 220 (intermediate) x 261 (non pungent), and their six basic generations (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub>, and BC<sub>2</sub>). The character showed predominance of additive gene effects and the magnitudes of the narrow sense heritability indicate that the capsaicin content can be effectively changed by simple selection.

### INTRODUCTION

Peppers are a widely cultivated species used as vegetables (sweet peppers) or spices (papikra, powder etc.) in the temperate zones as well as the tropics.

They are native to the New World tropics and belong to the genus *Capsicum* (Solanaceae). Five cultivated species are presently recognized (*C. annuum*, *C. baccatum*, *C. chinense*, *C. frutescens* and *C. pubescens*) and at least 20-30 wild species are related to the genus. All the cultivated species, as well as the wild ones for which counts have been reported, are diploids with  $2n = 2x = 24$ . Most of the species are self-compatible and among the cultivated ones there is predominance of self-pollination.

In the Tropical regions sweet peppers (non pungent types of *C. annuum*) have as major limiting factors some important diseases (viral, fungal and bacterial) and climate conditions (high humidity and temperature). These types have a narrow genetic base, since they were domesticated in Europe from a few sweet mutants and then reintroduced into the New World.

The sweet pepper breeding program of the Institute of Genetic at ESALQ/USP intends to extend its genetic base to other cultivated species, which are adapted to tropical conditions. The objective is to obtain plants with resistance to the principal diseases and that produce large and sweet fruits.

Pungency is one of the most important characteristics of the genus *Capsicum*. It is in *C. annuum* the major trait that distinguishes hot peppers from sweet ones, although nonpungent types can also be found among other domesticated and wild *Capsicum* species.

Most of the genetic studies on the genus, including pungency, have been based only on *C. annuum*. The first inheritance studies of pungency generally supported the single dominant gene hypothesis (Deshpande, 1935; Miller and Fineman, 1937; Odland, 1948), but they were carried out with a small number of F<sub>2</sub> plants and the evaluation of pungency was based on subjective organoleptic procedures. Afterwards the quantitative nature of the character was pointed out when chemical methods were developed to determine the capsaicin content, the pungent principle (Ohta, 1962; Thirumalachar, 1967; Quagliotti and Ottaviano, 1969).

*C. chinense* is a cultivated species widely spread in South America, and has its greatest diversity in the Amazon Basin (Pickersgill, 1969); so it is adapted to tropical conditions. Pungency in *C. chinense* is a dominant mendelian character according to organoleptic evaluations of 54 F<sub>2</sub> plants from a cross between two accessions: pungent Ca-1 and non pungent SA-75 (Pickersgill, 1966).

The present study aimed to determine the inheritance of pungency in *C. chinense*, based on a chemical method, and to give support to the *Capsicum* breeding program of the Institute of Genetic at ESALQ/USP, Piracicaba-SP, Brazil.

## MATERIALS AND METHODS

Three *C. chinense* accessions of the *Capsicum* collection of the Institute of Genetic, ESALQ/USP, all introductions from the Amazon region, were used:

- 157. Fruits pungent, elongated and yellow at maturity. Fruit size is the largest among the *C. chinense* accessions, however they are small when compared with commercial sweet peppers.
- 220. Fruits intermediate in pungency campanulated, small and red at maturity.
- 261. Fruits sweet (non pungent) campanulated, small and red at maturity.

The six basic generations viz.: P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>, were obtained from the crosses between the accessions 157 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group I, and 220 (P<sub>1</sub>) x

261 (P<sub>2</sub>), group II, which were grown in field conditions in a randomized complete block design with four replicates. The plot was represented by 5 plants for the P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub>, 50 plants for F<sub>2</sub> and 25 plants for BC<sub>1</sub> and BC<sub>2</sub> generations.

The pungency evaluation was based on the injection-extraction method for the rapid determination of total capsaicinoids in single whole pepper fruits, recently developed by Rymal *et al.* (1984).

Mature intact pepper fruits were injected with absolute methanol. After 30 minutes, pods were flushed and the capsaicinoids in the extracts were determined by absorbance at 275 nm (spectrophotometric determination). A standard curve was also obtained by linear regression from absorbance readings at 280 nm, using pure capsaicin (Sigma No. M-3773) diluted in absolute methanol. Pungency, in mg/100 g fruit (fresh weight basis), was obtained by comparing the absorbance reading with the standard curve  $x = 1.41 + 109.66 y$ , where  $x$  = capsaicin concentration in  $\mu\text{g/ml}$  of the extract and  $y$  = absorbance.

A simple analysis of variance was performed to compare generations. A weighted analysis of the within observed variances of the P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations was performed, according to the method of Mather and Jinks (1982), to test the goodness of fit and to estimate the genetic components of variation. The heritability, in the narrow sense, and the degree of dominance were also estimated.

## RESULTS AND DISCUSSION

The injection-extraction method for determination of pungency in single whole pepper fruits was effective and faster than other time consuming chemical methods.

The analysis of variance showed that the differences among generation means for both groups were highly significant, and the low magnitudes of the coefficients of variability indicated a fairly good precision of the experiments (Table I). The F<sub>2</sub> generation showed the largest observed variance as was expected, and P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub> generations showed the smallest ones, since their variances are due to environment effects, according to the model of Mather (1949).

It was observed that the non pungent parental line (261) also contained capsaicin, but at low concentrations (Figures 1 and 2). This fact was also pointed out by Quagliotti and Ottaviano (1969) and Kvachadze (1976) in sweet peppers (*C. annuum*). The F<sub>2</sub> and BC<sub>1</sub> generations, in both groups, showed transgressive segregation for the pungent parent and the distribution of F<sub>1</sub> generations showed complete and partial dominance in groups I and II, respectively.

Table I - Analysis of variance for capsaicin content (mg/100 g fruits) of the six basic generations from the crosses 157 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group I, and 220 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group II.

Source of variation	df	Mean square	
		Group I	Group II
Blocks	3	10.76 <sup>ns</sup>	7.58 <sup>ns</sup>
Generations	5	6032.55**	1993.75**
Error	15	10.57	9.36
Within P <sub>1</sub>	19	30.85	28.19
Within P <sub>2</sub>	19	11.97	15.29
Within F <sub>1</sub>	19	19.05	35.26
Within F <sub>2</sub>	199	1540.57	504.09
Within BC <sub>1</sub>	99	1050.97	350.67
Within BC <sub>2</sub>	99	804.98	278.84
Coefficient of variation		3.72%	5.83%

ns = not significant.

\*\* = significant at 0.01 level of probability.

The chi-square test ( $\chi^2$ ) of the weighted analysis (Table II), in both groups, indicated the adequacy of the model. The weighted analysis tested for goodness of fit and determined the best estimates of the components of variation and their standard errors (Table III). The standard errors and the variances estimates were of the same magnitude for the dominance component. According to Quagliotti and Ottaviano (1971); Mather's method gives a greater distinction for the additive ( $\sigma_A^2$ ) and environmental ( $\sigma_E^2$ ) components of variation, and magnitudes of the dominance component ( $\sigma_D^2$ ) oscillating around zero are frequently observed.

Narrow sense heritability estimates ( $\hat{h}_{ns}^2$ ), in groups I and II, were 83.67% and 78.33% respectively, which indicates the predominance of additive gene effects in the inheritance of capsaicin content. Similar results with regard to predominance of gene effects, but in *C. annum*, were reported earlier by Quagliotti and Ottaviano (1971) and Ahmed *et al.* (1982).

The degree of dominance estimate ( $\hat{d}$ ), 0.61 (group I) and 0.67 (group II) indicate partial dominance, although this is not evident when the histograms of the parental and F<sub>1</sub> generations (Figures 1 and 2) are compared. Probably the number of the plants evaluated, only 20 for the P<sub>1</sub>, P<sub>2</sub> and F<sub>1</sub> generations, was insufficient to show differences.

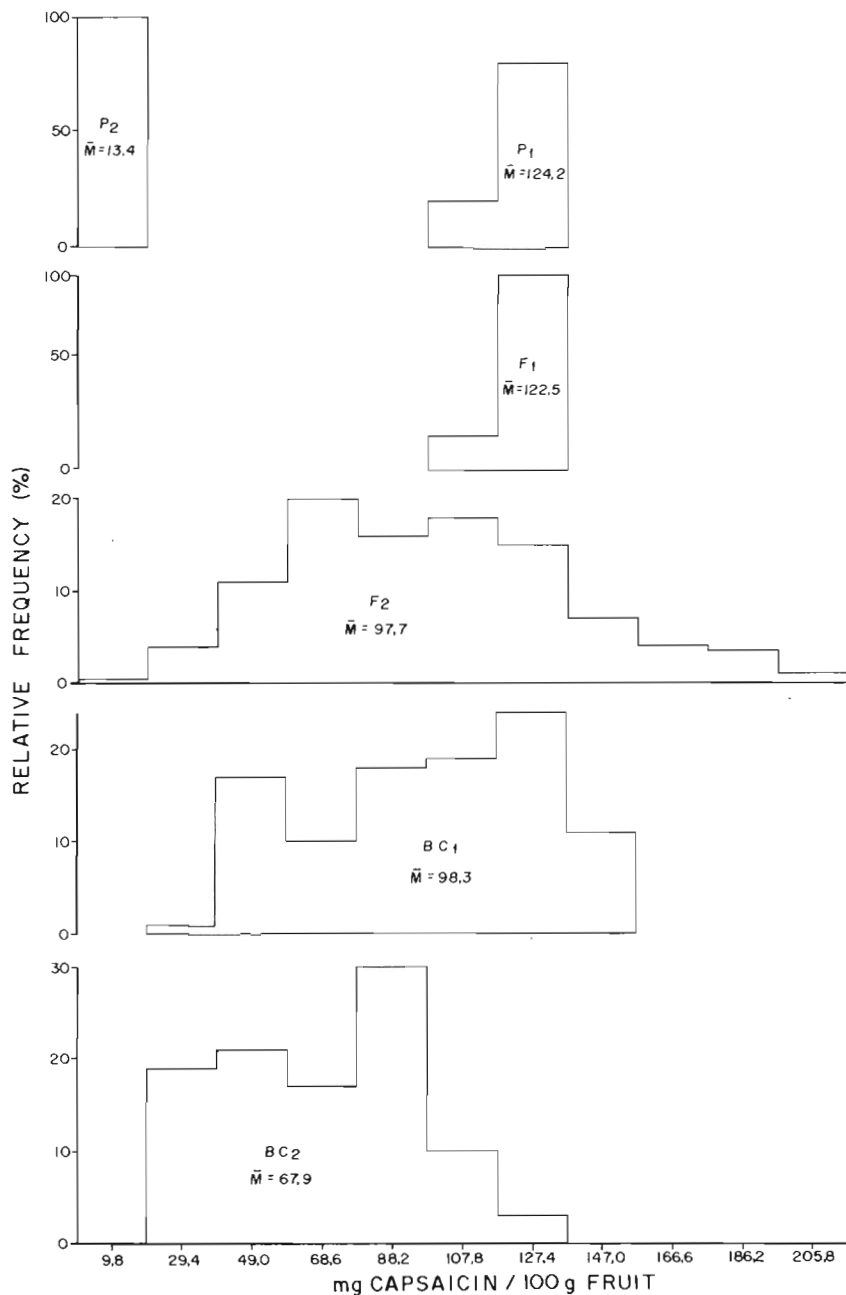


Figure 1 - Histogram of capsaicin content (mg/100 g fruit) of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations from the cross 157 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group I.

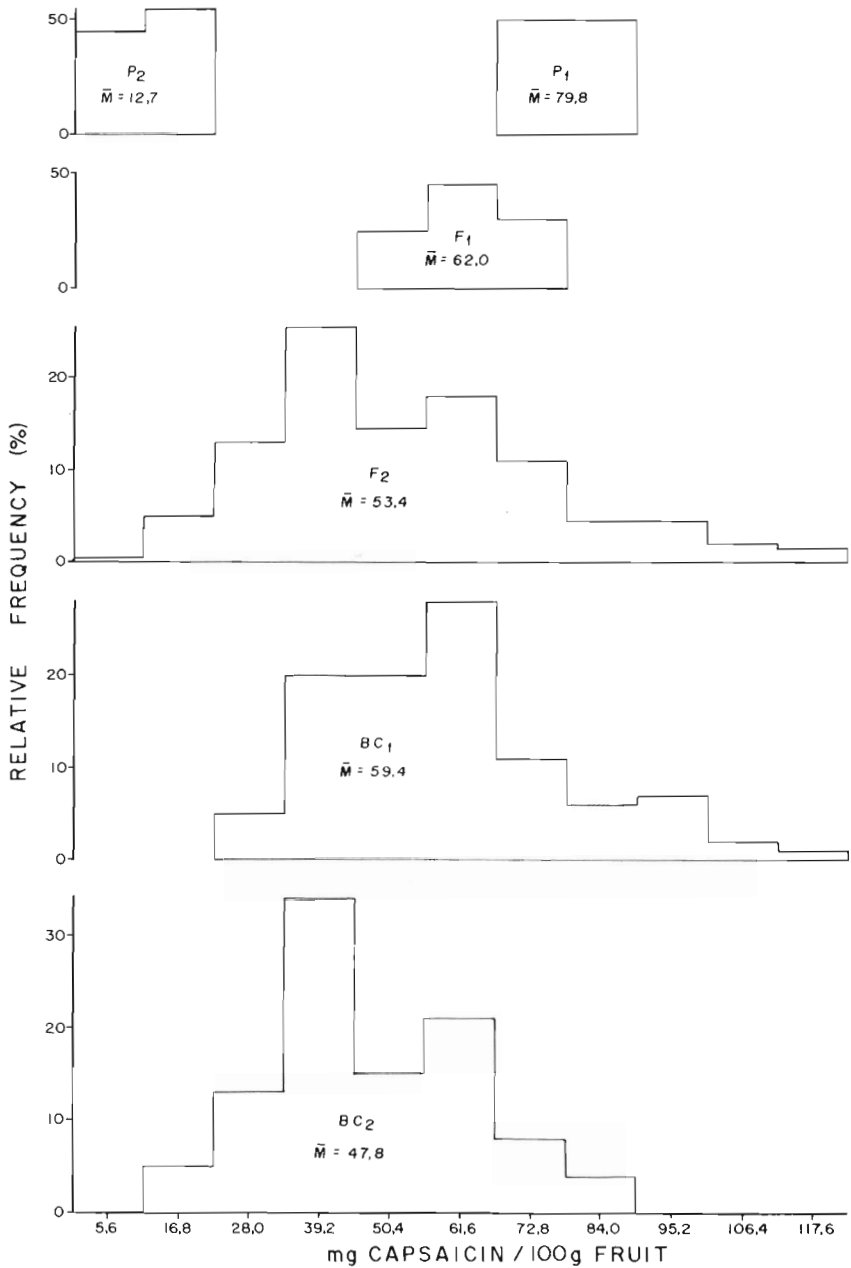


Figure 2 - Histogram of capsaicin content (mg/100 g fruit) of P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub> generations from the cross 220 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group II.

Table II - Weighted analysis of observed variances for capsaicin content (mg/100 g fruit) in different generations from the crosses 157 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group I, and 220 (P<sub>1</sub>) x 261 (P<sub>2</sub>) group II.

Generation	df	Observed variance		Model			Expected variance	
		Group I	Group II	( $\sigma^2$ )	( $\sigma^2$ )	( $\sigma^2$ )	Group I	Group II
P <sub>1</sub>	19	30.85	28.19	0	0	1	15.62	20.38
P <sub>2</sub>	19	11.97	15.29	0	0	1	15.62	20.38
F <sub>1</sub>	19	19.05	35.26	0	0	1	15.62	20.38
F <sub>2</sub>	199	1540.57	504.09	1	1	1	1540.38	504.09
BC <sub>1</sub>	99	1050.97	350.67	1/2	1	1	896.04	306.67
BC <sub>2</sub>	99	804.98	218.84	1/2	1	1	896.04	306.67
Chi-square test (3 df; 0.05)							5.22 <sup>ns</sup>	4.75 <sup>ns</sup>

ns = not significant.

Table III - Estimates of the genetic components of variation, heritability (narrow sense) and degree of dominance for capsaicin content (mg/100 g fruit) of the crosses 157 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group I, and 220 (P<sub>1</sub>) x 261 (P<sub>2</sub>), group II.

	Group I	Group II
( $\sigma^2$ )	1288.48 ± 358.24	394.85 ± 118.59
( $\sigma^2$ )	236.18 ± 238.40	88.86 ± 80.12
( $\sigma^2$ )	15.62 ± 3.12	20.38 ± 4.07
H <sup>2</sup>	83.67%	8.33%
dd	0.61	0.67

This study demonstrates that capsaicin content in *C. chinense* is controlled by several genes mainly acting additively. The high narrow sense heritability estimates indicate that the character can be effectively changed by simple selection.

The chemical method of pungency evaluation can be used in sweet pepper breeding programs when several plants must be screened. However, in a posterior step, organoleptic tests must be conducted to re-confirm sweetness of the selected plants and to evaluate other important organoleptic components.

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## RESUMO

A herança do conteúdo de capsaicina em *Capsicum chinense* Jacq. foi estudada a partir de dois cruzamentos entre as introduções 157 (pungente) x 261 (não pungente), e suas seis gerações básicas (P<sub>1</sub>, P<sub>2</sub>, F<sub>1</sub>, F<sub>2</sub>, BC<sub>1</sub> and BC<sub>2</sub>). O caráter mostrou predominância de efeitos aditivos e a magnitude da herdabilidade, sentido restrito, indica que o conteúdo de capsaicina pode ser modificado por métodos simples de seleção.

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