Family Size in Primary Trisomic Analysis

Por Ignacio Romagosa

Estación Experimental de Aula-Dei ZARAGOZA

Recibido el 24-VI-82

A B S T R A C T

ROMAGOSA, I., 1982. — Family Size in Primary Trisomic Analysis. *An. Aula Dei.* 16 (1/2): 67-94.

In the planning of any genetic experiment the minimum family size should be determined in order to minimize the total efforts, while fulfilling the objectives of the experiment. In the present study, the family size has been determined for different methods and extra chromosome transmission rates in primary trisomic analysis. The statistical criterion used was the *minimax* solution. Tables for both F_2 and backcross generation for different transmission rates and type of trisomic inheritance were developed.

A C K N O W L E D G E M E N T S

Supported by the U.S. — Spain Program of Cooperation in Science and Technology under the cooperative research project III P 3040, to whom the author acknowledges with thanks.

INTRODUCTION

Primary trisomics provide the most effective means of associating linkage groups and genes with their respective chromosomes in plants. Since there are three homologues chromosomes instead of two, the genetic ratios for genes located on these chromosomes, the so called "critical ratio", will differ from the 3:1 or 1:1 ratios found in the F_2 and backcross generation of a normal disomic heterozygous for a recessive gene. In order to minimize the total effort, the planning of any genetic experiment requires the identification of the minimum family size. This size is determined by the probability which a person is willing to accept that he or she will fail to meet the objective of the experiment. Even though reports on trisomic inheritance (BURNHAM, 1962; HERMSEM, 1970; KHUSH, 1973; TSUCHIYA, 1982) and on the adequacy of family size (MATHER, 1951; HANSON, 1959; STEEL AND TORRIE, 1981) can be found in the literature, no specific determinations of family size in primary trisomic analysis have ever been reported.

GENETIC STUDIES BY MEANS OF PRIMARY TRISOMIC ANALYSIS.

Two different methods may be used in primary trisomic analysis, depending on the generation used to study which type shows the critical ratio, namely F_2 and backcross techniques. The theoretical segregation ratios can be determined for the three types of trisomic inheritance: chromosome, chromatid and maximum equational segregations. The genetic ratios upon chromatid segregation are intermediate to those of the other two types of segregation, and therefore will not be discussed in this paper. Table 1 shows the theoretical genotypic ratios in F_2 and backcross generation for both types of mendelian genetic stocks: recessive and dominant. Phenotypic ratios for different female transmission of the extra chromosome, assuming no pollen transmission, appear in Table 2.

FAMILY SIZE IN PRIMARY TRISOMIC ANALYSIS

In primary trisomic analysis the statistical problem is to choose between two genetic, binomial, ratios, that of the critical combination and that of the standard disomic inheritance. How should we test

TABLE 1. — *Expected genotypic F_2 and backcross ratios for F_1 trisomic* for random chromosome and maximus equational segregation.*

																Backcross genotypes						
		Gametes					F_2 genotypes							Trisomic as male			Trisomic as female						
		x + 1			x		2x + 1 offspring				2x offspring			2x offspring			2x + 1 offspring				2x offspring		
F_1 genot.	Type of segreg.	AA	Aa	aa	A	a	AAA	AAa	Aaa	aaa	AA	Aa	aa	AA	Aa	aa	AAA	AAa	Aaa	aaa	AA	Aa	aa
AAa	Chromos	1	2	0	2	1	2	5	2	0	4	4	1	0	2	1	0	1	2	0	0	2	1
	Max eq	5	6	1	8	4	10	17	8	1	16	16	4	0	8	4	0	5	6	1	0	8	4
Aaa	Chromos	0	2	1	1	2	0	2	5	2	1	4	4	0	1	2	0	0	2	1	0	1	2
	Max eq	1	6	5	4	8	1	8	17	10	4	16	16	0	4	8	0	1	6	5	0	4	8

**Assumig 50% theoretical transmission, the 2x + 1 class would be equal in size to the 2x class. For other possibilities see Table 2.*

TABLE 2. —*Expected phenotypic F_2 and backcross ratios for different female transmission of the extra chromosome for F_1 trisomics under random chromosome and maximum equational segretation.*

Percent female transmission	F_2 phenotypes				Backcross phenotypes			
	AAa		Aaa		AAa		Aaa	
	Chrom.	Max. eq.	Chrom.	Max. eq.	Chrom.	Max. eq.	Chrom.	Max. eq.
	A:a	A:a	A:a	A:a	A:a	A:a	A:a	A:a
0*	8:1	8:1	1.25:1	1.25:1	2:1	2:1	0.5:1	0.5:1
10	9:1	8.73:1	1.37:1	1.34:1	2.33:1	2.24:1	0.58:1	0.56:1
20	10.25:1	9.59:1	1.50:1	1.43:1	2.75:1	2.53:1	0.67:1	0.62:1
30	11.86:1	10.61:1	1.65:1	1.54:1	3.28:1	2.87:1	0.76:1	0.69:1
40	14:1	11.86:1	1.81:1	1.65:1	4:1	3.29:1	0.88:1	0.76:1
50	17:1	13.40:1	2:1	1.77:1	5:1	3.80:1	1:1	0.85:1
100†	9:0	35:1	3.5:1	2.60:1	3:0	11:1	2:1	1.40:1
Noncritical combination	3:1	3:1	3:1	3:1	1:1	1:1	1:1	1:1

**Diploid plants.*

†*Trisomic plants, i.e., counting the ratio only in the trisomic offspring.*

against two ratios?. The criterion generally used is the X^2 test for both hypothesized ratios, accepting the genetic ratio not rejected by the test. If both hypothesis are tested, however, one may reach the wrong conclusion that either one is satisfactory. In these cases, it is clear that the sample size has been insufficient to distinguish between ratios at the chosen significance level.

MATHER (1951) discussed a criterion called the *ambiguous ratio*, for distinguishing between two ratios. First, express these ratios as 1_1:1 and 1_2:1, then the ambiguous ratio is $\sqrt{1_1 1_2}$:1. This value has the property that leads to the ambiguous segregation such that X^2 will have the same value, regardless of which ratio is proposed as the null hypothesis. Suppose that we need to distinguish the ratios 3:1 and 8:1 on the basis of 20 F_2 plants. The ambiguous ratio in $\sqrt{3x8}$:1 = 4.898:1. The dividing point of the two areas determined by the two ratios is at $[\sqrt{1_1 1_2}/(1 + \sqrt{1_1 1_2})]^n$ that is (4.898/(1+4.898))20 = 16.61. Consequently, we accept the 3:1 ratio if the potentially larger class has 16 or fewer individuals and the 8:1 if it has 17 or more. Note that for a hypothetically observed ratio of 16.61:3.39, the two X^2 would have the same value. Tested against 3:1, we would get a X^2 value of 0.691, and the X^2 in testing the 8:1 hypothesis also would be 0.691. Also note that for an observed ratio of 17:3, the two X^2 would be $X^2_{3:1}$ = 1.067 and $X^2_{8:1}$ = 0.308. They are not large enough to be rejected, $X^2_{.05,\ 1d.f.}$ = 3.84, and therefore both hypothesis would have to be accepted. Clearly, 20 is an insufficiently large sample size to distinguish between these two ratios. Mather's criterion to determine the family size was to insure that in the ambiguos region using the X^2 test, both alternative hypothesis could be rejected. For this approach it is necessary to note that we have two segregations 1_1:1 and 1_2:1 and the ambiguos ratio $\sqrt{1_1 1_2}$:1. The calculated X^2 using any of the two segregations as null hypothesis:

$$X^2_{\alpha,\ 1d.f.} = n\left(\frac{\sqrt{1_1} - \sqrt{1_2}}{1 + \sqrt{1_1 1_2}}\right)^2$$

and, then we can determine n for any significance level substituting the values of 1_1, 1_2 and $X^2_{-,\ 1d.f.}$

A very similar criterion was proposed by HANSON (1959). Like the one above, it was based on the normal approximation of the binomial distribution.

Let:

p_1 = expected proportion of the population having a certain character based on disomic inheritance.

q_1 = expected proportion of the population *not* having the character based on disomic inheritance.

p_2, q_2 = similar interpretation for the alternative, "critical ratio".

Then, n can be solved from the formula

$$t_{n-1\,d.f.} = n\left(\frac{p_1 - p_2}{p_1 q_1 + p_2 q_2}\right)$$

Where t correspondes to a one-tailed test for an probability of accepting the critical ratio when the disomic inheritance is in fact true and *vice-versa*.

However, these two criteria give sample sizes that are too large; and the probability of getting an observed ratio close to the ambigous ratio is, for the sample sizes given, very low. Also, the normal approximation, based on which, calculations were made, may yield very poor correspondence with the original binomial distribution for extreme expected ratios like the ones under consideration.

Another solution to the problem of choosing between two genetic ratios may be found in STEEL and TORRIE (1981). Since one of two genetic ratios is to be selected, two wrong decisions can be made: to decide that the first ratio is correct when the second is indeed the true value or to decide that the second is the true value when the first is correct. The probabilities of these two possible errors are fixed in advance and, then, the family size is chosen so that the probabilities are not exceeded. The method of solution, called *minimax*, is to minimize the maximum probability of an error of any kind. A detailed description of this technique can be found in STEEL and TORRIE (1981), and it is visualized in Fig. 1. This figure represents how to distinguish between the 3:1 ratio, that is a binomial distribution with $p_1 = 3/4 = 0.75$, and the 8:1 ratio, binomial distribution with $p_2 = 8/9 = 0{,}89$. The probability of obtaining exactly x individuals of the dominant class in a family of size n, is given by the probability function of the binomial distribution, $P(x) = C_x^n p^x q^{n-x}$. The probability functions for the two binomial distribution and for n = 25,50 and 75 are plotted in Fig. 1. Suppose that the true ratio is 3:1, if we obtain 21 or more individuals, and since the probabilities of obtaining these sumbers are higher for the 8:1 than for the 3.1 ratio, we wrongly accept the 8:1 ratio. The probability associated with this error is the sum of the probabilities of observing exactly 21, 22,..., 25 individuals computed from the 3:1 ratio. This probability is given by the light dotted area in Fig. 1, and it has a value of P = 0.22. Now suppose that the true ratio is 8:1. If we obtain 20 or fewer individuals with dominant pre-

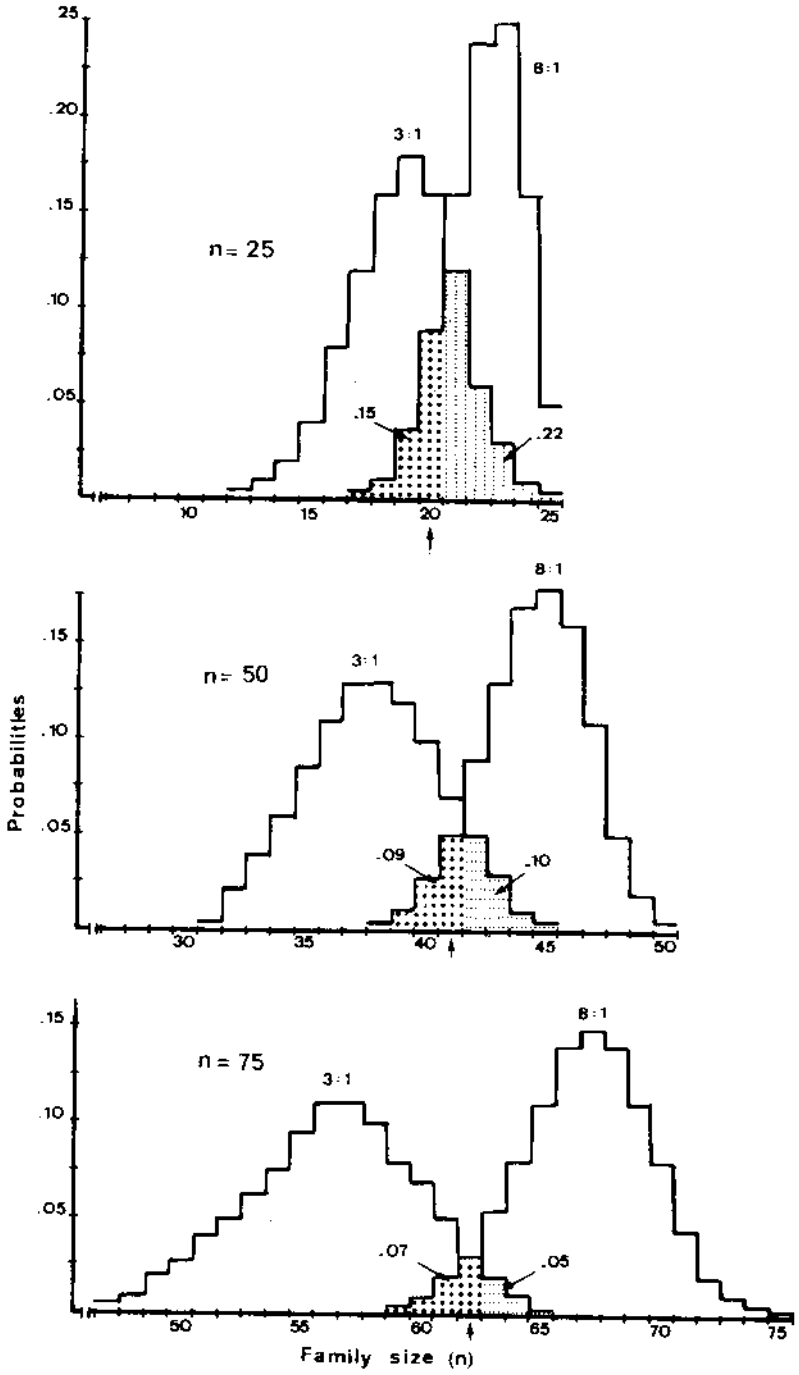

FIG. 1. —Binomial probability distributions for the 3:1, disomic, and 8:1, critical, ratios for different family size, n. Dotted areas correspond to Type I and II errors.

notype, we wrongly accept the 3:1 ratio. The probability of this kind of error is the sum of the probabilities of observing exactly 20, 19,..., 1,0 individuals of the dominant class which is the area marked by the bigger dots in Fig. 1, and it is exactly P = 0.15. It is clear in Fig. 1, that when n increases, the probability of making an error, area intersected by the two distributions, decreases very rapidly. According to the "minimax" criterion the maximum probabilities of an error of any kind in Fig. 1 are P = 0.22, 0.10, and 0.07 for n = 25, 50 and 75 respectively.

Here we will determine, based on this latter criterion, the regions of acceptance for the two genetic ratios, critical and disomic ratios, for the different methods and female transmissions, together with the probabilities of making a wrong decision about which hypothesis is true. These values appear in Tables 3, which give information *a priori* about the family size and *a posteriori*, once the experiment is performed, about the decision to make whether or not accept the critical ratio, and the extreme probability of making a wrong decision.

To ilustrate their use, consider Table 3a to distinguish between the genetic ratios 3:1 and 8:1, that is the critical (trisomic) and noncritical (disomic) ratios among diploid plants of the F_2 generation when the mutant is recessive. If the population size is 50, accept the noncritical combination (3:1) if 0-41 observations fall in the potentially larger group. If this group, plants with A- phenotype, contains 42-50 accept the critical combination (8:1) and assign the specific gene to that specific chromosome. At worst, one would be in error 10% of the time; this would be the case if data were always from the critical combination. If the true ratio were 3:1, on the average by chance we would have 41 plants of the A- phenotype 9% of the time.

Tables 4a,b,c give a summary of Tables 3, giving the minimum family size of the F_2 and backcross generation for an admissible error size of 0.10, 0.05 and 0.01. Table 4c gives the minimum family size, regardless of the type of chromosome segregation. For example, if the transmission of the extra chromosome to the next generation is 50% and we want to study the backcross generation when the mutant is recessive, and for an = 0.05, we need at least 30 plants.

FAMILY SIZE AND METHOD TO BE USED

If the trisomic plants show good pollen fertility and especially if male sterile genetic stocks are available, the backcross method using the trisomic F_1 as male, has an advantage in that no chromosome

TABLE 3a. —*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 8:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
10	3:1	0-8	0.24
	8:1	9-10	0.30
20	3:1	0-16	0.23
	8:1	17-20	0.18
30	3:1	0-24	0.20
	8:1	25-30	0.11
40	3:1	0-33	0.10
	8:1	34-40	0.15
50	3:1	0-41	0.09
	8:1	42-50	0.10
60	3:1	0-49	0.09
	8:1	50-60	0.06
70	3:1	0-57	0.08
	8:1	58-70	0.04
80	3:1	0-66	0.07
	8:1	67-80	0.03
90	3:1	0-74	0.04
	8:1	75-90	0.04
100	3:1	0-82	0.04
	8:1	83-100	0.03
110	3:1	0-91	0.02
	8:1	92-110	0.03
120	3:1	0-99	0.02
	8:1	100-120	0.02
130	3:1	0.107	0.02
	8.1	108-130	0.02
140	3:1	0-115	0.02
	8:1	116-140	0.01
150	3:1	0-124	0.01
	8:1	125-150	0.01

* Expected critical combination for the diploids in the F_2 of trisomic x recessive marker gene.

Mather's coefficient = 0.8305.

TABLE 3b.—*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 17:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
10	3:1	0-8	0.24
	17:1	9-10	0.10
15	3:1	0-13	0.08
	17:1	14-15	0.20
20	3:1	0-17	0.09
	17:1	18-20	0.10
25	3:1	0-21	0.10
	17:1	22-25	0.05
30	3.1	0-26	0.04
	17:1	27-30	0.08
35	3:1	0-30	0.04
	17:1	31-35	0.04
40	3:1	0-34	0.04
	17:1	35-40	0.02
45	3:1	0-39	0.02
	17:1	40-45	0.04
50	3:1	0-43	0.02
	17:1	44-50	0.02
55	3:1	0-47	0.02
	17:1	48-55	0.01
60	3.1	0-52	0.01
	17.1	53-60	0.02
65	3:1	0-56	0.01
	17:1	57-65	0.01

* Expected critical combination for a 50% female transmission in the F_2 of trisomic x recessive marker gene upon chromosome segregation. Mather's coefficient = 0.8772.

TABLE 3c.—*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 9:0 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
2	3:1	0-1	0.00
	9:0	2	0.56
4	3:1	0-3	0.00
	9:0	4	0.32
6	3:1	0-5	0.00
	9:0	6	0.18
8	3:1	0-7	0.00
	9:0	8	0.10
10	3:1	0-9	0.00
	9:0	10	0.06
12	3:1	0-11	0.00
	9:0	12	0.03
14	3:1	0-13	0.00
	9:0	14	0.02
16	3:1	0-15	0.00
	9:0	16	0.01

* Expected critical combination for de trisomics in the F_2 of trisomic x recessive marker gene upon chromosome segregation.

Mather's coefficient = 1.0000.

TABLE 3d.—*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 13.4:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
10	3:1	0-8	0.24
	13.4.1	9-10	0.15
20	3:1	0-17	0.09
	13.4:1	18-20	0.16
30	3:1	0-25	0.10
	13.4:1	26-30	0.05
40	3:1	0-34	0.04
	13.4:1	35-40	0.06
50	3:1	0-42	0.05
	13.4:1	43-50	0.02
60	3:1	0-51	0.02
	13.4:1	52-60	0.02
70	3:1	0-59	0.02
	13.4:1	60-70	0.01
80	3:1	0-68	0.01
	13.4:1	69-80	0.01

* Expected critical combination for a 50% female transmission the F_2 of trisomic x recessive marker gene upon maximum equational separation (m.e.s.).

Mather's coefficient = 0.8638.

TABLE 3e. —*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 35:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
5	3:1	0-4	0.24
	35:1	5	0.13
10	3:1	0-8	0.24
	35:1	9-10	0.03
15	3:1	0-13	0.08
	35:1	14-15	0.06
20	3:1	0-17	0.09
	35:1	18-20	0.02
25	3:1	0-22	0.03
	35:1	23-25	0.03
30	3:1	0-27	0.03
	35:1	28-30	0.01
35	3:1	0-31	0.01
	35:1	32-35	0.02
40	3:1	0-35	0.02
	35:1	36-40	0.01
45	3:1	0-40	0.01
	35:1	41-45	0.01

* Expected critical combination for the trisomics in the F_2 of trisomic x recessive marker gene upon m.e.s.

Mather's coefficient = 0.9111.

TABLE 3f. —*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 5:4 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
10	5:4	0-6	0.28
	3:1	7-10	0.22
20	5:4	0-13	0.14
	3:1	14-20	0.21
30	5:4	0-19	0.15
	3.1	20-30	0.11
40	5:4	0-26	0.09
	3:1	27-40	0.10
50	5:4	0-32	0.09
	3:1	33-50	0.06
60	5:4	0-39	0.05
	3:1	40-60	0.05
70	5:4	0-46	0.03
	3:1	47-70	0.05
80	5:4	0-52	0.03
	3:1	53-80	.0.03
90	5:4	0-59	0.02
	3:1	60-90	0.03
100	5:4	0-65	0.02
	3:1	66-100	0.02
110	5:4	0-72	0.01
	3:1	73-110	0.02
120	5:4	0-78	0.01
	3:1	79-120	0.01

*Expected critical combination for diploids in the F_2 of trisomic x dominant marker gene.

Mather's coefficient = 0.6595.

TABLE 3g. —*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 2:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
20	2:1	0-14	0.30
	3:1	15-20	0.38
60	2:1	0-42	0.24
	3:1	43-60	0.22
100	2:1	0-70	0.20
	3.1	71-100	0.15
140	2:1	0-99	0.13
	3:1	100-140	0.14
180	2:1	0-127	0.12
	3:1	128-180	0.10
220	2:1	0-156	0.08
	3:1	157-220	0.09
260	2:1	0-184	0.07
	3:1	185-260	0.07
300	2:1	0-212	0.06
	3:1	213-300	0.05
340	2:1	0-241	0.04
	3:1	242-340	0.04
380	2.1	0-270	0.04
	3.1	271-380	0.04
420	2:1	0-298	0.03
	3:1	299-420	0.03
500	2:1	0-355	0.02
	3:1	356-500	0.02
540	2:1	0-383	0.02
	3:1	384-540	0.02
580	2:1	0-411	0.01
	3:1	412-580	0.01

*Expected critical combination for a 50% female transmission in the F_2 of trisomic x recessive marker gene upon chromosome segregation. Mather's coefficient = 0.7101.

TABLE 3h.—*Family size and the probability of making a wrong decision between the 3:1 F_2 disomic ratio and the 1.77:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
20	1.77:1	0-13	0.38
	3:1	14-20	0.21
40	1.77:1	0-27	0.26
	3:1	28-40	0.18
60	1.77.1	0-41	0.20
	3:1	42-60	0.15
80	1.77:1	0-55	0.15
	3.1	56-80	0.12
100	1.77:1	0-69	0.12
	3:1	70-100	0.10
120	1.77.1	0-83	0.10
	3:1	84-120	0.09
140	1.77.1	0-97	0.08
	3:1	98-140	0.07
160	1.77:1	0-111	0.06
	3:1	112-160	0.06
180	1.77:1	0-125	0.05
	3:1	126-180	0.07
200	1.77.1	0-139	0.04
	3:1	140-200	0.04
220	1.77.1	0-153	0.03
	3.1	154-220	0.04
240	1.77:1	0-167	0.03
	3:1	168-240	0.03
260	1.77:1	0-181	0.02
	3:1	182-260	0.03
280	1.77:1	0-195	0.02
	3:1	196-280	0.02
300	1.77:1	0-209	0.02
	3:1	210-300	0.02
320	1.77:1	0-223	0.01
	3.1	224-320	0.02
340	1.77.1	0-237	0.01
	3:1	238-340	0.01

*Expected critical combination for a 50% female transmission in the F_2 of trisomic x dominant marker gene upon m. e. s.

Mather's coefficient = 0.6974.

TABLE 3i. —*Family size and the probability of making a wrong decision between the 1:1 disomic backcross ratio and the 2:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
10	1:1	0-6	0.17
	2.1	7-10	0.44
20	1:1	0-11	0.25
	2:1	12-20	0.19
30	1:1	0-17	0.18
	2:1	18-30	0.17
40	1.1	0-23	0.13
	2.1	24-40	0.14
50	1:1	0-29	0.10
	2.1	30-50	0.13
60	1:1	0-35	0.08
	2:1	36-60	0.11
70	1.1	0-41	0.06
	2:1	42-70	0.10
80	1:1	0-46	0.07
	2:1	47-80	0.07
90	1:1	0-52	0.06
	2:1	53-90	0.05
100	1:1	0-58	0.05
	2:1	59-100	0.04
110	1:1	0-64	0.04
	2.1	65-110	0.04
120	1:1	0-70	0.03
	2:1	71-120	0.03
130	1:1	0-76	0.02
	2.1	77-130	0.03
140	1:1	0-82	0.02
	2.1	83-140	0.03
150	1:1	0-87	0.02
	2.1	88-150	0.02
160	1:1	0-93	0.02
	2:1	94-160	0.01
170	1:1	0-99	0.01
	2:1	100-170	0.01

*Expected critical combination for (1) diploids the BC1 generation of trisomic x recessive marker genes and (2) trisomics in the BC1 generation of trisomic x dominant marker genes upon chromosome segregation.

Mather's coefficient = 0.5858.

TABLE 3j. —*Family size and the probability of making a wrong decision between the 1:1 disomic backcross ratio and the 5:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
5	1:1	0-3	0.19
	5:1	4-5	0.19
10	1.1	0-6	0.17
	5:1	7-10	0.07
15	1:1	0-10	0.06
	5:1	11-15	0.09
20	1:1	0-13	0.06
	5:1	14-20	0.04
25	1:1	0-17	0.02
	5.1	18-25	0.04
30	1:1	0-20	0.02
	5:1	21-30	0.02
35	1:1	0-23	0.02
	5:1	24-35	0.01
40	1:1	0-27	0.01
	5.1	28-40	0.01

*Expected critical combination for a 50% female transmission in the BC1 generation of a trisomic x recessive marker gene upon chromosome segregation.

Mather's coefficient = 0.6910.

TABLE 3k.—*Family size and the probability of making a wrong decision between the 1:1 disomic backcross ratio and the 3:0 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
2	1:1	0-1	0.00
	3:0	2	0.25
4	1:1	0-3	0.00
	3:0	4	0.06
6	1:1	0-5	0.00
	3:0	6	0.02
8	1:1	0-7	0.00
	3:0	8	0.01

*Expected critical combination for trisomic transmission in the BC1 generation of a trisomic x recessive marker gene upon chromosome segregation.

Mather's coefficient = 1.0000.

TABLE 31. —*Family size and the probability of making a wrong decision between the 1:1 disomic backcross ratio and the 3.8:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
10	1:1	0-6	0.17
	3.8:1	7-10	0.14
15	1:1	0-9	0.15
	3.8:1	10-15	0.07
20	1:1	0-13	0.06
	3.8:1	14-20	0.10
25	1:1	0-16	0.05
	3.8:1	17-25	0.06
30	1:1	0-19	0.05
	3.8:1	20-30	0.03
35	1:1	0-22	0.04
	3.8:1	23-35	0.02
40	1:1	0-26	0.02
	3.8:1	27-40	0.03
45	1:1	0-29	0.02
	3.8:1	30-45	0.02
50	1:1	0-32	0.02
	3.8:1	33-50	0.01
55	1:1	0-36	0.01
	3.8:1	37-55	0.01

*Expected critical combination for a 50% female transmision in the BC1 generation of a trisomic x recessive marker gene upon m. e. s. Mather's coefficient = 0.6609.

TABLE 3m.—*Family size and the probability of making a wrong decision between the 1:1 disomic backcross ratio and the 11:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
2	1.1	0-1	0.25
	11:1	2	0.16
4	1:1	0-3	0.06
	11:1	4	0.29
6	1:1	0-4	0.10
	11.1	5-6	0.08
8	1:1	0-6	0.04
	11:1	7-8	0.14
10	1:1	0-7	0.05
	11:1	8-10	0.04
12	1:1	0-8	0.02
	11:1	9-12	0.07
14	1:1	0-10	0.03
	11:1	11-14	0.03
16	1.1	0-11	0.01
	11.1	12-16	0.04
18	1:1	0-13	0.02
	11:1	14-18	0.01
20	1:1	0-15	0.01
	11:1	16-20	0.02
22	1:1	0-16	0.01
	11:1	17-22	0.01

*Expected critical combination for trisomics in the BC1 generation of a trisomic x recessive marker gene upon m. e. s.

Mather's coefficient = 0.7683.

TABLE 3n.—*Family size and the probability of making a wrong decision between the 1:1 disomic backcross ratio and the 0.5:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
10	0.5:1	0-3	0.44
	1:1	4-10	0.17
20	0.5:1	0-8	0.19
	1:1	9-20	0.25
30	0.5:1	0-12	0.17
	1:1	13-30	0.18
40	0.5:1	0-16	0.14
	1:1	17-40	0.13
50	0.5:1	0-20	0.13
	1:1	21-50	0.10
60	0.5:1	0-24	0.11
	1:1	25-60	0.08
70	0.5:1	0-28	0.10
	1:1	29-70	0.06
80	0.5:1	0-33	0.07
	1:1	34-80	0.07
90	0.5:1	0-37	0.05
	1:1	38-90	0.06
100	0.5:1	0-41	0.04
	1:1	42-100	0.05
110	0.5:1	0-45	0.04
	1:1	46-110	0.04
120	0.05:1	0-49	0.03
	1:1	50-120	0.03
130	0.5:1	0-53	0.03
	1:1	54-130	0.02
140	0.5:1	0-58	0.02
	1:1	59-140	0.03
150	0.5:1	0-62	0.02
	1:1	63-150	0.02
160	0.5:1	0-66	0.01
	1:1	67-160	0.02
170	0.5.1	0-70	0.01
	1:1	71-170	0.01

*Expected critical combination for diploids in the BC1 generation of a trisomic x dominant marker gene.

Mather's coefficient = 0.4142.

TABLE 3o.—*Family size and the probability of making a wrong decision between the 1:1 disomic backcross ratio and the 1.4:1 critical combination*.*

Family size n	*Ratio accepted*	*Classes in regions of acceptance*	*Probabily of making a wrong decision*
50	1:1	0-27	0.24
	1.4:1	28-50	0.31
100	1:1	0-54	0.18
	1.4.1	55-100	0.22
150	1:1	0-81	0.14
	1.4:1	82-150	0.16
200	1.1	0-108	0.12
	1.4:1	109-200	0.12
250	1:1	0-135	0.09
	1.4.1	136-250	0.09
300	1:1	0-162	0.07
	1.4:1	163-300	0.07
350	1:1	0-190	0.05
	1.4:1	191-350	0.07
400	1:1	0-216	0.05
	1.4:1	217-400	0.04
450	1:1	0-244	0.04
	1.4:1	245-450	0.03
500	1:1	0-270	0.03
	1.4:1	271-500	0.03
550	1:1	0-298	0.02
	1.4.1	299-550	0.03
600	1:1	0-325	0.02
	1.4:1	326-600	0.02
650	1:1	0-351	0.02
	1.4:1	352-650	0.02
700	1:1	0-379	0.01
	1.4:1	380-700	0.01

*Expected critical combination for trisomics in the BC1 generation of trisomic upon m. e. s.

Mather's coefficient = 0.5420.

TABLE 4a.—*Minimum family size in the F_2 generation for an probability of making a wrong decision in primary trisomic analysis for two types of trisomic inheritance.*

Female transmission	F_1 genotypes											
	AAa						Aaa					
	Chromosome segregation			Maximum equational separation			Chromosome segregation			Maximum equational separation		
	A:a	α	N	A:a	α	N	A:a	α	N	A:a	α	N
0*	8:1	0.10	50	8:1	0.10	50	1.25:1	0.10	40	1.25:1	0.10	40
		0.05	90		0.05	90		0.05	60		0.05	60
		0.01	150		0.01	150		0.01	120		0.01	120
50	17:1	0.10	25	13.4:1	0.10	30	2:1	0.10	220	1.77:1	0.10	120
		0.05	35		0.05	50		0.05	320		0.05	200
		0.01	65		0.01	80		0.01	580		0.01	340
100†	9:0	0.10	8	35:1	0.10	15	3.5:1	0.10	>1000	2.6:1	0.10	>1000
		0.05	12		0.05	25		0.05	>1000		0.05	>1000
		0.01	16		0.01	45		0.01	>1000		0.01	>1000
Noncritical combination	3:1			3:1			3:1			3:1		

**Diploid plants.*

†*Trisomic plants.*

TABLE 4b.—*Minimum family size in the BC1 generation for an a probability of making a wrong decisión in primary trisomic analysis for two types of trisomic inheritance.*

	F_1 genotypes											
	AAa						Aaa					
	Chromosome segregation			Maximum equational separation			Chromosome segregation			Maximum equational separation		
Female transmission	A:a	α	N	A:a	α	N	A:a	α	N	A:a	α	N
0*	2:1	0.10	70	2:1	0.10	70	1:2	0.10	70	1:2	0.10	70
		0.05	100		0.05	100		0.05	100		0.05	100
		0.01	170		0.01	170		0.01	170		0.01	170
50	5:1	0.10	15	3.8:1	0.10	20	1:1	0.10	--	0.85:1	0.10	>1000
		0.05	25		0.05	30		0.05	--		0.05	>1000
		0.01	40		0.01	55		0.01	--		0.01	>1000
100†	3:0	0.10	4	11:1	0.10	6	2:1	0.10	70	1.4:1	0.10	250
		0.05	6		0.05	10		0.05	100		0.05	400
		0.01	8		0.01	22		0.01	170		0.01	700
Noncritical combination	1:1			1:1			1:1			1:1		

**Diploid plants.*
†Trisomic plants.

TABLE 4c.—*Minimum family size in the backcross and F_2 generations for an a probability of making a wrong decision in primary trisomic analysis regardless of the type of trisomic inheritance.*

		N			
		F_2 generation		Backcross	
Female transmission	*a*	*AAa*	*Aaa*	*AAa*	*Aaa*
0*	0.10	50	40	70	40
	0.05	90	60	100	100
	0.01	150	120	170	170
50	0.10	30	220	20	>1000
	0.05	50	320	30	>1000
	0.01	80	580	55	>1000
100**	0.10	15	>1000	6	250
	0.05	25	>1000	10	400
	0.01	45	>1000	22	700

*Diploid plants.
**Trisomic plants.

counts are necessary in the backcross generation. Since transmission of the extra chromosome through the pollen is very low for most species (ROMAGOSA, 1982), most, if not all, plants are diploid; and the expected critical combination, depending on the F_1 genotype, will be 2.1 or 1:2, different from the 1:1 disomic noncritical ratio. Table 3i list the family size necessary to distinguish between these two ratios, n should be greater than 70, 100 and 170 for a = .10, 0.05 and 0.01 respectively. However, in some species the trisomic plants do not show good pollen fertility or the presence of self-fertile genetic stocks may result in poor hybrid seed set. In these cases the amount of seed needed to distinguish between the two ratios may be too high.

The F_2 method has an advantage in that no crossing after the initial hybridizations is needed. If the genetic stock is recessive, i.e. the F_1 trisomic genotype is AAa, then no chromosome counts are needed. A minimum of 50, 90 and 150 plants (Table 4c) are needed for a = 0.10, 0.05 and 0.01 respectively. In the case where the genetic stock is dominant, i.e. F_1 genotype Aaa, then chromosome counts are needed to distinguish between the critical and noncritical combination.

The backcross method using the trisomic as female has to be used when the F_1 trisomic is male sterile or it presents very low pollen fertility. It requires a second hybridization with the double recessive genotype. It does not have any apparent advantage or disadvantage as far as family size is concern with the F_1 method. Its use will be given by other factors as the one cited above.

RESUMEN

En el diseño de cualquier experimento genético, se debe determinar el tamaño mínimo de las familias que permita, minimizando el esfuerzo total, alcanzar los objetivos previstos. Utilizando el criterio estadístico "minimax" se han calculado los tamaños de familia mínimos en la localización de genes mediante trisómicos primarios.

REFERENCES

GURNHAM, C. R.
1962 Discussions in Cytogenetics. *Burgess, Minneapolis*. 375 pp.

HANSON, W. D.
1959 Minimum family sizes for the planning of genetic experiments. *Agron. J.* 51:711-715.

HERMSEN, J. G. Th.
1970 Basic information for the use of primary trisomics in genetic and breeding research. *Euphytica* 19:125-140.

KHUSH, G. E.
1973 Cytogenetics of Aneuploids. *Academic Press, New York*. 301 pp.

MATHER, K.
1951 The Measurements of Linkage in Heredity. *Methuen, London*. 131 pp.

ROMAGOSA, I.
1982 Primary Trisomics in Sugarbeet. PhD. Dissertation. *Colorado State University, Fort Collins*.

STEEL, R. G. and J. H. TORRIE
1981 Principles and Procedures of Statistics. A Biometrical Approach. *McGraw-Hill, New York*. 633 pp.

TSUCHIYA, T.
1982 Aneuploidy and Chromosome Mapping in Barley. *In press*.