

# The Concept of Genus

Subjects: Microbiology

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The genus concept and its implication in classifying pathogenic relevant microorganisms: The *Brucella* and *Ochrobactrum*

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## 1. Introduction

After Linnaeus, biologists used a binomial nomenclature in which the name for an organism was based on two terms, the genus and the species, and this naming convention has been maintained in modern taxonomy. While there have been numerous debates regarding the species concept in sexual and asexual organisms, the genus and other higher taxonomical taxa have received less attention because they are much more elusive than the species <sup>[1]</sup>, the entities active in nature. Since the genus and other higher taxonomical hierarchies result from averaging and factorizing common characteristics of known extinct and extant species within a group, they are undoubtedly artificial constructs of the human mind intended to bring a practical order to the observations of biological diversity <sup>[2][3]</sup>.

## 2. The Concept of Genus

Taxonomical ranks above the species are collective categories subjectively delimited. Therefore the pronouncement made by Linnaeus 285 years ago (1737), "It is the genus that gives the characters, and not the characters that make the genus," remains as a solid truth not only for the genus but for all categories above this rank. Within the bacterial realm, the taxonomical concepts are even more elusive because the population structure of the various groups may preclude recombination or undergo recombination within the same, close or distant "species."

In *stricto sensu*, taxonomy is an epistemological-based problem that requires two dialectically inseparable strategies: the analytical procedure and the typological analysis. While the first depends partly on quantitative techniques developed by scientists (for example, 16S rRNA and DNA sequencing), the second is a heuristic process that explores multidimensional properties such as adaptation, ecology, physiology, reproduction, homeostasis, commensalism, endosymbiosis, functional diversity, preferred niche, virulence, pathogenicity, and many other attributes. These qualities separate items in various dimensions based on an "ideal type." It is essentially an abstraction, and, as such, it corresponds to an ontological process. An excellent example of this epistemological analysis has been the separation of the intracellular brucellae pathogens and the free-living opportunistic ochrobacteria species, which, although phylogenetically related, have been kept apart based on analytical typological analysis in the genus *Brucella* and genus *Ochrobactrum*, respectively <sup>[4]</sup>.

### 2.1. The Analytical Process

The analytical process uses quantitatively measurable characteristics of the subjects organized in ranks, commonly depicted as cladograms or phylogenetic trees, which are hypotheses on the evolutionary course of the species. It must be borne in mind that, whereas this analysis is of fundamental importance in evolutionary studies, these representations are based on numerical values and thus, depend on the parameters quantified. Not surprisingly, in genomic sequence comparisons, the distance between two groups with different genome sizes (*Ochrobactrum* and *Brucella* <sup>[4]</sup>) may be enlarged or narrowed depending on whether the tree is constructed based on SNPs, core genomes, pangenomes, or nonsynonymous or synonymous sites, among several options <sup>[5]</sup>. Nonetheless, the punctuated ancestor-descendant relationships depicted through dichotomic nodes and branches in a tree are representations based on similarities presented as numerical values. Still, the interpretation of these values follows circular reasoning (the principle of *circulus in probando*) because a group of organisms descended from a common ancestor (premise) are closely related (conclusion), and they are closely related (premise) because they descended from a common ancestor (conclusion). In addition, drawing a cut-off line in a given branch for defining a cluster of organisms and including them in a taxon, such as a genus, is a decision that cannot be taken solely on quantitative parameters and thus, is usually based on assessments

made by other methods [6][7][8]. Moreover, the branching points are not fixed features of the possible trees because it was unknown that characteristics of the still undiscovered or extinct individuals not incorporated in the analysis. Consequently, the clustering or the division of groups (including the genus) reflects perspectives that, although obtained after analyzing multiple characteristics, are thus strictly speaking anthropocentric.

## 2.2. The Typological Process

The typological process follows a methodology that conceptually separates items in various dimensions by exploring common and exclusive properties to identify an “ideal type.” Therefore, this process is an intellectual construction that stresses specific properties of different realities that, although critically important, are not necessarily linked to quantitative characters (as those used in cladistics). Thus, the typological process is a flexible heuristic system that adapts to decision-making while working with complex data [9]. Typologies are crucial because they provide efficient and practical bases for comparisons and a framework for giving operative and predictive names, two essential conditions of taxonomy [2] that are particularly relevant for pathogenic bacteria.

Ideally, the analytical and typological essences coincide in a dialectic relationship. However, while acquiring the former (for example, DNA sequence comparisons) is a straightforward two-dimensional process often amenable to quantification, the typological essence (for example, ecology, lifestyle, pathogenicity, and so on) includes more than two dimensions and, therefore, requires qualitative assessments. For example, the biological species concept of the famous evolutionist Ernst Mayr (1904–2005) stated that, within a defined cluster (through the analytical process) of living organisms with common characteristics, species are those “groups of actually or potentially interbreeding natural populations, which are reproductively isolated from other such groups” [10]. This famous Mayr’s declaration, mainly used to define most species throughout the plant and animal kingdoms, stressed the typological essence of reproduction as the epistemological conceptualization of the species as a taxon on which evolution occurred through gene flow by interacting phenotypes. The typological characteristics are even more relevant when defining two different genera since they display different “types” precluding reproduction. As expected, in other live systems such as the prokaryotes, where conjugation can be entirely precluded or occur between the same species, between different species, or among species of different genera, the typological principles are more difficult to grasp; however, they cannot be ignored because they are at the core of the diversity of life that taxonomy aims to represent.

## 2.3. The Analytical and Typological Processes Define the Genus

The integration of the analytical and typological processes is reflected in different proportions in the two main ways biologists interpret the genus, for example, cladistics and evolutionary systematics [11]. The cladistic definition relies heavily or solely on the quantitative analytical process and proposes that a genus is a group of species more closely related among them than with the species of another genus, implying that it must be monophyletic. However, this definition makes no provision that paraphyletic subsets in a monophyletic group can be diverging evolutionary units occupying widely different ecological niches. Furthermore, as discussed above, defining monophyly using quantitative approaches (for example, strict cladistics) is not straightforward and cannot avoid subjective considerations. A 94.5% or lower sequence identity for two 16S rRNA genes has been proposed as evidence for distinct genera. However, this represents a practical convention to introduce order in the taxonomy of uncultured archaea and bacteria, not a taxonomically objective truth [8]. In fact, the authors of this proposal explicitly acknowledge that such a threshold is a minimum value that does not preclude the formation of separate genera with higher sequence identities if supported by other phenotypic, genetic, or environmental data [8], as for *Ochrobactrum* and *Brucella*. [4]

Moreover, it has been emphasized that such a “lower cut-off window” of 16S rRNA gene sequence similarity, while reasonable for the above-cited practical purpose, was based on the evaluation of genera previously delineated by a broad spectrum of methods [7][8]. Clearly, these cautions in applying “lower cut-off windows” illustrate why integrating the analytical and typological process is necessary and support the second interpretation of the genus, for example, the systematic evolutionary definition. This definition postulates that a genus is a group of species of common ancestry (or a single species for monospecific genera) that occupies an ecological situation different from that occupied by the species of another genus. Following this definition, the genus can be monophyletic or paraphyletic (when the latter is a subset of a monophyletic group), thus, bypassing the problem of strictly defining the branching nodes that occurs in cladistics. Emphasizing ecology (and, therefore, its structural and physiological bases) also introduces typology and thus, becomes operative and predictive. The need to incorporate ecology in taxonomy is obvious, and it is entirely relevant for those bacteria (commensal or pathogens) that colonize and thrive in a given host. In addition, the systematic evolutionary definition considers the evolutionary hypotheses derived from cladistic analyses and puts them in a biologically and taxonomically meaningful perspective. Specifically, in the context of *Brucella* and *Ochrobactrum*, it is necessary to consider hypotheses on how bacterial pathogens emerge and evolve in nature.

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