

# Proposed Nomenclature for Mutants of Adenoviruses

HAROLD S. GINSBERG,<sup>1</sup> JAMES F. WILLIAMS, WALTER H. DOERFLER, AND HIROTO SHIMOJO

*Department of Microbiology, School of Medicine, University of Pennsylvania, Philadelphia, Pennsylvania 19174; Medical Research Council Virology Unit, Institute of Virology, Glasgow, Scotland; Institut für Genetik, University of Cologne, Cologne, West Germany; and Department of Tumor Virus Research, The Institute of Medical Sciences, University of Tokyo, P.O. Takanawa, Tokyo, Japan*

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In accord with the nomenclature proposed for mutants of simian virus 40 the same rules, with minor modifications, are recommended for naming mutants of adenoviruses. It is further suggested that these rules, which pertain to a system of classification based primarily upon complementation analysis, also be applied to mutants of other DNA-containing animal viruses.

Investigations into the regulation of replication, cell transformation, and oncogenicity of adenoviruses have inevitably led to a need for mutants deficient in different properties. Host range (11, 12) and conditionally lethal temperature-sensitive (2-5, 7-10, 13, 14) mutants have been isolated, and predictably, their discovery has led to the utilization of a variety of nomenclature systems.

The value to be derived from a standardized nomenclature for mutants was recognized by Demerec and his colleagues (1), and investigators studying simian virus (SV40) mutants saw the advantage of a single accepted system (6). Similarly, several investigators isolating and utilizing adenovirus mutants accepted the desirability of a standardized nomenclature at the Tumor Virus Meeting at the Cold Spring Harbor Laboratory (August 16-19, 1972), and it was recommended that the nomenclature for adenovirus mutants follow where possible the general rules proposed for SV40 mutants (6). To avoid misunderstandings a summary of the general rules for nomenclature will be restated as modified for adenovirus mutants although to do so is largely repetitious.

(i) The major modification of the rules accepted for SV40 (6) follows from the numerous known adenovirus species. Thus, the first term of the mutant name should designate the natural host (i.e., H = human, S = simian, A = avian, C = canine, M = murine, B = bovine, O = ovine, P = porcine) and the immunological type (Table 1).

(ii) The entire name should be in italics or underlined, and except for the first term and the complementation group designation (A, B, C, etc.) all letters should be in lower case.

(iii) If a mutant should have more than one form (for example, temperature-sensitive and host range), the characteristic for which it was originally screened should be used for the designation of the mutant type (e.g., ts). However, if a second characteristic is considered of major importance or if a second characteristic is subsequently introduced by a separate mutation, it may be designated (e.g., ts [hr]).

(iv) At the present time, the determination of complementation groups can be accomplished through the exchange of mutants. If complementation studies have not been performed, a hyphen should be used in the complementa-

TABLE 1. A proposed nomenclature for all mutants of adenovirus (examples for naming mutants)

Term	Adenovirus	Natural host <sup>a</sup>
First	viral species	H5 A1
Second	mutant type	ts hr cyt hs pm
Third	complementation group	A, B, C, etc.
Fourth	mutant number	1, 2, 3, etc.

<sup>a</sup> Abbreviations: H5, human type 5 adenovirus; A1, type 1 avian or "CELO" adenovirus; ts, temperature-sensitive; hr, host range; cyt, cytotoxic; hs, heat stable; pm, plaque morphology.

<sup>1</sup> Present address: College of Physicians and Surgeons, Columbia Univ., New York, N. Y. 10032.

TABLE 2. *Initial assignment of block numbers to adenovirus mutants*

Type virus	Numbers assigned	Reference
H5	0-99	Williams, Gharpure, Ustacelebi, and McDonald (13)
	100-199	Ensinger and Ginsberg (2)
	200-299	Takahashi (10)
H12	0-99	Takemori, Riggs, and Aldrich (11, 12)
	100-199	Lundholm and Doerfler (5)
	200-299	Shiroki, Irisawa, and Shimojo (7)
	300-399	Rubinstein and Ginsberg (Unpublished)
H31	0-99	Suzuki and Shimojo (8, 9)
A1	0-99	Ishibashi (3, 4)

tion group space. If the mutant does not complement when tested against representative mutants of all known complementation groups, an asterisk should be used in the complementation group space. When data become available identifying the cistron for each mutation, the complementation group designation will be modified to indicate the actual gene.

(v) Arabic numerals should be used to designate the mutant number, and each number should be used only once (i.e., each mutant of a viral species should have a unique number).

(vi) The original publication describing and characterizing each mutant should contain in Materials and Methods all information concerning the origin of the wild-type virus stock from which the mutant was obtained and methods of mutagenesis, selection, and propagation of the mutants. In the text, only the mutant number in italics need be used unless the paper contains discussion of mutants of more than one viral species (e.g., H5 ts 1 and H 12 ts 1). Under some circumstances it may also be desirable to give the mutant's complementation group designation.

(vii) Blocks of mutant numbers can be obtained from James F. Williams (Institute of

Virology, Glasgow, Scotland). As indicated above, each viral species should be assigned new numbers. The blocks of numbers suggested are assigned, in order, to the laboratories that have reported the isolation and characterization of adenovirus mutants (Table 2).

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