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Inheritance of Eight Characters in Intra- and Interspecific Crosses Among Five *Carica* Species[1]

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Abstract. **The inheritance of 8 monogenically controlled plant, fruit, and seed characters in *Carica* species is reported. The gene for red stem is dominant to that for green stem and the gene for red petiole is dominant to that for green stem and the gene for red petiole is dominant to that for green petiole. Genes for white and purple-blush flower colors are dominant to those for pale yellow; while the gene for red skin color of ripe fruit is dominant to that for yellow. However, the gene for red skin color is not dominant to that for orange skin color; the heterozygote has pink-skinned fruits. The gene for ridging on the fruit (carpel fusion lines) is dominant to that for wide groove, which in turn is dominant to that for narrow groove. Spiny vs. non-spiny seed coat produces an intermediate F_1, indicating no dominance. The gene for succulent fruit pulp is dominant to that for dry pulp. The gene for bushy branching is dominant to that for sparse branching.**

Genetic studies of vegetative characters in the Caricaceae have largely been confined to cultivars of *Carica papaya* L., the only species of commercial importance. These investigations were motivated by attempts to discover sex-linked characters which might allow the identification of sexes in the early seedling stages. Recent studies on compatibility and interspecific hybridization among several *Carica* species (7, 8) provided an opportunity to determine the genetics of 8 characters.

Usually, color of organs of plants has been reported to be controlled by a single gene pair. Variations in color intensities usually were not investigated, but were attributed to modifying gene action. In a biochemical survey of factors determining flower color, Scott-Moncrief (10) showed that many different gene types were involved in flower color variations, some exhibiting independent action with their effects being purely additive, while others expressed interactions of a complex nature.

Pigmented stem and petiole generally show monogenic inheritance with pigmented stems and petioles dominant over green in Spanish clover (*Desmodium sandwicense* E. Mey) (9), carrot (*Daucus carota* L.) (1), and guava (*Psidium guajava* L.) (6), although exceptions have been reported in jute (*Corchorus capsularis* L.) (4), okra (*Hibiscus esculentus* L.) (3), and sesame (*Sesamum indicum* L.) (2).

In *Carica papaya* the gene for yellow flower color was dominant to that for white (5). This gene was sex-linked. In the 'Kapoho Solo' purple-tinged flower color was also found to be a sex-linked character limited to hermaphrodites. Female flowers were all white (Nakasone, unpublished data). However, sex vs. flower color linkages offer no practical value inasmuch as sex can also be determined by floral morphology at flowering.

Hofmyer (5) found also that purple stem and petiole in *C. papaya* were dominant over green stem and petiole. The observed differences in intensity of the purple color were not analyzed but modifying factors affecting intensity were suggested.

Inheritance studies of skin color of ripe fruits have not been reported in *Carica,* largely due to the lack of color variations in *C. papaya.* There is a mutant yellow cultivar (with yellow leaves and fruits) in which the gene for yellow color of both leaves and skin of immature fruits is recessive to that of normal green

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Table 1. Inheritance of stem color in progenies of crosses between parents of the same color.

Parents (P_1)	Parents (P_2)	F_1	No. of plants F_2 Red	F_2 Green	BC-P_1 Red	BC-P_1 Green	BC-P_2 Red	BC-P_2 Green
C. goudotiana (A)R Sib-mated (Red x Red)		Red	70	0				
C. goudotiana (B) sib-mated (Red x Red)		Red	55	0				
C. goudotiana (A)G sib-mated (Green x Green)		Green	0	60				
C. monoica selfed (Green)		Green	0	38				
C. cauliflora (A) x *C. monoica* (Green x Green)		Green	0	96	0	116	0	76
C. cauliflora (A) x *C. pennata* (Green x Green)		Green	0	110			0	50

color (Nakasone, unpublished data).

Materials and Methods

We used 7 collections representing 5 species of *Carica* from 4 Central and South American countries:

1) *C. pennata* Heilborn, Svensk. Dioecious, green-stemmed species from Costa Rica.
2) *C. cauliflora* Jacq. Dioecious, green-stemmed species from El Salvador, designated as A to identify collections from 2 different sources.
3) *C. cauliflora* Jacq. Dioecious, green-stemmed species from Venezuela, designated as B.
4) *C. goudotiana* (Tr. & Pl.) Solms. Dioecious species A from Colombia with red (R) and green (G) pigmented stem types.
5) *C. goudotiana* (Tr. & Pl.) Solms. Dioecious, green-stemmed species from Venezuela, designated as B.
6) *C. monoica* Desf. Monoecious, green-stemmed species from Venezuela.
7) *C.* species No. 203. Unidentified, dioecious, red-stemmed species from Colombia.

All pollinations were made at the mature bud stage before anthesis. When *C. monoica* was used as a seed parent, all staminate flowers were stripped, leaving only the terminal pistillate buds for pollination. All pollinated buds were enclosed in small glassine bags which were tied firmly around the peduncle with the tag string.

Plants were grown in 19-liter containers on nursery benches on the Manoa Campus and in the field at the Waimanalo Experimental Farm. Field-grown plants were spaced 1.52 x 3.04 m. To minimize effects of the "replant problem" (root rot associated with *Phytophthora palmivora* Butl. and *Pythium aphanidermatum* (Edson) Fitzpatrick), the soil in the fields replanted to *Carica* was pretreated with 40 kg captan/ha. Orchard management for irrigation, fertilization, and weed and pest control followed standard papaya culture methods.

Color of flowers, stem, petiole, and fruit, and branching habit were determined visually. Fruit skin color was rated only for ripe fruits. Fruit configurations refer to the grooves and ridges delineating carpel fusion lines (11, 12). Fruit pulp in *Carica* species is either succulent (fleshy) or dry and these types are easily distinguishable.

Results and Discussion

Stem color. Progenies obtained from sib-mating and selfing any one collection were true-breeding (Table 1). Crosses between species with the same stem color also produced progenies with the same parental stem color, indicating identical genes in different species.

Crosses between red- and green-stemmed trees within and between species produced F_1 progenies with red stems (Table 2). F_2 and backcross segregations indicated that the factor for red stem color is dominant to green stem color. Chi-square tests showed close fits of the observed ratios to the theoretical 3:1 and 1:1 ratios for the F_2 and the backcross to the recessive parent, respectively.

Differences in intensity of the red color were observed in the F_1, F_2 and backcross progenies. Variations ranged from dark to light red, but in determining genetic ratios, all red-pigmented stems were combined as one group. An attempt to determine the mode of inheritance for these color variations did not show any definite pattern, probably due to difficulty in classification.

Petiole color. Crosses between species with red petioles produced plants with red petioles, while crosses between green-petioled plants produced only plants with green petioles. Crosses between red- and green-petioled species showed all F_1 hybrids with red-colored petioles (Table 3). The F_2 segregation showed a close approximation to the 3:1 ratio with genes for red-colored petiole dominant to those for green-colored petiole. The backcross to the green-colored parent produced an approximate ratio of 1:1.

All red-stemmed plants also produced red petioles but some

Table 2. Inheritance of stem color in progenies of crosses between parents of different colors.

Parents (P_1 = Red)	Parents (P_2 = Green)	F_1	No. of plants F_2 Red	F_2 Green	BC-P_1 Red	BC-P_1 Green	BC-P_2 Red	BC-P_2 Green
C. goudotiana (A) x	*C. goudotiana* (A)	red	202	62	78	0	40	36
C. goudotiana (B) x	*C. monoica*	red	78	27	–	–	–	–
C. species 203 x	*C. monoica*	red	53	21	–	–	26	30
C. goudotiana (A)R x	*C. monoica*	red	190	75	65	0	50	58
Total			523	185	143	0	116	124
Chi-square for single gene difference			0.48				0.27	
P value			0.49				0.63	

Table 3. Inheritance of petiole color in 3 crosses between red-petioled and green-petioled parents.

Parents (P_1 = Red)	(P_2 = Green)	F_1	No. of plants F_2 Red	F_2 Green	BC-P_2 Red	BC-P_2 Green
C. goudotiana (B) ×	*C. monoica*	Red	78	27	32	29
C. species 203 ×	*C. monoica*	Red	91	32	27	33
C. goudotiana (R) ×	*C. monoica*	Red	140	56	99	111
Total			309	115	159	173
Chi-square for single gene difference			1.89		0.68	
P value			0.19		0.44	

green-stemmed plants produced red-pigmented petioles. This seems to suggest that the modifier genes which control distribution of anthocyanin in the stems are different from those controlling the distribution of red color in the petiole. Erickson and Couto (3) reported a similar case in okra (*Hibiscus esculentus*). They found plants with red stems possessing red petioles and green plants with green petioles but among the green-stemmed plants, some showed red-pigmented petioles. They concluded that there were 2 dominant genes for pigmentation: 1 giving red stems and petioles and the other affecting petioles only.

Our results (Table 3) agreed with those obtained by Hofmyer (5), who reported a single, dominant gene for purple petiole color in *C. papaya.*

Flower color. Carica goudotiana (A) had purple-blush colored flowers (purple stripe on a greenish background); *C. monoica* had pale yellow flowers; while *C. cauliflora* (A) and (B), from El Salvador and Venezuela, respectively, and *C. pennata* produced white flowers. All species bred true for flower color.

The cross, *C. cauliflora* (A) x *C. monoica* (white x pale yellow), produced F_1 progeny with white flowers (Table 4). The F_2 progeny produced plants with white or yellow flowers in numbers expected on the single gene difference hypothesis (Table 4). The backcross ratios supported the monogenic inheritance hypothesis with genes for white flower color from *C. cauliflora* dominant to those for pale yellow color from *C. monoica.* Hofmyer (5) found white and yellow flower colors of *C. papaya* to be under control of a single pair of genes but, in papaya, the gene for yellow flower color was dominant over that of white. The flower color difference between *C. cauliflora* and *C. monoica* is therefore dependent on genes other than those reported in *C. papaya.*

The F_1 plants of the cross *C. goudotiana* (A)R x *C. monoica* (purple-blush x pale yellow), produced purple-blush flowers (Table 5). The F_2 segregation produced purple-blush and pale yellow flowers in proportions that showed close fit to the theoretical 3:1 ratio. The backcross ratios were as expected of monogenic inheritance with genes for purple-blush color dominant to those for pale yellow flower color.

Ripe fruit skin color. One form of *C. goudotiana* from Colombia designated as (R) has red stem and petiole and produces red-skinned fruits. The other, designated as (G), has green stem and petiole and produces yellow-skinned fruits. Since the species is dioecious, the ♂ plant could be identified by stem color only, and the fruit color was unknown. The ♂ parent selected for crossing with ♀ of both color variants possessed red stem.

Table 4. Inheritance of white and pale yellow flower colors in a cross between *C. cauliflora* (white) x *C. monoica* (yellow).

Generation	No. of plants white	yellow	Ratio white	yellow	X^2	P
F_1	63	0	1	0		
F_2	70	25	3	1	0.09	0.77
BC to *C. cauliflora*	93	0	1	0	0.00	
BC to *C. monoica*	26	28	1	1	0.47	0.49

Table 5. Inheritance of purple-blush and pale yellow flower colors in a cross between *C. goudotiana* (A) (purple-blush) x *C. monoica* (pale yellow).

Feneration	No. of plants purple	yellow	Ratio purple	yellow	X^2	P
F_1	24	0	1	0		
F_2	56	26	3	1	1.97	0.18
BC to *C. goudotiana* (A)	111	0	1	0	0.00	
BC to *C. monoica*	32	39	1	1	0.69	0.43

Table 6. Inheritance of red and yellow ripe fruit colors from sibmatings of *C. goudotiana* (A) (♂ plant was red-stemmed).

♀ parent	No. of plants red	yellow	Ratio red	yellow	X^2	P
Red-fruited	31	7	3	1	0.88	0.38
Yellow-fruited	19	25	1	1	0.82	0.39

A cross between the red-fruited ♀ and the red-stemmed ♂ produced 31 red-fruited and 7 yellow-fruited plants (Table 6). The cross between the yellow-fruited ♀ and the same ♂ parent produced 19 red-fruited and 25 yellow-fruited plants. These ratios approximate 3:1 and 1:1 segregations. Assuming that a dominant gene, *R,* was responsible for the red fruit color and its recessive allele, *r,* for the yellow fruit color, the genotypes *RR* and *Rr* will both produce red-fruited plants. The genotype of the yellow-fruited plant would be *rr* and the genotype of the red-fruited ♀ parent and the ♂ parent must have been *Rr.* It appears reasonable to conclude that the red and yellow fruit colors of *C. goudotiana* are governed by 1 allelic pair with the gene for red color dominant to that of yellow.

Table 7. Inheritance of red, pink and orange ripe-fruit colors in a cross between red-fruited *C. goudotiana* (A) and orange-fruited *C. monoica.*

Cross (generation)	No. of plants red	pink	orange	Ratio red	pink	orange	X^2	P
Red x orange (F_1)	0	21	0	0	1	0		
Pink selfed (F_2)	11	28	13	1	2	1	0.46	0.80
Pink x orange (BC–P_2)	0	35	41	0	1	1	0.47	0.79

The cross between *C. goudotiana* (red-fruited) and *C. monoica* (orange-fruited) produced F_1 plants with pink fruits (Table 7). An approximate ratio of 1 red:2 pink:1 orange was observed in the F_2. Backcrossing the F_1 to the orange-fruited parent produced orange- and pink-fruited plants in a ratio of approximately 1 orange:1 pink. Backcross to the red-fruited parent was not made because the original *C. goudotiana* ♀ parent was lost before the F_1 plants began to flower. It appears that orange vs. red fruit color is controlled by 1 pair of genes with no dominance.

Fruit configuration. We have observed 3 distinct types of fruit configurations in some *Carica* species. In *C. cauliflora* and *C. pennata* the lines occur as narrow grooves (Fig. 1). In *C. goudotiana* fusion lines occur as narrow ridges (Fig. 2), giving the fruits a markedly pentagonal shape in cross-section. In *C. monoica* and *Carica* sp. 203 the grooves are wide, shallow and barely distinguishable (see *C. monoica* in Fig. 1 and 2).

To test the homozygosity of fruit configurations, crosses were made within ridged-types, within narrow-grooved types,

and within wide-grooved types. All crosses produced their respective fruit configurations, indicating that all 3 types bred true.

The F_1 from a cross between narrow groove (*C. cauliflora*) and wide groove (*C. monoica*) produced only wide-grooved fruits like those of *C. monoica* (Table 8, Fig. 1). The F_2 population produced fruits with wide- and narrow-grooved fruits in numbers expected on the single locus hypothesis (Table 8). The segregations observed in the backcross progenies also suggest monogenic control of this character with genes for wide, shallow grooves from *C. monoica* dominant over those for narrow grooves from *C. cauliflora.*

A cross between ridge (*C. goudotiana*) and wide groove (*C. monoica*) produced F_1 plants with ridged fruits (Table 9, Fig. 2). The F_2 segregation showed a close fit to a 3:1 ratio with genes for ridge dominant to those for wide groove. Results of the backcrosses also showed monogenic control with genes for ridged configuration from *C. goudotiana* dominant to those for wide grooves from *C. monoica.* The data in Table 8 and 9 show that the gene for wide groove is dominant to that for narrow groove but the gene for the former trait is recessive to that for ridged configuration. Unfortunately, crosses between narrow

Table 8. Inheritance of narrow- and wide-grooved fruits in a cross between *C. cauliflora* (narrow grooves) and *C. monoica* (wide grooves).

Generation	No. of plants		Observed ratio		X^2	P
	wide	narrow	wide	narrow		
F_1	45	0	1	0		
F_2	75	21	3	1	0.50	0.49
BC to *C. cauliflora*	23	27	1	1	0.32	0.59
BC to *C. monoica*	39	0	1	0	0.00	

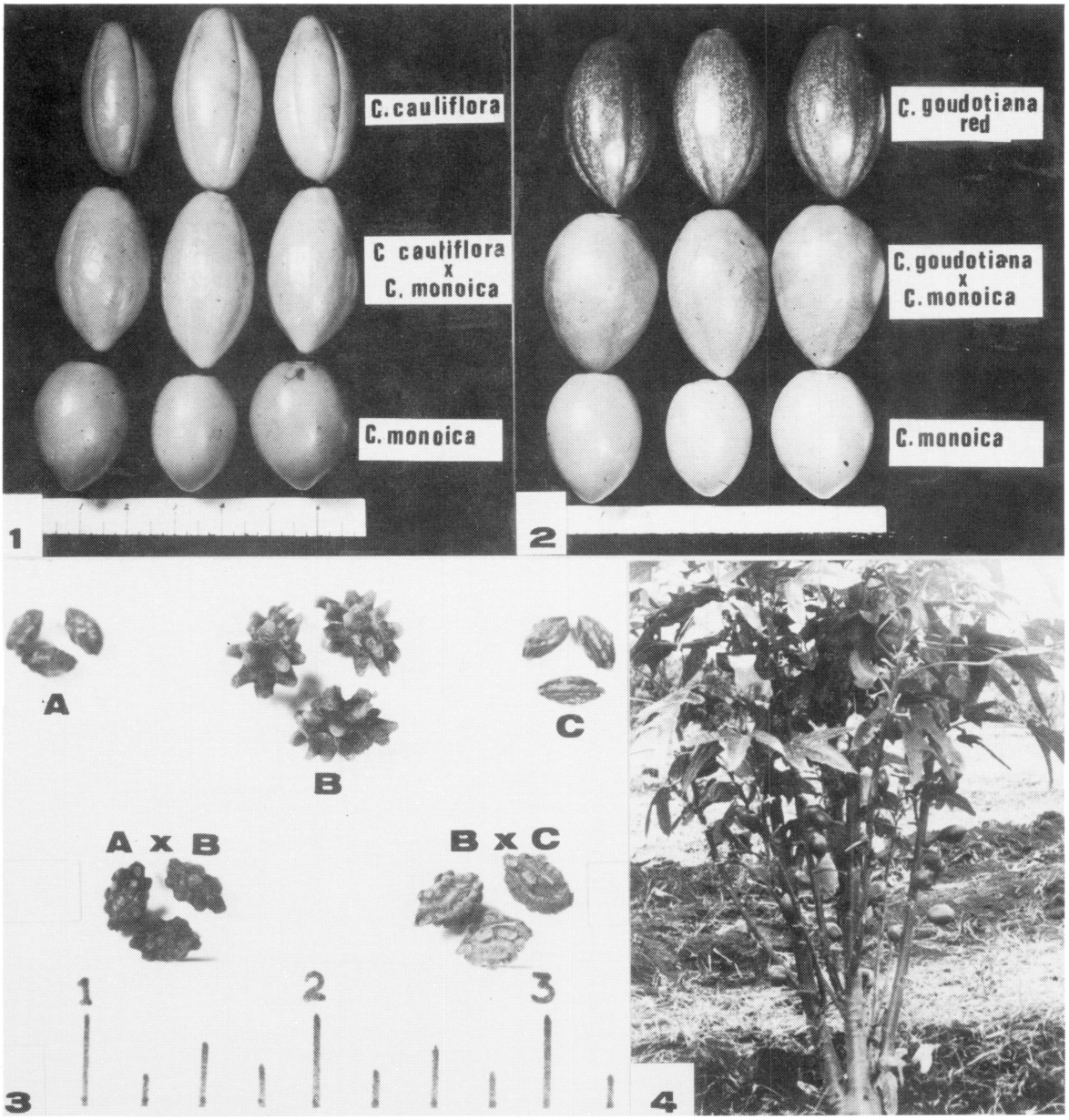

Fig. 1. Narrow-grooved fruits of *C. cauliflora;* wide, shallow; almost indistinguishable grooves of *C. monoica;* and the dominant, wide-grooved fruits of the F_1 progeny.

Fig. 2. Narrow-ridged configuration of *C. goudotiana* fruits; wide, shallow grooves of *C. monoica;* and the dominant, ridged configuration of the F_1 progeny.

Fig. 3. A and C are non-spiny seeds of *C. goudotiana* and *C cauliflora,* respectively; B shows spiny seeds of *C. monoica;* seeds with intermediate spines of F_1 hybrids, *C. goudotiana* x *C. monoica* (A x B) and *C. monoica* x *C. cauliflora* (B x C).

Fig. 4. Profuse branching characteristic of *C. monoica.*

Table 9. Inheritance of ridged and wide-grooved fruits in a cross between *C. goudotiana* (ridged) and *C. monoica* (wide-grooved).

Generation	No. of plants		Observed ratio		X^2	P
	ridged	grooved	ridged	grooved		
F_1	21	0	1	0		
F_2	37	14	3	1	0.16	0.71
BC to *C. goudotiana*	52	0	1	0	0.00	
BC to *C. monoica*	35	38	1	1	0.12	0.74

Table 10. Inheritance of succulent and dry fruit pulp in crosses involving *C. cauliflora, C. goudotiana* (both succulent pulp), and *C. monoica* (dry pulp).

Cross	F_1	F_2		BD–P_1		BC–P_2	
		Suc.	Dry	Suc.	Dry	Suc.	Dry
C. cauliflora (P_1) x *C. monoica* (P_2)	all succulent	61	25	52	0	18	20
C. goudotiana (P_1) x *C. monoica* (P_2)	all succulent	35	17	40	0	30	38
Total		96	42	92	0	48	58
Chi-square for single gene difference		2.17				0.94	
P value		0.16				0.36	

groove and ridge types could not be made due to cross incompatibility.

Pulp texture. All species except *C. monoica* produced fruits with soft, succulent pulp. That species produced fruits with dry, cottony pulp. Pulp texture was determined easily when fruits were fully ripe.

Crosses of *C. monoica* as 1 parent and 2 species with succulent pulp produced F_1 hybrids with succulent-pulped fruits (Table 10). The F_2 plants of the cross between *C. cauliflora* and *C. monoica* produced succulent pulp and dry pulp approximating the 3:1 ratio. Trees of the backcross to *C. cauliflora* (succulent) yielded fruits with all succulent pulp. The backcross to *C. monoica* (dry pulp) produced approximately equal number of plants with succulent pulp and dry pulp. A similar segregation pattern was obtained for the cross, *C. goudotiana* x *C. monoica* and the data were pooled for analysis.

The F_2 segregation ratio approximated 3 succulent:1 dry pulp and the backcross to the dry pulp parent produced a segregation approximating the 1:1 ratio. These results indicate monogenic inheritance with genes for succulent pulp dominant to those for dry pulp.

Seed coat spines. Two types of seed coat morphology were observed among the species studied. In *C. monoica* the mature seeds were covered with numerous spines or protuberances (Fig. 3B). These spines, described by Warmke et al. (13) as prominant horn-like projections, are referred to in this study as seed coat spines.

In the other species mature seeds were covered with slightly raised protuberances that gave the appearance of spines having absciced, leaving only scar-like structures. The scar-like structures were described as low, irregular protuberances (13), but the seeds are referred to here as non-spiny.

Crosses between *C. goudotiana* (non-spiny, Fig. 3A) and *C. monoica* (spiny) and between *C. cauliflora* (non-spiny, Fig. 3C) and *C. monoica* produced F_1 hybrids with spines intermediate in size between those of the parents (Table 11, Fig. 3, A x B and B x C). The F_2 populations segregated plants with spiny, intermediate, and non-spiny seeds in proportions close to the 1:2:1 ratio. The backcross to the spiny parent produced intermediate and spiny seeded plants in the 1:1 ratio. Similar ratio of intermediate and non-spiny plants was obtained from the backcross to the non-spiny parent. The data were pooled for chi-square analysis, which showed a close fit of the observed ratios to the the theoretical values and indicated a simple mode of inheritance without dominance. These results confirm those of Warmke et al. (13) in their cross, *C. goudotiana* x *C. monoica.*

Branching habit. Two forms of branching were observed among the species studied. Sparse branching, typical of *C. cauliflora,* refers to few branches (0-4 branches per plant) produced late during vegetative growth. The main stem remains dominant. Bushy branching, typified by *C. monoica,* refers to several to many branches per plant produced near the base of the main trunk (Fig. 4). Branching occurs early during vegetative growth and the branches attain the size of the main trunk.

The F_1 hybrids from the cross, *C. cauliflora* x *C. monoica,* branched profusely from the basal areas like the latter parent. The F_2 population produced plants with bushy and sparse branching closely fitting the 3:1 ratio (Table 12). The progeny of the backcross to *C. cauliflora* produced approximately equal numbers of bushy and sparsely branched trees. The backcross to *C. monoica* produced all bushy-branched plants.

These results suggest a difference of a single pair of genes

Table 11. Inheritance of spiny and non-spiny seed coats in crosses involving *C. monoica* (spiny) and *C. cauliflora* and *C. goudotiana* (both non-spiny).

Cross	F_1	No. of plants						
		F_2			BC–P_1		BC–P_2	
		Spiny	Interm	Non-spiny	Interm	Non-spiny	Spiny	Interm
C. cauliflora (P_1) x *C. monoica* (P_2)	interm	19	54	23	22	28	22	17
C. goudotiana (P_1) x *C. monoica* (P_2)	interm	10	27	14	19	23	37	29
Total		29	81	37	41	51	59	46
Chi-square for single gene difference		2.40			1.09		1.61	
P value		0.32			0.59		0.46	

Table 12. Inheritance of branching habit in a cross between *C. monoica* (bushy branching) and *C. cauliflora* (sparse branching).

Cross	Branching habit		Ratio observed		X^2	P
	bushy	sparse	bushy	sparse		
C. cauliflora x *C. monoica*	45	0	1	0		
F_2	68	27	3	1	.59	.46
BC to *C. cauliflora*	40	45	1	1	.29	.61
BC to *C. monoica*	39	0	1	0		

with bushy branching dominant to sparse branching. It appears reasonable to suggest that *C. cauliflora* possesses strong apical dominance, while *C. monoica* has weak apical dominance.

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Colonization of Almond by *Aspergillus flavus*[1]

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Abstract. **The *Aspergillus flavus* group was associated with both sound and insect damaged kernels of almond *Prunus dulcis* (Mill.) D.A. Webb during 1972 and 1973. About 1 of 2,000 sound kernels and 1 of 200 insect damaged kernels were colonized. Surface contamination was common on sound and damaged kernels. In orchard plots, spores inoculated on the fruit colonized hulls, shells, and kernels of maturing almonds. Aflatoxins were detected in harvested kernels and hulls. Almond fruits were susceptible to colonization from the time of hull-split, when rapid drying of the fruit began, until after harvest when moisture of the kernel dropped below about 5% based on the fresh weight of the kernel. Infestations by the navel orangeworm, *Paramyelois transitella* (Walker), increased colonization of the kernels by *A. flavus* from experimental plots.**

The drupe of the edible sweet almond has a distinct pericarp enclosing the kernel. This pericarp consists of an outer fleshy hull and inner hard shell. Fruits usually mature on the tree, and a longitudinal suture on one side of the hull splits exposing the shell, allowing rapid drying of the fruit. Cultivars vary in shell thickness and dehiscense (20).

Drying fruits are shaken onto the ground, picked up mechanically, transported to a location where the hulls are removed, and sent tot a plant for shelling, storing, and processing.

Many kinds of micro-organisms are found on almonds (12, 13, 14, 18) and may colonize the hull while the fruit is on the tree (14) or on the ground (12, 13).

Toxigenic species of *Aspergillus* are widespread on seed and other crops (8, 9, 10). *Aspergillus flavus* is a "group" species (16) containing 11 species. *A. flavus* Link, and *A. parasiticus* Speare both are included in this group and may produce toxic metabolites called aflatoxins. In the Central Valley of California, where most almonds are produced in the U.S., fungi in the *A. flavus* group occurs sporadically on cotton (2). Of 345 objective samples of almonds taken in the period 1970-1974, 8% had detectable aflatoxins at the average level of 20 μg/kg total aflatoxins and a range of 2-84 μg/kg (Dr. L. Stoloff, Food and Drug Admin., personal communication). These fungi may colonize almonds while they are drying on the tree or soil (6) and might lead to a pre- or postharvest invasion of kernels by *A. flavus* and contamination by aflatoxins. Preliminary information (Harry W. Schroeder, USDA, College Station, Texas, unpublished report) indicated *A. flavus* occurred on insect-damaged almonds more frequently than on sound nuts. We studied the susceptibility of the almond fruit to *A. flavus* colonization with emphasis on the role of the navel orangeworm (NOW) that commonly damages both kernel and hull.

Materials and Methods

Analysis for Aspergillus flavus. Surface disinfested and non-disinfested almond kernels, shells, or hulls were tested for presence of the *A. flavus group.* For surface disinfestation, samples were dipped in 70% (v/v) ethanol/H_2O for 10 sec, then immediately soaked in 0.5% sodium hypochlorite solution for 5 min. Without further washing, samples were then aseptically placed on plates of malt-salt medium (MSM) containing 7.5% NaCl, 2% malt extract and 2% agar. Non-disinfested samples were plated directly on MSM plus 13 μg/ml 2,6-dichloro-4-nitroaniline to inhibit growth of some *Rhizopus* spp. Five almond kernels or 5 half-shells, or 5 half-hulls were placed on each plate. After incubation for 1 week at 30°C, colonies of *A. flavus* were

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