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ESSAY

Homology: Homeostatic Property Cluster Kinds in Systematics and Evolution

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Abstract Taxa and homologues can in our view be construed both as kinds and as individuals. However, the conceptualization of taxa as natural kinds in the sense of homeostatic property cluster kinds has been criticized by some systematists, as it seems that even such kinds cannot evolve due to their being homeostatic. We reply by arguing that the treatment of transformational and taxic homologies, respectively, as dynamic and static aspects of the same homeostatic property cluster kind represents a good perspective for supporting the conceptualization of taxa as kinds. The focus on a phenomenon of homology based on causal processes (e.g., connectivity, activity-function, genetics, inheritance, and modularity) and implying relationship with modification yields a notion of natural kinds conforming to the phylogenetic-evolutionary framework. Nevertheless, homeostatic property cluster kinds in taxonomic and evolutionary practice must be rooted in the primacy of epistemological classification (homology as observational properties) over metaphysical generalization (series of transformation and common ancestry as unobservational processes). The perspective of individuating characters exclusively by historical-transformational independence instead of their developmental, structural, and functional independence fails to yield a sufficient practical interplay between theory and observation. Purely ontological and ostensional perspectives in evolution and phylogeny (e.g., an ideographic character concept and PhyloCode’s ‘individualism’ of clades) may be pragmatically contested in the case of urgent issues in biodiversity research, conservation, and systematics.

Keywords Characters • Individuals • Monophyly • Natural kinds • Phylogeny • Similarity • Taxonomy • Transformational and taxic homology

Introduction

Taxa (hereafter, monophyletic groups) have been construed as *classes* (which have members and are not spatio-temporally continuous and cohesive entities embedded in the evolutionary contingency), or alternatively as *individuals* (which are wholes having parts and are spatio-temporally continuous and cohesive entities embedded in the evolutionary contingency; Rieppel, 2006). This seeming philosophical dichotomy between classes and individuals has generated renewed approaches and debates in contemporary systematics – theoretically, methodologically, and philosophically – such as the elaboration of an ideographic character concept (Grant and Kluge, 2004) and the clash between phylogenetic nomenclature and Linnaean taxonomy (Keller *et al.*, 2003; Nixon *et al.*, 2003; Pleijel and Härlin, 2004; Wheeler, 2004; Rieppel, 2006; Cantino and de Queiroz, 2007; and references therein).

However, this dichotomy is considered largely irrelevant for contemporary systematics by those arguing that taxa can be conceptualized as *homeostatic property cluster (HPC) kinds* (Keller *et al.*, 2003; Franz, 2005; Rieppel, 2005a, b, 2006, 2007a; Assis, 2009). Originally introduced by Richard Boyd (1991, 1999), the HPC construal of kinds attempts to reconcile the fact that kinds in the biological and social sciences are typically heterogeneous and cannot be defined by necessary or sufficient conditions (essences, which define classes), with the observation that such categories are not formed in an arbitrary fashion and epistemically permit scientific generalizations and explanations (Wilson *et al.*, 2009). The approach suggests that a kind is ontologically characterized by a *property cluster*, i.e., a larger set of properties that exhibit a relevant degree of correlation, where each kind member possesses several (though usually not all) of these properties, and no single property must necessarily be shared by all kind members. Such a kind is a natural kind (rather than an arbitrary collection of objects) if the clustering of the various properties is due to underlying causal processes, so-called *homeostatic processes*.

In the context of phylogenetic systematics, the property cluster characterizing a taxon consists of taxic homologies or synapomorphies (Keller *et al.*, 2003; Franz, 2005; Rieppel, 2006). Common descent (involving reproduction across generations) is here the ‘homeostatic process’ that accounts for the clustering of these characters and the fact that phylogenetic classifications have a rich information content, e.g., “the characterizations of 38,000 kinds of spiders by their spinnerets (silk-producing glands), or of 250,000 kinds of flowering plants by their endosperm (resulting from the process of double fertilization)” (Franz, 2005, p. 497). Thus, homeostatic property cluster kinds are “scientific categories posited by our theories as epistemological devices; insofar as they have ontological status, it is as features of the ways in which causal structures in the world interact with our classificatory practices in such a way as to support reliable induction and explanation” (Keller *et al.*, 2003, p. 102). This thesis is claimed to allow natural kinds to be historically delimited, because of the reference to common ancestry in the case of taxa (Keller *et al.*, 2003; Rieppel, 2007a, b).

A few have suggested that there is no incompatibility between a taxon being construed both as a kind and as an individual (Dupré, 1999; LaPorte, 2004; Brigandt, 2009), for both constructions are context sensitive. However, the conceptualization of taxa as natural kinds even in the sense of homeostatic property cluster kinds has been criticized by some systematists (e.g., Kluge, 2003; Grant and Kluge, 2004), as it seems that even such kinds cannot evolve due to their being based on homeostatic processes.

However, we reply by arguing that the treatment of transformational and taxic homologies, respectively, as dynamic and static aspects of the same homeostatic property cluster kind offers a good perspective for supporting the conceptualization of taxa as kinds. The focus on a phenomenon of homology (i.e., the relation of correspondence between parts of two or more organisms) based on causal processes (e.g., topology, connectivity, activity-function, ontogeny, genetics, inheritance, and modularity in development and evolution) and implying relationship with modification yields a notion of natural kinds conforming to the phylogenetic-evolutionary framework.

While assuming that ontologically speaking an individual and a kinds approach are consistent, we focus on articulating how to construe taxa and in particular homologues as HPC kinds, because some still argue that this is impossible, and – more importantly – because we explore new perspectives, showing how the HPC approach motivates and successfully addresses them. This paper recommends the notion of HPC kinds for its heuristic and theoretical fruitfulness in tying taxic to transformational homology, combining empirical-pragmatic and theoretical-explanatory aims in taxonomy and evolutionary biology, and making accounts of homology germane to a plethora of issues. This embraces evolvability, adaptation, diversification, research on the developmental-functional make-up of organisms, the phylogeny-taxonomy link, biodiversity and conservation policies, as well as the continuity of philosophy with empirical science. We do not maintain that the individuals perspective is wrong, but challenge it on the grounds that it has not previously motivated the indispensable issues in systematics and evolution we explore in these pages.

From properties of classification to events of generalization

Some metaphysically realist systematists influenced by the purely ontological conception of species and monophyletic groups as individuals such as Grant and Kluge (2004, p. 25) have criticized the construal of character states as properties: “character-states have generally been conceptualized as properties (attributes, features), which logically denies their ability to transform or evolve, since properties are class concepts and, as such, immutable.” Instead they propose an ideographic character concept: “as transformation series, characters are historical individuals akin to species and clades” (Grant and Kluge, 2004, p. 23). Accordingly, character states are “*the least inclusive historical individuals that result from heritable transformational events*” (Grant and Kluge, 2004, p. 26; emphasis in original). And “because the basic or fundamental unit in phylogenetic inference is the transformation event, the relevant independent parts of organisms are those that have undergone independent, heritable transformation events. What matters in individuating character-states (and more inclusive transformation series), therefore, is not the structural, developmental, or functional independence of a part, but its historical/transformational independence” (Grant and Kluge, 2004, p. 26; contra Rieppel and Kearney, 2002). Hence, a strict ontological character concept is proposed that represents the primacy of generalization (e.g., an explanatory theory of historical singular processes) over classification (e.g., contextual patterns of membership relations by properties) in phylogenetic systematics (cf. Rieppel, 2004). Correspondingly, Grant and Kluge (2004, p. 25) reject the possibility of construing species as kinds, even as homeostatic property cluster kinds, claiming that “in being homeostatic, such kinds cannot evolve.”

However, when assuming that a character, as a relation of ‘sameness’ captures the notion of transformational (e.g., the homologues A and A’) and taxic homologies (e.g., A’), the tenet of Kluge (2003) and Grant and Kluge (2004) about the non-phylogenetic-evolutionary nature of HPC kinds fails to meet its target, because a hypothesis of transformational and taxic homologies – as we will see below – are critical for making the idea that homologies and taxa are HPC kinds conform to an evolutionary framework. An important point is that the fundamentals of transformational and taxic homologies in phylogenetic theory and practice are not strictly ontological like an ideographic character concept is. They are also epistemological and, as such, instantiate a relation of classification (or knowledge of observational facts) to generalization (or explanatory theories of unobservable phenomena). In fact, conjectures of transformational and taxic homologies are firstly established by the empirical-contextual delineation of characters (i.e., by similarity or correspondence) with their subsequent polarization (i.e., definition of relatively correspondent plesiomorphic and apomorphic character states within characters onto the phylogenetic hierarchy; Bryant, 2001) by cladogram rooting (see Grant *et al.*, 2006, as an example of these empirical and logical approaches). And only after the hierarchical construction the evolutionary explanation is carried out. It is in this way that the conceptualization of taxa as HPC natural kinds and their accommodation to evolutionary properties and events (contra Grant and Kluge, 2004) must be further investigated through the treatment of transformational and taxic homologies as dynamic and static aspects of a homology, and thus as different aspects of the same HPC kind, which thereby permits phylogenetic relatedness and modification.

Transformational and taxic homologies, modification and homeostasis

It turns out to be erroneous to assume (as Kluge, 2003 and Grant and Kluge, 2004 do) that an entity whose identity is based on homeostatic processes – at least as this notion is used in the HPC construal of kinds – is essentially unchanging in most of its features. Rieppel (2005a, p. 482) discusses the meaning of homeostasis as “the maintenance of a dynamically stable internal environment in an open system.” In this way, an individual organism is a dynamically stable system that keeps many properties during its life time, despite undergoing ontogenetic development as change in other properties (e.g., its series of semaphoronts; see Hennig, 1966). There are ‘homeostatic’ processes that explain both why the individual keeps its identity across time and can change as an integrated entity, including self-maintenance as a variety of cellular, physiological, and behavioral processes (Wagner and Laubichler, 2001), phenotypic plasticity and developmental constraints (Rieppel, 2005a, b).

The same idea applies to a species taxon construed as an HPC kind (Wilson *et al.*, 2009). Conspecifics share many features in certain combinations – the cluster of properties characterizing an HPC kind. This correlation and distribution of properties is explained by processes accounting for species cohesion, as laid out by different species concepts. One such process is gene flow. Gene flow across conspecifics is not at all incompatible with evolutionary change; in fact, it accounts for why a species changes *as a coherent unit*, should it change due to natural selection and other influences, since change in some populations is transmitted via gene flow to the rest of the species. Thus, the so-called ‘homeostatic’ processes account for why the members of an HPC kind existing at the same point in time exhibit similarities, and why change typically affects all kind members, so that the kind changes as a unit. Gene flow and the ability to interbreed are relational rather than intrinsic properties, but the HPC approach permits such properties and considers them as important for the identity of biological kinds, including the relational property of common descent.

This brings us to the ability of characters to evolve, as emphasized by Grant and Kluge (2004). An important issue for construing characters as HPC kinds consistent with an evolutionary framework is the relation between ontogeny, inheritance, and phylogeny, where the concepts of homologue and homology as well as semaphoront and ‘complex semaphoront’ are fundamental. A homologue is “a part of an organism” and homology is “a phylogenetic relationship between parts, or homologues of different organisms” (Nelson, 1994, p. 104). According to Hennig (1966, p. 65), “the semaphoront corresponds to the individual in a certain, theoretically infinitely small, time span of its life, during which it can be considered unchangeable,” whereas “a ‘semaphoront complex’ can be constructed by aspect fusion of several aspect continua representing the same organism at different ontogenetic stages” (Rieppel, 2003, p. 172). As an organism is contextually composed of parts (homologues), each such part, throughout its ontogenetic stages, is characterized by a complex semaphoront. Developmental and genetic constraints act in the construction of the ‘semaphoront complex’ as a dynamic entity integrated by homeostatic processes, so that each one of its semaphoronts corresponds to a static, ‘unchangeable’ stage in a certain time span of the organism’s life. “But just as a ‘semaphoront complex’ [i.e., an ontogenetic unity] can be constructed for a single organism, so it can also be constructed by aspect fusion for species and higher taxa” (Rieppel, 2003, p. 172). As such, taxa can be conceptualized as “phylogenetic relationships […] of ontogenetic parts of life” (Nelson, 1989a, p. 279), so that these parts are homologues (e.g., A or A') of a character in different organisms, and these homologues, in the phylogenetic-evolutionary hierarchy, capture relations of transformational and taxic homologies.

The *transformational* perspective on homology, i.e., the relation between different states of a character found in two or more organisms, is concerned with change (e.g., A→A') and need not imply grouping (Patterson, 1982; Rieppel, 1988). The *taxic* perspective, i.e., the relation between identical, apomorphic character states shared by two or more organisms, is concerned with common ancestry and grouping (e.g., A'), being operationally established by the overall congruence of characters in a hierarchy (Patterson, 1982) (i.e., a set-theoretical notion irrespective of causal phenomena, unless it is qualified by causal-contextual efficacious properties; Rieppel, 2004). The transformational account with its focus on evolutionary change represents the *dynamic* aspect of the HPC kind (i.e., a phenomenon of homology), whereas the taxic account with its relation to the monophyly and classification of groups represents the *static* aspect of the same HPC kind.

This is possible as there are different properties ontologically associated with an HPC kind, some of which are more static, while others are more dynamic. Some of these properties are causally more basic, while others are the effects of the former; some are non-observational, while others are observable (Brigandt, 2009). In the case of a higher taxon as an HPC kind, descent from a particular ancestral species is a (non-observational) causally basic feature that *explains* why the (observable) apomorphies of the taxa members – some further properties of the HPC cluster – are shared, and common ancestry is a property shared by taxa members that permits other properties (characters) to change and evolve. A species taxon construed as an HPC kind is ontologically characterized by many features that stand in complex and reciprocal causal relations, e.g., genetic properties of individuals, their phenotypic features, gene flow and the ability to interbreed, ecological competition, and developmental constraints (Wilson *et al.*, 2009). Rieppel (2008) emphasizes that a particular scientific approach is typically interested in only certain aspects tied to a kind, be it phylogenetic, developmental, functional, anatomical, or ecological features. Indeed, there are different species concepts based on different biological features and operational approaches (see Wheeler and Meier, 2000; and references therein). Yet the fact that only some features of a taxon or a homology are of epistemological or pragmatic interest in a certain scientific context does not entail that there are no other features ontologically tied to this entity that may be relevant given other scientific interests; and the HPC approach explains how different perspectives on a kind can be consistent and related.

In the case of a homology (a character across generations) as an HPC kind, certain genetic-developmental properties of the character permit that it can be inherited across generations and undergo change of state while remaining the same morphological unit (Wagner, 1996, 2001; Jamniczky, 2008). Wagner (2007) presents evidence that the identity of a character is established by *certain* gene regulatory networks, which have been stable across evolutionary change (so that the character is present in several extant species), while *other* genes have evolved leading to this character taking different states in ancestral and extant species. This illustrates how different features are tied to an HPC kind – some of which are more evolutionary stable, some of which are subject to change – and that a character construed as an HPC kind can evolve (contra Grant and Kluge, 2004).

Grant and Kluge (2004) restrict the notion of homology to the transformational account. But by regarding homology as both a homeostatic property cluster kind and a relation between parts, we conceive homology within a broader scope. In this manner, the same phenomenon of homology (as an HPC kind) encompasses the *transformative-dynamic* aspect of homologues (e.g., A→A') and the *taxic-static* aspect of one such homologue or character state (e.g., A') shared ontologically by all descendants and their most recent common ancestry. Monophyly integrated with developmental and genetic constraints are the homeostatic processes that determine a taxon's boundary (Brigandt, 2009). As taxic homologies are responsible for the identification and classification of monophyletic groups, their importance over transformational homologies has been pragmatically endorsed in phylogenetic theory and practice (see Patterson, 1982; Rieppel, 1988; de Pinna, 1991; Brower and Schawaroch, 1996). Criticisms have been made regarding the ontological nature of a transformation series (see Rieppel, 1988). But whereas most of the papers concerned with the integration of the theory of natural kinds and phylogenetic systematics focus on the treatment of taxic homologies (or synapomorphies) as HPC kinds (e.g., Keller *et al.*, 2003; Franz, 2005; Rieppel, 2005a, b, 2006), transformational homologies – the most critical feature to dispel the idea that an HPC kind cannot evolve – have only recently been considered (see Brigandt, 2007, 2009).

Since a taxic homology, i.e., the apomorphic homologue that identifies a phylogenetic relationship as a taxon, is included in a series of transformations, it is an ongoing phenomenon in the world (Keller *et al.*, 2003). As such, it is subject to modification. Moreover, by regarding the causal-contextual properties (or tokens) that define a taxon (qua natural kind) as embedded in the evolutionary contingency, one has to expect the occurrence of some reversions (i.e., the appearance of an apomorphic condition within a natural kind, so that this condition is similar to the plesiomorphic condition found at a more inclusive level in which that natural kind is contained) and derivations (new character states). Other homologues (as HPC kinds) found in the taxon are also subject to change and consequently promote diversification and novelty within it. For instance, in the phylogeny of Reptilia, the position of turtles (Testudines, classically considered anapsids) within Diapsida reveals that the lack of holes behind the eye socket is – following the phylogenetic levels of universality – a reversion in Reptilia, an apomorphic or derivate condition in Diapsida (which is phylogenetically circumscribed by the presence of two holes behind the eye socket), and a synapomorphy of Testudines (see Rieppel, 1999; and references therein). In this way, lack and presence of holes behind the eye socket are states that characterize the skull of Diapsida and Reptilia as a causal, historical, and dynamic unit integrated by homeostatic processes, which is related to certain events of origin and diversification within these groups.

Since the notion of homologies as HPC kinds embraces relationship with modification, it is germane to evolvability, “the capacity of a developmental system to evolve” (Hendrikse *et al.*, 2007, p. 394). In other words, evolvability “is a disposition that an organism and its homologues can possess” (Brigandt, 2007, p. 712). In line with this, morphological organization into distinct homologues, developmental constraints, and modularity explain evolvability (Yang, 2001; Brigandt, 2007; Jamniczky, 2008). This perspective plus the theory of HPC kinds can also be used in studies of diversification, selection, and adaptation (e.g., Yang, 2001). According to Brigandt (2007), in contrast to what has often been assumed, developmental constraints and selection are not antagonistic forces, but complementary. For developmental constraints are related to the developmental generation and evolutionary maintenance of homologues as units of morphological variation across generations (identity of a morphological unit despite its phenotypic change), while natural selection subsequently operates on the produced variation (resulting in character transformation).

In fact, Yang (2001) argues that developmental aspects of juveniles and adults stages of hemi- and holometabolous insects can be conceived of as modules (or causal properties) of evolutionary change relative to events of diversification and adaptation. The author highlights that, based on these features, Holometabola was found to have a significant rate of diversification when compared to its sister-group Eumetabola (traditionally a hemimetabolous). In addition, Yang (2001) shows that the characters in more modular monophyletic groups partake in greater levels of variation due to their independence. This may imply that developmental constraints and selection act complementarily in the static and dynamic aspects of these insects' parts or modules (i.e., homologues as a HPC kinds), and consequently, in their events of origin and diversification.

Similarity again and forever

Identical or similar character states in a monophyletic group are *one* aspect of an HPC kind. However, Ereshefsky (2007, p. 296) charges that "HPC's emphasis on similarity is at odds with phylogenetic approaches to taxonomy." We reply by pointing out that apart from members of the same HPC kind sharing certain internal features, there are also *relations to members of other kinds*, which in this case account for a character (a homology) being a unit of evolutionary transformation. Some of the genetic-developmental properties of a morphological structure (or developmental module) pertain to how this structure is partially developmentally dissociated from other structures, so that across generations it can vary and evolve largely independently of other structures (Brigandt, 2009). Among other things, the growing literature on modularity works towards an explanation of how structures that exhibit some developmental and functional relations can be sufficiently dissociated so as to permit morphological change (von Dassow and Munro, 1999; Schlosser and Wagner, 2004; Rieppel, 2005b). What makes a character a phylogenetic unit is its ability to evolve independently of other characters (Wagner and Laubichler, 2001). Construing a character as an HPC kind is not only consistent with a character being able to evolve, but some of the developmental relations and dissociations w.r.t. other characters – an aspect of the HPC kind in addition to internal similarities – explain this ability to evolve in a character-by-character fashion (Brigandt, 2007).

To be sure, the relations of correspondence among different character states (i.e., transformational homology as a dynamic aspect of an HPC unit) and the same homologues (i.e., taxic homology as a static aspect of an HPC unit) are causally and contextually evidenced according to heterogeneous criteria of comparative biology, as a way of seeing the biological world whereby similarity / correspondence between parts of organisms (homologues) is empirically and theoretically justified by activity-function, ontogeny, genetics, inheritance, and modularity in development and evolution. Yet it is important to bear in mind that these developmental, functional, and modular phenomena are largely unexplored for characters in phylogenetic inferences, and that these relations need to be established by classical approaches to comparative biology, such as topological relations and/or connectivity (the resemblance in position and arrangement between structures) (Rieppel, 1988; Rieppel and Kearney, 2002; Kearney and Rieppel, 2006). These two classical criteria of correspondence are conventionally and more or less successfully used throughout the systematic and comparative endeavor as the panacea for solving problems of the common origin of homologues (Rieppel and Kearney, 2002; Kearney and Rieppel, 2006). Indeed, as monophyly is not immediately given, it must be parasitic on homology (see Dupré, 1981; Nelson, 1994; Rieppel, 2003, 2006). Taxa and characters delineation is empirical-contextual (Franz, 2005).

Following the thesis of individualism, Grant & Kluge (2004) stress that developmental independence is not fundamental for individuating historical character-states in phylogenetic systematics, whereas Ghiselin (2005) realizes that homologies as historical entities / individuals are grounded among other things in developmental processes. In the context of an empirical-contextual discourse, homologies and taxa as individuals are levels of biological organization with asymmetric construction. Homologies can be construed by substantial knowledge (see Ghiselin, 2005), but taxa cannot. Specific parts or processes (e.g., developmental and taxic homologies) do not define taxa as individuals, for these are whole-part relations. Hence, the individualism of taxa cannot be grounded in data matrix and cladogram construction (contra Cantino and de Queiroz, 2007; Ereshefsky, 2007). The only way of making reference to their individualistic monophyly is by stipulation plus ostensional indication (i.e., by ‘pointing out’ paradigmatic exemplars of a taxon without any empirical-contextual knowledge about its referent; cf. Rieppel, 2007b, 2008). Accordingly, the perspective of individuating characters exclusively by historical-transformational independence instead of a part’s developmental, structural, and functional independence (e.g., Grant and Kluge, 2004) is, in the language of systematics, virtually devoid of any practical interplay between theory and observation.

Conclusions

Taxa and homologues can in our view be construed both as kinds and as individuals depending on the context of a certain scope of discourse. Consequently, both constructions face the problem of instantiating theoretical-causal entities and the terms that name them w.r.t. two indispensable and reciprocal approaches – the epistemological knowledge of systematics and the metaphysical phenomenon of evolution. A successful perspective for making the theory of homeostatic property cluster kinds conform to phylogenetic systematics depends upon the treatment of transformational and taxic homologies, respectively, as dynamic and static aspects of the same phenomenon of homology (i.e., as modification and relationship in a hierarchical reconstruction) grounded in efficacious causal-contextual properties. These properties capture relations of similarity (in language by predicates; Rieppel, 2007b), which are fundamental for phylogenetic reconstructions, classifications of biodiversity, and related approaches (Assis, 2009). The transformational account of homology focuses on how a character is inherited and gradually modified through generations and species, while the taxic approach focuses on a split in a lineage (formation of different taxa) and the resulting marked differences between extant species of different taxa.

An adequate notion of HPC kinds establishes an epistemological and ontological basis for the naturalization of the Linnaean taxonomy – as a verbal reference system for systematics – grounded in Hennigian phylogenetic systematics – as a general reference system for systematics (Hennig, 1966) –, and the consequent replacement of paraphyletic groups or nominal kinds by monophyletic groups or natural kinds (Rieppel, 2006). Nevertheless, the conceptualization of taxa as classes, in Linnaean taxonomy, and individuals, in Hennigian phylogenetics, can fruitfully be replaced by a construal of taxa as natural kinds (Keller *et al.*, 2003; Rieppel, 2006). For in addition to theoretical-explanatory aims HPC natural kinds satisfy simultaneously historical, empirical, and methodological demands of contemporary systematics. Thus, we recommend the HPC approach because of its heuristic fruitfulness for a variety of issues, not because it would metaphysically exclude the individualism approach.

Even though species and higher taxa are pragmatically and contextually circumscribed in different ways (i.e., there are different species concepts, and higher taxa are phylogenetically delimited by synapomorphies distributed in a cladogram), their ontological status in the systematics-evolution link is the same – they can be construed as HPC natural kinds. Therefore, it is false to assume an empirical difference between species and higher taxa as units of systematics and evolution (see Nelson, 1989b). Both are contextually delineated based on (relational) properties and homeostatic processes at distinct levels of universality.

Historically, extensional and intensional definitions – empirically based accounts of characters, homologues, and taxa – when compared to an ostensional individuation or baptism (cf. Rieppel, 2007b), have provided great conceptual advances in our epistemological and ontological schemata in the context of systematics and the evolution of biodiversity. Substantial knowledge is consequently required for homologies' construal both as kinds and as individuals. In contrast, Grant and Kluge's (2004) metaphysical realism about individuals and characters does not provide an advancement in our knowledge of observational beliefs, concepts and terms relative to the language of systematics and everyday life. At the end of the day, their ideographic character concept has merely ontological status that fails to do justice to the essential continuity of philosophy with empirical science.

As homeostatic property cluster kinds in systematics, evolution, and biodiversity research are fundamentally and historically rooted in the epistemological primacy of classification (e.g., homology and taxonomic hierarchy) over generalization (e.g., series of transformation and common ancestry) (see Rieppel, 2004), it emerges as an appropriate approach in an attempt to provide that continuity. As a result, a purely ontological assumption, stipulation, and ostension in evolution and phylogeny, e.g., the ideographic character concept (Grant and Kluge, 2004) and the ‘individualism’ of clades as endorsed by the PhyloCode (Cantino and de Queiroz, 2007; see also Ereshefsky, 2007), may be pragmatically contested in the case of urgent issues in contemporary systematics. These include the renaissance of taxonomy and comparative morphology, homology assessment, as well as the crisis, knowledge (e.g., faunas, floras, monographs, and revisions), phylogenetic classification, and the conservation of biodiversity (Wheeler, 2004; de Carvalho *et al.*, 2008; Assis, 2009).

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