NOTAS BREVES

CHROMOS: A COMPUTER PROGRAM FOR THE MORPHOLOGICAL CHARACTERIZATION OF CHROMOSOMES.

CHROMOS: UN PROGRAMA DE ORDENADOR PARA LA CARACTERIZACIÓN MORFO-LÓGICA DE LOS CROMOSOMAS.

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The general studies in cytogenetics are centered on the correct characterization of the species chromosomes, in view of describing their organization in homologous pairs. It can be attained by using the external characteristics of the chromosomes with morphometrical criteria (chromosome's number, form and lengths).

In this subject the computers are giving us great help. We find described several programs adjusted to the standard methodology followed in the cytogenetic laboratories for the mathematical treatment of the chromosome lengths.

Since the 1960's, the literature which concerns the chromosome analysis in the morphometrical aspects, has been widely available (Ledley, 1964 and Gilbert, 1966). The most recently published and more complexly developed are the Maggurk and Rivlin program (1983) and the Green *et al.* Chrompack III (1984). Both are very similar, in that they incorporate the use of digitizers and operate in APPLE system.

In the present paper we offer an improved computer program of easy use, operative in IBM and compatibles, that aport as principal characteristics its simple management and its functionality in this widely distributed system, moreover which is opened to standard statistical and graphic programs across a data base, and is completely adjusted to the cytogenetic methodology in the morphometrical analysis. Our program does not precise special inversions in software infrastructure, because of it is operative in the most widely distributed computers in Europe.

This program works with the chromosome arm lengths submitted by the operator, only one, for the acrocentric chromosomes, and two for biarmed (longer arm length and shorter arm length). These lengths are measured on microphotographs using the standard method with precision calipers.

The program presents three beginning modules: The first for metaphases which presents only acrocentric chromosomes, the second for metaphases where monoarmed and biarmed chromosomes are present and are defined, and the third for metaphases which presents undefined mono and

biarmed chromosomes.

The third module categorizes the chromosomes into acrocentric, telocentric, subtelocentric, submetacentric and metacentrics, following the recommendations of Levan *et al.* (1964), attending to the arm ratio. Here the program sequences the chromosomes from largest to smallest within the categories.

The program calculate, whatever the module, the relative lengths with respect to the haploid or diploid complement. These relative lengths are obtained with a view to neutralize the "metaphase state" effect (early or late metaphase) upon the chromosome length. With the relative lengths, a normalized variable is obtained, which permits the use of statistical normality test in the investigation of the specie karyotypes.

The program have two output possibilities, to a printer, or to a data base for the accumulation of several metaphase data, in order to the posterior application of standard statistical programs.

We offer a copy of this program, with instructions, without charge, in the form of diskette, providing us with one (5 1/4" or 3 1/2").

References

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