Primary Trisomic Series: Theoretical Sample Size

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ABSTRACT

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A theoretical sample size needed to isolate all different trisomic types is developed. Calculations are based on equal transmission of gametes with different extra chromosome. The probability of all types being isolated in a sample of size n, in a species with haploid chromosome number r, is given by the formula:

$$P(\bar{B}) = 1 - \sum_{i=1}^{r} (-1)^{i-1} C_i^r (1 - i/r)^n$$

Probabilities of obtaining all primary trisomic types as a function of the sample size for species with haploid chromosome number ranging from 6 to 12 are determined.

ACKNOWLEDGEMENTS

INTRODUCTION

In the process of isolating a complete series of primary trisomics from progenies of triploids, one question of interest is to determine what size population of trisomics is needed for isolation of all types. For this calculation some unproven assumptions must be made. It is reasonable to assume that the frequency of gametes with one extra chromosome is approximately equal for all chromosomes. This would result from random anaphase I distribution to the poles of the chromosomes of the third genome of the triploid. Most plant species studied showed random anaphase I assortments (BALOG, 1979, RO-MAGOSA, 1980). However, it is not known whether the effect of the extra chromosome in gamete function or zygote survival is the same for all types. There are some indications that the transmission depends on each specific chromosome in plant species, such as maize, tomato, barley (KHUSH, 1973). If the transmission freguencies are very different for some types, the estimated sample size will not be large enough to assure the presence of all types with any given probability. The calculated sample size would be minimum when the frequencies of the different trisomic types are all the same. Therefore, the given sample size is a lower bound of that required at any probability level. The same methodology could also be applied directly to other sources of trisomics or to the isolation of addition lines and so forth.

PROCEDURE

Let n = number of trisomic plants isolated from progenies of triploid or from any other source, r = maximum number of primary trisomic types for a given species. Therefore, $r = x$ haploid chromosome number and p_i = probability of a specific type i. It is assumed hereafter that $p_i = 1/r$, equal frequency for all types. Let us first determine the probability of B when at least one trisomic type is not present in the sample. B is a function of the A_i's, where A_i is the event of type i not present. Thus,

$$B = \bigcup_{i=1}^{r} A_i$$

Note that the A_i's are not disjointed events, since $A_i \cap A_j = A_{ij} \neq \phi$, where A_{ij} represents the event of both trisomic types i and j not present.

$$P(B) = P\left(\bigcup_{i=1}^{r} A_i \right) =$$

$$= \sum_{\substack{i=1}}^{r} P(A_i) - \sum_{\substack{i=1 \\ i \neq j}}^{r} \sum_{j=1}^{r} P(A_{ij}) + \sum_{\substack{i=1 \\ i \neq j}}^{r} \sum_{\substack{j=1 \\ i \neq k}}^{r} \sum_{\substack{k=1 \\ j \neq k}}^{r} P(A_{ijk}) - \ldots =$$

$$= \sum_{i=1}^{r} (-1)^{i-1} S_i \quad ,$$

where S_i is the probability of the intersection of i *events*; i varies from 1 to r.

$$S_i = C_i^r \; P(A_{1\ldots i})$$

The probability of at least i types not present, $P(A_{1\ldots i})$, can be expressed as

$$P(A_{1\ldots i}) = \left[\frac{r - i}{r} \right]^n = (1 - i/r)^n$$

Therefore,

$$P(B) = \sum_{i=1}^{r} (-1)^{i-1} S_i = \sum_{i=1}^{r} (-1)^{i-1} C_i^r (1 - i/r)^n$$

If the probability of all trisomic types present in a sample is needed, n should be substituted in the following formula:

$$P(\bar{B}) = 1 - P(B) = 1 - \sum_{i=1}^{r} (-1)^{i-1} S_i = 1 - \sum_{i=1}^{r} (-1)^{i-1} C_i^r (1 - i/r)^n$$

The sample size for a given probability is also given by the solution of the above equation. This equation is plotted for different values of r and n in Fig. 1. It is obvious that for values of $n < r$, the probability of having all types is zero. The theoretical sample size for a given probability level or the probability at a given sample size can be easily found by interpolation.

R E S U M E N

Se determina el tamaño teórico de muestra necesario para aislar todos los grupos de trisómicos primarios de una especie. Los cálculos se basan en una frecuencia de transmisión del extra cromosoma idéntica para todos los grupos. La probabilidad de obtener todos los tipos trisómicos en una muestra de tamaño n, para una especie de número cromosómico haploide r viene dada por la expresión:

$$P(\bar{B}) = 1 - \sum_{i=1}^{r} (-1)^{i-1} C_i^r (1 - i/r)^n$$

La probabilidad de obtener todos los grupos trisómicos primarios en función del tamaño de la muestra está calculada para especies con número cromosómico haploide 6 hasta 12.
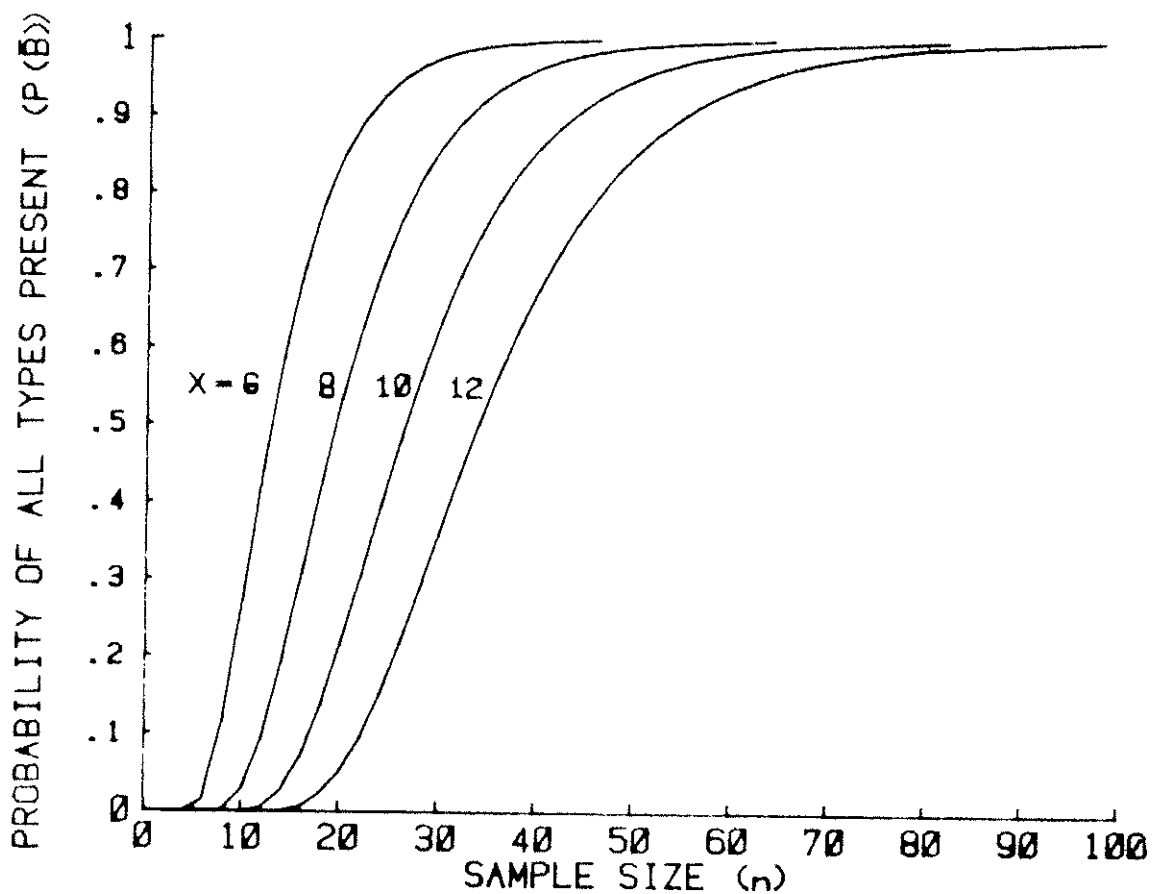
FIG. 1. --Probability of obtaining all primary trisomic types as a function of the sample size and the haploid chromosome number (x).

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