Commentary

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Standard nomenclature applies to cell lines too

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The recent report by Henderson et al. (1981) raises a number of issues that are of general concern to cytogeneticists. Foremost among these is a question of nomenclature: how to refer to specific chromosomes in cell lines. The authors have referred to the chromosomes in mouse L-cells in a line-specific manner, i.e., LT1-LT9 and L10-L34. Their table listing possible homologies with normal mouse chromosomes suggests some uncertainty in their identification of particular chromosomes, but that is not of such general concern as the introduction of a totally new system of nomenclature. Their system serves to emphasize the uniqueness of each independently derived hetero-ploid cell line and the possibility that some of the chromosomes have undergone structural changes undetectable by standard chromosome banding techniques. The disadvantages of this system are that it conceals otherwise obvious similarities and differences

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among cell lines and that it is at variance with the standard nomenclature so widely used by workers who have analyzed the chromosome complements of cell lines. Is such a new system really needed?

Chromosome banding techniques have been used with great success in characterizing unusual chromosomes (variants, trans-locations, inversions, insertions, deletions, rings, amplified segments, etc.) in patients, tumors, cell lines, and somatic hybrids, and in comparing the chromosomes in related species, as attested by hundreds of papers in this and other journals. Scientific communication in much of this work has been facilitated by the development and use of an agreed-upon standard nomenclature for each species. Such systems are in widespread use for the human and primates (ISCN, 1978), the mouse (Committee on a Standardized Genetic Nomenclature for Mice, 1972; Lyon, 1979), the rat (Committee for a Standardized Karyotype of *Rattus norvegicus*, 1973), and *Peromyscus* species (Committee for Standardization of Chromosomes of *Peromyscus*, 1977). A system has been proposed for the Chinese hamster

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(Committee on Chromosome Markers, 1976) but has not won general acceptance over alternative systems which have several advantages (e.g., see Kitchin and Sager, 1980). It is to be hoped that an acceptable standard system will soon be agreed upon by the workers in this field; a committee is being organized by Dr. Francis Arrighi to attempt this. Agreement on a system for the rabbit has nearly been reached (R. Fox, personal communication).

In each species, the standard nomenclature provides a means of referring to any chromosome and, therefore, is applicable to cell lines. This applicability is particularly well documented in the mouse, where the standard system of nomenclature for mouse chromosomes (Committee on

Standardized Genetic Nomenclature for Mice, 1972; Lyon, 1979) has been widely used to report findings in mouse cell lines derived from renal adenocarcinoma (Hashmi et al., 1974), Ehrlich ascites tumor (Sasaki et al., 1974), sarcomas (Hashmi et al., 1974; Russell et al., 1974), myelomas (Shepard et al., 1974; Schröder et al., 1980), plasmacytomas (Shepard et al., 1976), melanomas (Jonas-son et al., 1977; Bostock et al., 1979), teratocarcinomas (Martin et al., 1978; McBurney and Strutt, 1980), erythro-leukemias (Miller et al., 1979), other leukemias (Klein et al., 1980), and lymphomas (Francke and Gehring, 1980). It has also been used for such common L-cell derivatives as A9 and B82 (Allderdice et al., 1973; Russell et al., 1977). These studies have indicated that L-cell derivatives have highly characteristic features which serve to emphasize their relatedness to each other and to distinguish them from cell lines of different origins, many of which have typical karyotypic features of their own.

The system of nomenclature used by Henderson et al. (1981) conceals such similarities and differences, as well as the origin of specific marker chromosomes. This seems too high a price to pay just to be reminded of the uniqueness of each cell line. Each individual or inbred strain is also unique, but that reduces only minimally the usefulness of a standard nomenclature for the chromosomes of each species. Hopefully, the development of standard systems for additional species will conform to general principles, which will make it easier for cyto-geneticists to understand each other and to refer even to chromosomes in interspecific hybrids in a consistent manner.

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