Pruned trees consistently produced larger and heavier nuts (Table 1 and Fig. 2). Average nut volumes from pruned and unpruned trees were 0.40 and 0.32 cm³, and the average nut weights were 0.33 and 0.20 g respectively. Percent kernel was nearly the same and percent full nuts was much greater for nuts coming from pruned trees as compared to nuts from unpruned trees. Unauthorized harvesting precluded accurate determination of seed yield. However, it is doubtful that seed number was affected since primodia were initiated prior to pruning.

Basal pruning may prove to be a valuable technique for stimulating quality of piñon nut production due to an increase in nut size and decreased percentage of poor nuts. Fewer empty nuts and increased weight will reduce labor investment per unit weight of harvested seed.

Basal pruning will spare cone bearing branches in the upper crown and will remove lower branches likely to be net consumers rather than producers of energy. Pruning can be easily combined

Table 1. Effect of pruning treatment on weight, percentage kernel and percentage filling of piñon nuts.

Treatment	Avg nut wt (g/nut)	Kernel ^z (%)	Full nuts ^z (%)	
Unpruned	0.20	55	84	
Pruned	0.33**	54	99**	

²Based on 50 nut sample.

******Significantly different from unpruned at 1% level.



Fig. 2. Nut sizes from purned and unpruned piñon trees.

with other operations such as Christmas tree harvest and thinning or fuel wood cutting.

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Identification of Nucellar and Zygotic Seedlings of *Citrus* with Leaf Isozymes¹

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Abstract. The distinction between apomictic nucellar and zygotic 5-month-old seedlings of Citrus was made using two genetically defined isozyme markers: phosphoglucose isomerase and phosphoglucose mutase. Of 123 seedlings of attempted crosses of 'King' (seed parent) × 'Parsons Special', 18 had the 'King' genotype and were therefore nucellars. Segregation ratios for both markers were as expected among the zygotics.

Several economically important spe-

cies of *Citrus* either produce asexual nucellar embryos exclusively or a polyembryonic mixture of nucellar and recombinant sexual embryos (3). One of the major problems in citrus breeding is to distinguish between these while the seedlings are young (ca. 2 months). Nucellar gene combinations are already available in the seed parent and resources spent growing plants with them could be saved with early identification. Other workers (1, 2, 4, 5) have examined various biochemical characteristics in attempts to determine the genetic origin of seedling populations prior to fruiting (ca. 5 years).

Torres et al. (6) proposed that some isozymes would provide excellent single gene markers because they are colinear with the gene, codominant, little affected by the environment and are identical in leaves of young and mature plants of the same cultivated variety. The rationale for using isozymes for addressing the problem and the electrophoretic techniques were noted. The genetic control of 3 enzyme systems coded by 4 genes with 12 codominant alleles was analyzed in citrus and near relatives. Among the variable isozyme systems were phosphoglucose isomerase (PGI) and phosphoglucose mutase (PGM). The former is specified by the gene Pgi-1 and the latter by Pgm. For each enzyme, F is used to specify a fast migrating subunit, S a slow migrating subunit and I an intermediate one. The W subunit for Pgi-1 was named for the cultivar 'Willial' in which it was first

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located (6). It migrates faster than the F band.

Here we wish to show how these markers were used to analyze a 5-monthold seedling population of the polyembryonic seed parent 'King' tangor (probably C. sinensis (L.) Osbeck x C. reticulata Blanco) pollinated by 'Parsons Special' mandarin (C. reticu*lata*). The genotype of 'King' is F/Ffor Pgi-1 and F/S for Pgm (Table 1, Fig. 1), and of 'Parsons Special' is W/Sfor Pgi-I and F/I for Pgm. Note that Pgi-1 by itself could provide positive nucellar vs. zygotic identification because the presence of the isozymes specified by W or S could alone document the zygotic contribution of 'Parsons Special'. However, the 2 markers together afford an interesting double check because a seedling with the nucellar ('King') F/F genotype for Pgi-1 must always also have the F/S genotype for Pgm. Two further conditions can be predicted and tested: one is that among the zygotic seedlings the segregation ratio of W/F:F/S for Pgi-1 should be 1:1; the second is that the Pgm ratio for the F/F:F/I:F/S:S/I genotypes, after the nucellars are subtracted from the F/S class, should be 1:1:1:1. In brief, zygotic seedlings of 'King' must be either W/F or F/Sfor Pgi-1 and 1 of 4 possible Pgm genotypes. While Pgm alone could not be used to distinguish all nucellars from zygotics, any seedlings of the three Pgm genotypes, F/F, F/I or S/I, would be zygotics since they too demonstrate the gametic contribution of 'Parsons Special'.

The results of the analysis of a sample of 123 seedlings are given in Table 2. The 18 seedlings that were F/F for Pgi-1 were also, as predicted, F/S for Pgm. Thus 14.6% of the sample was undoubtedly nucellar. Of the remaining 105 seedlings we would expect half to be W/F for Pgi-1 and the other half to be F/S. The observed 61:44 ratio did

Table	1.	Pgi	-1	and	Pgm	ger	notyj	pes	of	'King	',
'Pa	rsc	ns	S	pecia	ul', i	nuce	llar	and	1	zygoti	C
see	dli	ngs.									

Parent	Genotypez			
or progeny	Pgi	Pgm		
King	F/F	F/S		
Parsons Special	Ŵ/S	$\dot{F/I}$		
Nucellar sdlgs.	F/F	F/S		
Zygotic sdlgs.	W/F, F/S	F/F, F/I F/S, S/I		

²Migration speed of subunit W>F>I>S



Fig. 1. Schematic illustration of 'King', 'Parsons Special' and the 8 zygotic phenotypes for *Pgi-1* and *Pgm*. Origin at 0, anode toward the top, *Pgi-1* genotypes below, those of *Pgm*, above.

Table 2. Genotypes of 'King' \times 'Parsons Special' seedlings.

No. of seedlings	No. of seedlings							
	Pgi-1			Pgm				
	F/F	W/F	F/S	F/F	F/I	S/I	F/S	
Observed Expected	18 ^z	61 52.5	44 52.5	26 26.25	26 26.25	24 26.25	29+18 ^z 26.25	

²Nucellar seedlings of the 'King' genotype.

not differ significantly from the expected $(\chi^2 = 2.15, p = 0.10)$. The observed segregation ratio of the *Pgm* zygotic seedling genotypes, less the 18 *F/S* nucellars (Table 2), agrees very well with the expected $(\chi^2 = 0.69, p = 0.70)$.

Older, fruiting populations of 'King' as the seed parent were identified by Frost and Soost (3) principally on morphological bases, as having 21% nucellars out of 391 plants. Our analysis shows 14.6%. Given the variable production of nucellars (3) and the likelihood that weak seedlings were not field planted in the Frost and Soost populations, the percentages are considered to be in close agreement.

This demonstration of the use of isozymes to help solve a long-standing citrus breeding problem emphasizes the importance of developing yet more markers so that young seedlings of each possible cross could be analyzed. If, for example, only Pgm markers had been available in the above case, only 62% rather than 100% of the zygotics could have been identified and which of the 47 plants with the Pgm F/S genotype were nucellars would not be determinable.

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