15 Nomenclature

This chapter is devoted to nomenclature: systematically formulated names for specific entities.

Biological nomenclature dates back at least to the 18th century. Since the mid-20th century, many biomedical disciplines have established committees to develop and promulgate official systems of nomenclature.

Accelerating knowledge, particularly from molecular biology, necessitated the official biomedical nomenclature systems, sometimes with dramatic results. For instance, a single coagulation factor had been referred to by 14 different names.[4] An investigator deemed the official coagulation nomenclature ''one of the most significant, even if only semantic, recent advances in the field.''[5(p16)] The results, probably true in other disciplines as well, were that an ''impenetrable confusion was cleared away, apparent disagreements were often shown to be conflicts of terminology, not of fact, and a much freer exchange of information was made possible.''[5(p16)]

In microbiology, with publication of the approved list of bacterial names in 1980, the number of names of bacteria decreased by an order of magnitude, from around 30 000 to around 2000[6,7] (now nearly 7500[8]). The CD (clusters of differentiation) nomenclature is thought to have prevented mistakes in laboratory and clinical research.[9]

Those are some indications of the compelling need for systematic nomenclature, which requires the ongoing work of international groups. The development of nomenclature, however, faces challenges besides multiplicity of names. There is tradition—''the ruins of previous systems''[10(p7)]—which investigators are often reluctant to give up. When disciplines converge—for instance, when the genetics of a physiologic system are delineated—preexisting systems of nomenclature may operate in parallel, and names proliferate.[11] For instance, concerning the homologous human HLA and mouse H-2 tissue antigen systems, it has been observed:

> The situation is perhaps similar to what one might have encountered in the field of immunoglobulins had researchers working with immunoglobulins in different species not realized relatively early that the classes of heavy chains and light chains they were working with were homologous and been willing to adopt a common nomenclature. We might then have separate names in each species for IgM, IgG, IgA, kappa, lambda, and so on.[12(p578)]

A system of nomenclature may face the test of sheer numbers. The count of assigned gene symbols has increased from several hundred[13,14] to more than 23 000,[15] with more than 25 000 human genes anticipated.[16,17] The system was devised with a foresight that has allowed transition from typescript to print to online database.[18-20]

Another challenge is to remain flexible. Those who deal with nomenclature accept it as a construct[21-24] and have noted the need to reflect new knowledge.[22,25] Biomedical classification is arbitrary and ''artificial,'' created by humans.[26,27] Nomenclature needs to ''evolve with new technology rather than be restrictive as sometimes occurs when historical . . . systems are applied.''[28(p12)]

Such flexibility, however, places a burden on clinicians, who must replace familiar names with new ones.[29] Often, ‘‘colorful or descriptive names,’’[9(p1245)] which are more easily retained,[30] give way to more efficient terms, such as the alphanumeric epithets of many systems.

Nomenclature systems may differ markedly in approach. Stability is an overriding principle of the codes of taxonomic nomenclature, which avoid name changes.[31] For instance, the bacteriologic code has a provision that a name may be rejected ‘‘whose application is likely to lead to accidents endangering health or life or both or of serious economic consequences.’’[32(p43)] For example, the name *Yersinia pseudotuberculosis* subsp *pestis* for the plague bacillus was rejected and the name *Yersinia pestis* retained[32,33] because of concerns about public health hazards (owing to confusion of the name of the plague bacillus with that of the less virulent *Yersinia pseudotuberculosis*[34,35]). In contrast, currency is an overriding principle of the official human gene nomenclature, with genes renamed to reflect new knowledge. (Of the approximately 260 gene symbols in the first Catalog of Gene Markers following introduction of the current system of gene nomenclature, more than half have been renamed.[14,36]) Yet the principles of stability and currency are not mutually exclusive; for instance, the bacteriologic code requires name changes necessitated by revisions of taxonomy, and the human gene nomenclature acknowledges former names and aliases.

Nomenclature is ‘‘the means of channelling the outputs of systematic research for general consumption’’[37] and aims for international scope (‘‘ ‘. . . Science should unite Nations . . . ’ ’’[38[p10]]). Giangrande[39(p710)] writes that international nomenclature efforts in coagulation ‘‘provide[d] an outstanding early example of international collaboration to resolve a scientific problem. This sort of co-operation is now commonplace, but was certainly not typical in [the post–World War II] period.’’ To facilitate worldwide access to the latest terms, large computerized databases have been created. But computerized databases require consistent use of nomenclature.[11] Unique identifiers provide a home base for terms in large databases but are not practical for referring to entities throughout published articles and textbooks[40]—hence, names.

Our purpose in the nomenclature chapter is to explain not how names should be devised (although we cite the sources of such rules) but rather which names should be used and how they should be styled. Official systems of nomenclature are not universally observed to the letter (literally or figuratively), but style that is consistent with official guidelines and within publications reduces ambiguity. Editors have the task of mediating between official systems and authors’ actual usage. To that end, the goals of this chapter are to present style for terms and to explain terms in hopes that they are more easily dealt with.

In medical nomenclature the stylistic trend has been toward typographic simplicity, driven by computers. Terms lose hyphens, superscripts, subscripts, and spaces. However, such features have not been eliminated completely, either within or beyond these pages. In 1950 standardized terms in pulmonary-respiratory medicine and physiology were put forth, and typographic features impossible on a typewriter were expressly retained, seen as indispensable components of a systematic and enlightening nomenclature.[25] Computers are increasingly capable of generating unusual characters, and typographic simplification and electronic sophistication may

cross paths before medical nomenclature loses its last defining flourishes.

An umbrella resource for biomedical terminology is the Unified Medical Language System (UMLS), a project of the National Library of Medicine. The UMLS is intended to provide integrated terminology (including synonyms and relationships among terms) for use in electronic applications, ie, computer systems.[41,42] A major component of the UMLS is the Metathesaurus, a comprehensive repository of biomedical terms and their relationships. The Metathesaurus is accessible online at the UMLS Knowledge Source Server, http://umlsks.nlm.nih.gov. (Complimentary registration is required.) That site offers concept and term searches that can be useful to medical authors and editors seeking explanations of particular terms, including their relationships to other terms (eg, human gene, protein, condition, and animal counterparts).[42]

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