Ontic and epistemic differentiation: mechanistic problems for microbiology and biology

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Abstract

Species are considered the basic unit of biological classification and evolution. Hence, they are used as a benchmark in several fields, although the ontological status of such a category has always been a matter of debate. This paper aims to discuss the problem of the definition of species within the new mechanistic approach. Nevertheless, the boundary between entities, activities, and mechanisms remains difficult to establish and always requires an analysis of what is meant by explanation. As a case study, the paper describes the debate concerning the species category by considering different kingdoms: Animals, Bacteria, and Fungi. The inherently biological differences between those groups prevent the use of a single, universally applicable concept of species that could fit the mechanisms responsible for the variability present in these kingdoms. The same issue is encountered within each group, as highlighted through a focus on mammals and microbes. This controversy has given rise to opposite approaches, namely: monism, which looks for a single definition that might account for all species, and pluralism, which admits that different groups of organisms require somewhat different definitions. In order to develop an adequate definition of species, we propose to apply a new mechanistic framework, which considers the ontic-epistemic dimensions of scientific explanation in close parallel. The apt correlation between epistemic and the ontic aspects highlights the way in which the concept of species and the reference to data are strictly co-determined. This suggests that the concept of species is better understandable within a dual ontic-epistemic approach.

Keywords: species, explanation, causality, ontic-epistemic differentiation

1. Introduction

Can the question of whether the species is real receive a yes-or-no answer? “A species, be it plant or animal, is a fiction, a mental construct without objective existence” (Burma, 1949, p. 369). Is this indeed the case, or are species real? This is the dilemma of trying to find a univocal definition and answer to the so-called “species problem”. Anyone who wades through the scientific and philosophical literature on this issue will note that the solutions offered to the problem of the species have not decreased over the years, but multiplied. The debate is open (Wheeler-Meier, 2000): it has led to intermediate solutions (Kitcher, 1993) and different approaches (Nathan & Cracraft, 2022), not always with optimistic results (Hey, 2006). We assume there is little hope of an imminent solution to the problem.

A solution could be the analysis of both the ontological status of the species and its epistemological nature. We took into consideration the concept of scientific explanation that allowed us to connect the ontic and epistemic side of the concept of species. The scientific explanation of what species are, in fact, can make this explicit via the various epistemic roles played by such a concept in biological investigations, and via certain ontological assumptions about what is denoted by such a term. In other words, “species”:

- explains the taxonomy of living beings since this concept is based on certain ontic assumptions about the properties of species and the cause of an individual’s belonging to a species;
- and/or it describes this membership as a consequence of methodological operations and conceptual assumptions used in biological research.

In this paper, we will show that the new mechanistic discussion contributes to highlighting the epistemic and ontic reasons for the lack of a single definition of species. A consequence of this is often an irreconcilable distinction between the concept of species as the basic unit for classification and the concept of species as the basic unit for evolution (Dupré, 2001). Indeed, we will emphasize some incongruities in the concept of species by referring to different biological kingdoms. “Kingdoms”, in turn, is a problematic concept that has been discussed since the 1960s (Whittaker, 1969; Kwok, White, Taylor, 1986; Cavalier-Smith, 1981, 1986, 1989; Barr, 1992) and still has an obvious and direct connection with the problem of species definition. Therefore, we will focus on the latter and the consequent need to consistently clarify the epistemic and ontic references in every species definition.

To achieve our main aims, we will divide the paper into four sections. In section 2 we will show that since the advent of Darwinism, the concept of species has been transformed by shifting from hierarchical Linnean ranks to a long series of parent-offspring relationships. Such a change will be discussed from the perspective of the definition of the species, up to recent proposals. We will point out that the idea of species is limited in terms of its explanatory power by emphasizing that there are two main issues concerning the species problem: at the epistemic level species are treated as categories with various constraints, but at the ontic level they are the outcome of speciation events. We will start by pointing out the ontic-epistemic origin of the species problem. In the section 3 we will follow this distinction by further exploring epistemic and ontic issues concerning the species problem in relation to the dominant philosophical approaches. We will point out that the nominalism-realism metaphysical debate underpins the debate on species, noting that the realism vs nominalism debate is orthogonal to the monism vs pluralism one. We especially focus on pluralism since it has become a major approach in dealing with the species problem in recent decades.

In section 4 we will clarify that the new mechanistic philosophy is engaged in the species problem, since it concentrates on one of the species accounts, that is, the Homeostatic Property Cluster (HPC) approach to natural kinds. On the one hand, we will argue that the latter must be understood within the nominalism vs realism debate about the species category. On the other hand, we will emphasize some problems stemming from the realist assumptions of HPC, that is, the problematic role of explanation within such a theory (its theory-dependence) and the risks arising from the application of the notion of mechanism to natural kinds. After that we will show that the new mechanistic account relies on the HPC theory and contributes to the nominalism vs realism debate about the species category. We will point out that the new mechanistic approach is merging the ontological distinctness of natural kinds with the pluralist approach in its theory-dependent guise. Furthermore, we will discuss three epistemic problems (the boundary problem, the complexity problem, and the circularity one), showing why the new mechanistic approach should be regarded as the theory-dependent one. Finally, we will formulate three conclusions: 1) the concept of causal mechanism is not a decisive argument for realism about natural kinds or species; 2) the perspectival character of the concept of mechanism is not a decisive argument for nominalism about natural kinds or species; 3) the use of the mechanistic explanation entails a sort of theory-dependent pluralism about natural kinds or species.

In section 5 we will describe the debate on the species concept in relation to different kingdoms (Bacteria, Fungi, and Animalia). In botany, zoology, and microbiology there are those supporting the existence of a single definition of species based on the ontological differences between the various groups. On the contrary, some studies have suggested the use of different criteria, which take different biological aspects into consideration, for specific classificatory purposes. This last approach reinforces the need for a pluralism of species concepts to explain the complexity of biological world. Furthermore, we will show that although there are biological differences that characterize the different research fields, the question about the realism of species remains unsolved and creates two opposite approaches: an approach seeking to find the ontological status of real species and one seeking to establish methodological boundaries to divide organisms into different groups. Finally, in this section we will explain how the new mechanistic approach has the merit of having shown that the concept of mechanism always has a two-sided nature: on the one hand, mechanisms are natural kinds; on the other, they are a model-theoretical construction and a means of scientific representation. Mechanisms, if applied to the species problem, are central for constructing a scientific explanation, though they are placeholders, indicators around which a theory is built. The paper ends with a discussion of main conclusions.

2. Problems surrounding the classification of species

The natural selection of species has attracted considerable attention since Darwin's time. In the "Origin of Species", Darwin (1859) referred in many ways to the idea that species become increasingly matched to their respective environments. The celebrated principle of natural selection derives from other principles, particularly that of variation within every species and that of inheritance in relation to the inheritability of certain variations. The principle of competition between different populations and the principle of variation in fitness are needed to complete the Darwinian theory. This theory long remained incomplete and replete with misconceptions. According to Mayr, the success of the Darwinian explanation is due to its ability to treat confused or misconceived concepts, especially the idea of variation, as "black boxes". In other words, Darwin understood that while it was impossible to explain such processes in detail, for his purposes it was not necessary to find a deep causal explanation (Nathan, 2021, pp. 49-55). He pursued his research anyway and left many questions unanswered.

Finding satisfactory answers remained difficult and the founders of the New Synthesis (Dobzhansky, 1935) were aware of this. In particular, the biological species concept took shape: species are historical entities, and the reproductive barrier became the sole criterion of delimitation, with Mayr and Dobzhansky. Furthermore, in this case, the difficulty was clear from the beginning:

> "This new concept is not applicable to asexually reproducing organisms. (…) The supporters of the Biological Species Concept, therefore, agree with their critics that the Biological Species Concept does not apply to asexual" (uniparental) organisms. (Mayr, in Wheeler-Meier 2000, 17-29, p. 23).

This concept does not apply in two cases. First, it does not apply to fossil organisms (Mayr,1949): in this case, the problem is obviated by defining the species in an operational sense or in a sense such that the scientific concepts are constructed based on the set of operations conducted on the entities studied (Bridgman, 1938). Secondly, in the case of microorganisms, for which sexual reproduction is not necessary or absent, even the ecological definition of species does not solve the problem, based on the line of descent and therefore on the causal mechanism. Indeed, excluding that it is sexual reproduction that determines the adaptive zone of the species, the environment and the ecological needs of organisms are used. The definition of the "ecological niche" of the species becomes equally ambiguous, both for reasons of circularity in relation to the very concept of species (Lewontin, 2000) and because there are species that can cross several "niches" during their evolution.

Other definitions of species run up against analogous problems (Ereshefsky, 2017; Ghiselin, 1974; Stamos, 2003; de Queiroz, 2007). It emerges from this literature that every concept of species is based on criteria that justify the classification and formation of groupings.

> “The proposed solutions to the species problem are usually evaluated according to their agreement with the unifying framework of the theory of evolution. For example, a good definition of the species concept must apply to every organism, but also according to their operational value in demarcating such or such species. Putting these two requirements on the same level amounts to mixing up the definition of a taxonomic category (i.e., the definition of a concept) and the criteria that may be used to identify the taxa that fall under this category” (Samadi and Barberousse, 2006, p. 509).

Divergence and diversification, as well as the reconstruction of phylogeny, are elements necessary for an ontological interpretation of taxonomy (Henning, 1996); the more complex and numerous the data are, the more difficult the ontological interpretation becomes (Haber and Molter, 2019). The issue is felt to represent an insoluble problem (Hey, 2006; Haber and Molter, 2019). This insolubility is so great according to some researchers that they have suggested removing the problem from the list of those to be solved and reducing it to an operational issue; for others, this insolubility requires temporary solutions that, although incomplete, can be effective from an operational viewpoint. The need for a universal definition of species does not imply that all the criteria to distinguish species should be indifferently applicable to every group of organisms. Instead of insisting on the soluble/insoluble dichotomy, another approach can be adopted.

A recent proposal offers interesting perspectives, even if it does not solve all problems (Galtier, 2018). The idea is to take as a reference system a category of taxa around which there is a high degree of consensus. The criteria that justify the organization of this category and distinguish it from the next one, can become the criteria to configure other species: in this way, you have a versatile method, which can be adapted to any type or amount of data. Moreover, the taxonomy is already based on a comparative system, to the point of making the discussion on the identification of new species very heated. The essential element is the reference to datasets, as well as scientists’ views: hence, the rule that manages the datasets is important but, above all, it is exportable from one case to another. According to Galtier, the issue of which taxa we should take as our reference points remains to be decided: in his study, he looked at *Homo sapiens* and its close relatives. From this, we get two rules (Galtier, 2018, p. 661):

> Rule 1: Any set of entities showing greater divergence/differentiation than that observed between humans and chimpanzees should be considered distinct species.
> Rule 2: Any set of entities showing less divergence/differentiation than that observed between distinct human populations should be considered a single species.

The rules outlined here cannot solve the most difficult cases of species differentiation, but offer an operational criterion in many cases, both to differentiate species and to assess the belonging of each element to the species. The continuum between the species is supposed, but is not demonstrated: the two rules tend toward a nominalist interpretation of the species problem, but, beyond the operational criterion, they also offer cues to deal with the ontological problem: they recall the interdependence established at the level of formal rules (modes of data collection and calculation) and the extra-formal point of reference (the relationship between data and reality of the taxon).

The state of affairs regarding the species problem is intriguing and the debate on the correct definition of the notion of species continues. It is not at all the case that this problem – which has been raging since Darwin’s time – has been solved. Why is it so? There are two main issues concerning the species problem:

1) at the epistemic level there is the conflict between various theoretical constraints imposed by proposed concepts and the operational methods applied to the identification of species;

2) at the ontic level species are the product of speciation events; in this case the term “species” denotes various ontological meanings, e.g., species denoting a category of classes or a category of spatiotemporally limited entities.

At the epistemic level species are treated as categories with various constraints. They help researchers identify organisms by creating distinct groups which can be used in the process of recognition, and thus classification, of unknown entities based on their similarity to known objects. Among the very general virtues of establishing divisions by species, one may indicate for instance comprehensiveness or reasonably sharp boundaries between groups (Dupré, 2001, pp. 209-212). But species are also the product of speciation events (Hey, 2001). In this case they are “things” in the world. At the ontic level species may be treated as individuals or classes. However, some authors suggest that such a dichotomy is misplaced, since the units of evolution may be considered to be not species, but lineages. The latter are conceived of as “sequences of entities related by ancestry and descent” (Dupré 2001, p. 213). The relevant entities in this case will be populations. Our concern here is not to discuss all ontological commitments entailed by the term “species” (Reydon, 2005), but to point out that this term may denote various ontological categories: classes, concrete entities, populations, etc. We have tried to describe the ontic-epistemic origin of the species problem. Now we will discuss the main proposals for grounding the species concept, with special attention to the traditional opposition between nominalism and realism which lurks in the background of the species problem.

3. Various accounts of species

Before offering an overview of various accounts of species, let us note that biologists may say a lot of things about the descriptions of traits possessed by the individual object of their inquiry, i.e., they may describe its typical behaviors, physiology, habitat, etc. However, they may wish to describe not an individual object, but the species as a whole. Even if biologists are interested in describing particular traits of particular objects, they do not focus only on individual-level descriptions but seek higher-level descriptions, by focusing on certain kinds of things, traits, properties, etc. On the one hand, in order to collect a certain group of individuals together in the same species, one needs to have clearly identified a specific characteristic that they share as a fundamental element; on the other hand, as a general term “species” seems to be fruitful from an explanatory standpoint, since it allows inferences from few samples to general statements. Those elements which afford the inductive fruitfulness of species may be interpreted as genuine features of the world, rather than merely our own way of arbitrarily classifying them. Indeed, there seems to be a contrast between classifying species and grouping elements in some aggregates (Slater 2013, pp. 6-11).

What we have just stated may be expressed in more philosophical terms as two different approaches – the nominalist and the realist one – which “carve nature at its joints”. The first approach seeks to carve nature between concrete particulars, since it divides the world up into concrete objects, composed of further elements. According to the nominalist perspective, successful determination of the boundaries between objects means adequately carving nature at its joints. Species are treated as concrete particulars located in spacetime: they are as real as other composite objects. In contrast to the thesis that species are individuals, one may treat species as natural kinds (or sets, classes, universals, etc.). Indeed, there is a long-standing debate as to whether the term “species” denotes a category of concrete entities with organisms as their elements rather than abstract classes (Ghiselin, 1974; Hull, 1976, 1978). According to this second approach the term species conveys “the idea of a class of objects, members of which shared certain defining properties” (Mayr, 1996, p. 268). Although the term “natural kind” does not have a univocal meaning (Hacking, 1991), we assume that, in the case of the species problem, natural kinds may be treated as universals, that is, as repeatable and abstract features of reality that may be instantiated.

As it turns out, the crucial metaphysical issues about the species problem is the nominalism-realism debate. In some circles the nominalist stance is called the antirealist one. The nominalist theory rejects general concepts, being only focused on particulars; the realist stance avoids the unique role of particulars, as it concentrates on genuine properties present in the world. Nominalists regard classificatory divisions as arbitrary inventions reflecting our epistemic conventions and strategies; for the realist, on the contrary, such divisions are to be discovered in the world. We should bear in mind that the realism vs. nominalism debate is orthogonal to the monism vs. pluralism debate (Nathan, 2019, p. 3), although very often the two are connected. Monism is the thesis that there is a single, uniquely correct species division. Pluralism suggests that there are in fact many equally legitimate ways of establishing such a division. If there are many equally good ways of carving up the world into species, it may seem that no classification of species is objectively better than any other. While accepting species pluralism seems to entail antirealism with regard to species problem, monism entails a realist stance. Although some authors have defended the nominalist version of pluralism (Stanford, 1995; Ereshefsky, 1998; Devitt, 2009), others have combined realism with pluralism (Kitcher, 1984; Dupré, 1993, 1999; Boyd, 1999; Slater, 2013). The apparent connection of the monism-pluralism debate with the realism-nominalism one stems from the fact that, without further specification, the realist stance can virtually mean anything, that is: both worldly things and abstract concepts or theory-dependent entities may be considered real. In short, the realism-antirealism debate and the monism-pluralism one on the species problem are conceptually independent, but often intertwined.

In recent decades, pluralism has become a major approach in dealing with the species problem. Some authors suggest that there are equally legitimate species concepts and that the reason why there are many species concepts is that biologists are legitimately interested in a heterogeneous set of questions, each of which requires logically independent and equally valid concepts of species (Pigliucci, 2003). On the contrary, monists seek a single, universal definition accounting for all species (Dobzhansky, 1940; Mayr, 1970). Among the latter, De Queiroz (2007) suggested that an essential prerequisite for the species category is being the most general category at its level of biological organisation. The situation seems to become increasingly complex if we also consider recent studies (Doolittle, 2019; Dupré, 2017) suggesting a shift of focus from the “ontology of the substance” to the “ontology of the process”. Nathan scrutinizes species pluralism by distinguishing its basic two theses:

> “The first one is […] ‘heterogeneity.’ This is the claim that the species category is an ontologically mixed bag of entities. More precisely, the species category includes multiple types of species taxa, presumably because different species may be produced by a variety of natural phenomena. The second strand of pluralism involves a view that can be dubbed ‘theory dependence.’ Here, the guiding thought is that assignments of species-level taxa crucially depend on both the organisms and the evolutionary processes in question, and on the explanatory target at hand. Theory-dependence entails that there is no uniquely correct, objective, or natural way of grouping organisms into species, or into any other rank of the Linnaean hierarchy” (Nathan, 2019, p. 7).

The meaning of these two dimensions of pluralism changes considerably across three influential stances present in the current literature on the species problem (second-order pluralism, encompassing the variety of taxonomic practices; eliminativism regarding the species concept; and pragmatism, which retains the centrality of the species concept in biology). The pluralism of pluralisms makes it hard, even impossible, challenging or even impossible to solve this problem at the ontic level.

Let us point out the main theoretical problems emerging from our discussion of various accounts of species. At the epistemic level, first of all, the criteria that allow the induction of general entities (species as classes) starting from a multiplicity of individuals, or the criteria that allow the opposite operation, i.e., descending from species to individuals (class elements), must be explicated and justified in every explanation. Secondly, carving up the species is a theory-dependent problem. Many interpretations of species entail that its definition can be interpreted both within the realist paradigm (i.e., that it can be taken to mean something that exists in reality before any conceptual abstraction) and within the nominalist one (i.e., as a conceptual instrument that is not necessarily related to the structure of reality (Bridgman, 1938). At the ontic level, first of all, there are various kinds of species present in nature and natural phenomena prove to be highly complex. Secondly, the boundaries between living species are often flexible and it seems impossible to fix them univocally: natural phenomena are not sharply divided. There are therefore various epistemic and ontic issues surrounding the species problem. In the following section we will show how the mechanistic literature contributes to that specific debate.

4. Mechanistic strategies and the species problem

Since the 2000s, the concept of mechanism has received significant attention in the philosophy of science, especially in the domain of the life sciences (biology, medicine, cognitive science, and neuroscience) (Glennan & Illari, 2018; Levy, 2013). It has three fundamental meanings: the first, more general, has to do with the life and behavioral patterns of living things; the second concerns the structure enabling the repetition of these mechanisms; finally, the third meaning enhances the explanatory power of the concept of mechanism with respect to natural phenomena (Nicholson, 2012). One may ask why the new mechanistic philosophy should be involved in the species problem. The answer is that all three aspects just mentioned impact the species problem. First, because the concept of species directly and obviously has to do with defining the behaviours of living things. Moreover, this concept is used as a pattern to achieve classifications and identify regularities. Finally, many life-world problems are related to the definition of species. We will move now within the boundaries drawn by the mechanistic approach. First, we will discuss if the HPC approach to natural kinds has to be understood within the nominalism vs realism debate about the species category, and after that then we will show whether – and, if so, in what way – the mechanistic literature contributes to that this specific debate.

4.1 The homeostatic property cluster theory and mechanisms

Boyd (1999) proposed the homeostatic property cluster theory (HPC) as a regulatory standard for all natural kinds: according to it, some mechanisms maintain recurrent properties in a cluster by decreasing the possibility of deviations. Boyd sought to defend property cluster kinds against a merely instrumentalist interpretation (i.e., kinds as a conceptual instrument not related to the fundamental structure of reality). Instead, he aimed to find some natural basis for them. According to Boyd, the postulated existence of homeostatic mechanisms is capable of explaining the stable properties displayed by various members of the same kind and also plays a crucial role in epistemic practices like induction and prediction. His theory advocates a weakened form of essentialism: it explains that species are characterized not by a property or a defined group of properties, but by a cluster containing many properties that need not be simultaneously possessed either individually or jointly by each element of the species conceived as a kind.

Reflection on Boyd's HPC conception of kinds has been particularly exciting for those philosophers of biology who are unhappy with traditional essentialism and approaching biological kinds as historical entities. Its general concern is with the causal underpinning of the relevant clusters of properties by homeostatic causal mechanisms. Moreover, it presupposes a class ontology of species, since it focuses on the role of species as denoting units of generalization. It attempts "to ground the role of species as generalization-supporting groups of organisms in external evolutionary factors rather than in the intrinsic nature of organisms" (Reydon, 2005, p. 148), insofar as HPC pertains to the organizational level of clusters of organisms. Boyd (1999, pp. 165–167), conceptualizes species as natural kinds with populations as their members. To summarize, his approach merges realism with pluralism and, in relation to the latter, fits with the theory-dependence strand.

Looking for a deeper understanding of HPC realist assumptions, some scholars have recently advanced some critiques by pointing out, on the one hand, the problematic role of explanation within such a theory (its theory-dependence) and, on the other, some risks arising from an interpretation of

Boyd’s theory through the notion of mechanism. We will briefly focus on the former issue; then, in the next section, we will dwell on the new mechanistic view of HPC.

It may be noted that homeostatic mechanisms are the foundation of HPC-type natural kinds in so far as they are the basis of their stability. The lurking presumption, then, is “that something is a natural kind if and only if it accords with the HPC notion of natural kinds” (Lipski, 2020, p. 96). This presumption entails the risk of over-generalization, as it may lead to the conclusion that HPC works as a normative criterion for kindhood and applies to all natural kinds. Moreover, the reading of HPC according to which the properties of natural kinds arise out of uniform underlying mechanisms, may become problematic. The price we have to pay in this case is very high. Although the investigation of lower-level properties is scientifically very useful, there are ways of identifying specific natural kinds other than lower-level implementation (e.g., molecular pathways). In the life sciences, there are very common functional explanations in which valuable groupings are identified by the specific functional roles of various parts or entities. If such explanations range from the very detailed to the very schematic, properties can be clustered, regardless of the fact that their lower-level components display a certain degree of diversity. The homogeneity of lower-level mechanisms is theory-dependent and it does not appear capable of yielding a final verdict as to whether the higher-level grouping sustained by mechanisms counts as a natural kind. Besides, there are good reasons to think that there are exceptions to such a notion of stable kinds, as we will be discussing later in relation to microbiology and zoology.

Moreover, some authors pointed out that natural phenomena exhibit peculiar characteristics, such as being scale-free and having a small-world organization, that prevent the researchers to use the original idea of mechanisms as well-delineated systems. In this perspective, Bechtel stated (2015, p. 92) that “mechanisms are viewed not as entities in the world, but as posits in mechanistic explanations that provide idealized accounts of what is in the world”.

4.2 The new mechanistic philosophy and the species problem

This section is concerned with how the new mechanistic account relies on the HPC theory and how it contributes to the debate about the species category. Craver (2009) has directly brought together the mechanistic agenda and the HPC approach to natural kinds. He notes that the normative constraint following from the HPC view

> “is that taxonomies of natural kinds are adequate to the extent – and only to the extent – that the kinds in that taxonomy track mechanisms, that is, that the recognized kinds correspond to the mechanisms that constitute the causal structure of the world. Kind concepts cut nature at its joints, and according to this normative constraint, nature’s joints are located at the boundaries of mechanisms” (Craver, 2009, p. 575).

The core aspect of the HPC theory, which perfectly fits within the new mechanistic agenda, is that it draws the boundaries between property clusters by identifying the underlying mechanisms which sustain those properties. In other words, phenomena are product of interacting mechanisms. The latter are made up of components that can be isolated and described according to HPC theory. Thus, the explanation of phenomena can be achieved through the examination of those single parts. On the one hand, it makes it possible to support the ontological distinctness of natural kinds and thus fits very well with the realist stance. However, this distinctness at the ontic level should not be interpreted from a monist point of view: according to Craver, it is a “flawed assumption” to believe “that there must be a uniquely correct and orderly taxonomy of the mechanistic structure of the world” (Craver, 2009, p. 592). The new mechanistic approach instead merges the ontological distinctness of natural kinds with the pluralist approach in its theory-dependent guise. We will now discuss three epistemic problems to show why this is the case.

The first problem is the boundary one, widely discussed in the mechanistic literature. The question concerning the criteria for identifying the boundaries between different entities, activities, and mechanisms themselves is difficult to solve (Tobin, 2018; Kaiser, 2018). Replacing the boundary problem for kinds with the boundary problem for mechanisms does not resolve the issue but only postpones it. One can point out different principles that guide the carving of the components of mechanisms, such as the natural boundaries of biological objects (e.g., the cell membrane, the skin, the mountain range bordering a specific ecosystem) (Darden, 2008), or invoke the strength of interactions (e.g., in nearly decomposable systems, the interactions between the various parts are generally stronger than those between the object's parts and the environment) (Simon, 1962; Wimsatt, 1972). Furthermore, Craver's account of constitutive relevance has been considered a prominent way of solving the boundary problem (Craver, 2007, pp. 139-160): it concerns the way in which the activities of parts make a difference to the activities of wholes. Whether Craver's account is successful in solving the problem of constitutive relevance is the subject of much ongoing discussion (Leuridan, 2012; Romero, 2015, Baumgartner & Gebharter 2016; Harinen, 2018, Craver et al., 2021).

The second difficulty is the complexity of the mechanisms problem. Craver was aware of the challenge of trying to divide the world into kinds on the basis of the complex activity of mechanisms. For instance, the human body has many co-occurring and continuously interacting systems which are responsible for the various activities of the body, such as the cardiovascular, respiratory, nervous, endocrine, and musculoskeletal systems. The deeply problematic issue, then, is not whether a homeostatic mechanism explains why the properties in the cluster regularly co-occur, but which mechanism is responsible for the *explanandum*. Craver dwelt on the two common strategies embodying the central commitments of the HPC theory, that is: the lump methodology and the split one (Craver, 2009, p. 581). These may be described as strategies for producing scientific taxonomies that track the mechanistic underpinning of phenomena. For instance, in the case of a speciation event where the differentiation of ecological conditions is significant, this differentiation changes the mechanism for the subset of the species population that evolves under selective pressures and experiences random events different from the rest of the population. In this case, one is forced to split the species into two separate ones, given the operation of the new mechanism. However, tracking the mechanistic underpinning of a phenomenon like speciation is far from straightforward, considering that what we are dealing with here is neither a sequential and linear process, nor a highly regular one (Skillings, 2015). Although this splitting-lumping strategy seems to be very attractive, Craver emphasized that very often the decision to lump or split involves conventional and contextual elements: the boundaries of a mechanism depend on our choice of the property cluster (*explanandum*) and on how we choose to describe that cluster (degree of abstraction).

We can now explicate the third problem, the circularity problem, which lies in the background of the previous ones. We have noted that the application of mechanisms for clustering properties of natural kinds works in the following way: we start by delineating property clusters on the basis of mechanisms, but when addressing the issue of the identification of mechanisms in scientific practice, we require kinds of property clusters. Mechanisms and property clusters thus become inter-translatable.

Does the mechanistic reading of the HPC theory, then, provide a better grounding of taxonomic judgements? Does it solve the species problem? We will offer three answers, connecting each of them to the debate on species definition.

First of all, some scholars, such as Slater (2015) and Ali Khalidi (2018), have suggested replacing the notion of mechanism with other causal notions. While Khalidi postulates replacing the notion of mechanism with causal processes captured by causal graphs, Slater argues that natural kinds are characterized by stable cluster properties. Although a detailed analysis of both approaches is beyond the scope of this article, we wish to stress that – leaving aside the mechanistic perspective and metaphysical discussion on the grounding of property clusters – these two refinements of cluster theories of kinds cannot provide an unproblematic way of making inductive inferences concerning natural kinds (Onishi & Serpico, 2022). Both the consideration of underlying causal processes and explanatory interests play an indispensable role in these alternative approaches to natural kinds, showing that the ontic and epistemic aspects of mechanistic explanation work together. A few consequences can be outlined. First, the concept of causal mechanism is not a decisive argument for realism about natural kinds or species. Second, the identification and decomposition of mechanisms as an inherently perspectival (epistemic) matter does not imply that parts are not mind-independent, even though the parts in different decompositions may overlap. The interconnected character of nature hinders the description of sharp boundaries among the mechanisms, but this does not entail that the epistemic perspective is necessarily arbitrary or unconstrained. The scientists are not merely cutting nature at conveniently chosen joints, but they discover and localize natural mechanisms through heuristics (Bechtel, 2015; Craver, 2001). The second corollary is that the perspectival character of the concept of mechanism is not a decisive argument for nominalism about natural kinds or species.

Thirdly, the mechanistic literature shows that strategies of abstraction or idealization are abundantly used in life sciences, especially to elucidate system-level patterns of organization that cannot be predicted from or derived *ab initio* from the features of the system (Levy & Bechtel, 2013). The presence of abstractions and idealizations in the models often leads to the misrepresentation of the causal relations between parts and activities in mechanistic explanations (Love & Nathan, 2015). Although some authors have pointed out certain conceptual inconsistencies in the debate on the nature of idealization and abstraction as employed in mechanistic explanations (Zach, 2022), both epistemic strategies remain essential and irreducible features of scientific explanation. On the one hand, this is because explanation involves a necessary trade-off between explanatory power and descriptive accuracy; on the other, the goal of explanation is to provide not an all-encompassing model of the target phenomenon, but rather a series of many complementary and partial descriptions similar – to a certain degree – to what is being investigated. As Glennan (2017, pp. 59-105) has argued, this means that we cannot understand mechanism kinds without using models of particulars (organized entities and activities) which are highly abstract and idealized. The interplay between the explanatory interests of the modeler and the objective features of the target determine whether a model is good enough for an actual target. An interesting example of this approach was given by Poliseli and coworkers (2022), who demonstrated that the heuristic gathers the instruments that guide scientists' actions in model building. They showed that show that, even though a mechanistic model was developed, it was nonetheless substituted for a broader theoretical model that fitted best the ecological system. Thus, the use of mechanistic explanations entails theory-dependent pluralism about natural kinds or species. The monist stance is rejected.

Let us make explicit three points on how the new mechanistic philosophy contributes to the debate about the species category via the development of the HPC's main assumptions:

1) the concept of causal mechanism is not a decisive argument for realism about natural kinds or species;
2) the perspectival character of the concept of mechanism is not a decisive argument for nominalism about natural kinds or species;
3) the use of the mechanistic explanation entails theory-dependent pluralism about natural kinds or species.

Point 3 shows that the pluralist stance is the viable option from the mechanistic point of view. The interest-relativity of our classificatory categories, such as species, entails that various epistemic strategies and constraints remain essential and irreducible features of any scientific explanation. Points 1 and 2 entail that neither realism nor nominalism about natural kinds or species is the solution to the problem. What can we offer instead of them? While mechanists do not explicitly formulate the third metaphysical option, we believe that the mechanistic proposal can be formulated in the form of the following prescription: we should moderate the ontological implications we draw from our explanations of natural kinds or species. Close attention to the various accounts of species shows that they play important and distinct roles within the sciences. On the one hand, they work as metaphysical posits; on the other, as explanatory postulates. In the former case, the objectivity of species is what grounds the objectivity of explanations, and sound explanations of species require us to identify the relevant factors at work in evolutionary processes. As explanatory postulates, they play a specific role restricted to the context of a particular theoretical framework or model (Nathan, 2020). In this case, species are essentially preliminary hypotheses or theoretical units awaiting to be replaced by more perspicuous explanatory elements. This distinction between species *de re* and explanatory species provides the conceptual resources to rethink the presence of ontic and epistemic aspects in the long-standing debate on natural kinds and the notion of species. The inconclusiveness of the first and second point can be expressed through the following philosophical maxim: "distilling metaphysical implications from scientific explanations requires close attention to explanatory practice" (Nathan, 2015, p. 773).

5. The biological species problem

The concept of species is not arbitrary, but certainly proves very fluid. The following paragraphs aim to show the species debate in different biological fields related to mammals and microbes that are characterized by different mechanisms of genetic recombination. This is the physical exchange of DNA between two genetic elements and represents the main source of variability. In mammals the variability is due to Homologous Recombination (HR), i.e., the exchange between paired chromosomes, while in microbes Horizontal Gene Transfer (HGT) is the mechanism that produces diversity. The former mechanism underlines a particular faculty of mammals, namely sexuality, or rather the presence of two separate sexes. On the contrary, in microbes sexuality is absent or elective and thus the mechanism of recombination consists in the movement of genetic material among organisms that are not in a vertical relationship (parent-offspring).

The different frequencies of these two mechanisms between the two domains (High HR and the near-absence of HGT in mammals vs. High HGT and the absence of HR in microbes), make the application of the same theoretical concept difficult. Hence, Novick and Doolittle (2021) proposed that we consider the species concept a patchwork concept generated by the application of various notions of species to new domains.

5.1 The species problem in mammals

Taxonomy in the kingdom of Animalia, to which mammals belong, was originally based on the idea that species are separated by gaps (Poulton, 1904). However, the presence of geographic varieties introduced the concept of subspecies, which were considered taxonomic entities immediately subordinate to species. This evidence led Richard Lydekker to follow "the principle of classing nearly related kinds of animals as races of a single species, rather than as distinct species" (Lydekker, 1913, 1-249), spreading the concept of polytypic species, which made it possible to further divide all the members of a class into a minimum of two subspecies (Rothschild, Hartert, & Jordan, 1903). Around 1920 the science of genetics began to focus on the properties of populations and the ways in which such properties could be maintained or altered, so there was a shift from considering the individual differences between organisms to evolution at the population level. This paved the way for the definition of species as "groups of actually or potentially interbreeding natural populations which are reproductively isolated from other such groups", as stated by Mayr when outlining the so-called biological species concept (BSC) (Mayr, 1942). In his review of Primate taxonomy, Groves (2014) reported an example demonstrating that different species can interbreed, even when they are sympatric: it was found that two consistently different species of North American deer, the white-tailed deer (*Odocoileus virginianus*) and the mule deer (*O. hemionus*), had historically been interbreeding in areas where their ranges overlap. This confirmed the objections raised against the BSC but did not discourage realists from searching for the best explanation for the presence of discrete groups. De Queiroz, for instance, acknowledged that the common idea underlying the different concepts of species was to compare them to groups of interconnected populations forming an extended reproductive community; he thus postulated the General Species Concept, according to which species are separately evolving metapopulation lineages (De Queiroz, 2007). The main issue raised by this definition is its applicability: as Zachos has pointed out, "if species are really to be objective entities without arbitrary delimitation criteria as to their inclusiveness, then any two allopatric populations cannot be conspecific" (Zachos, 2018, 153-159) because they would not be included in the same species. Groves and Grubb (2011) tried to overcome this limitation through the phylogenetic species concept (PSC), according to which "[a] species is the smallest population or aggregation of populations which has fixed heritable differences from other such populations or aggregations". According to Groves, shifting from the "old way of thinking" – represented both by the polytypic species concept and the biological species concept – to the phylogenetic species concept, supported by a gradual rethinking of species as evolutionary lineages, it is possible to achieve a new understanding of primate biodiversity. Groves thus affirmed that PSC avoids misleading biases concerning interrelationships, "by insisting on simply identifying the units of biodiversity", and avoids concealing what may be strong biological differences, "by splitting the population to the smallest diagnosable units" (Groves and Grubb, 2011).

Zachos (2018) questioned the use of PSC because, according to him, there is no objective way of deciding where the line should be drawn along the trajectory of the evolution of two species. The point when it comes to addressing the species problem for Zachos is to recognize the inconsistency of any species delimitation grounded in the effort to reduce continuous variability to discrete, binary, taxonomic classifications, so as to stress the inherently fuzzy boundaries present in nature. As he states, "[t]he only remedy would be a very crude yardstick such as genetic similarity based on certain marker genes" (Zachos, 2018, 156), which would create meaningful taxonomic units based on some measure of phylogenetic diversity.

This section has highlighted the debate on the definition of species in relation to mammals, which are genetically characterized by a high degree of internal cohesion that ensures similarities between organisms belonging to the same population and increases the divergence between the different populations. This characteristic should have helped zoologists to determine the proper mechanisms that maintain recurrent properties, and with them to arrange organisms into natural kinds. The two positions described here (the phylogenetic species concept (PSC) vs the meaningful taxonomic unit) emphasize the effort to find a unique definition, based on ontological aspects and the need to establish operational criteria to distinguish organisms according to an epistemological method. In conclusion, the question of the reality of the species remains unsolved in relation to mammals.

5.2 The species problem in Microbes

5.2.1 Pluralism in microbial species definition

The discussion on the ontological status of species gets more complicated when microbial species are taken into considerations. Indeed, the absence or elective character of sexuality rules out the possibility of using the mechanism of reproductive isolation to delimit those groups of organisms. Moreover, the high degree of HGT complicates the establishment of precise boundaries, thus limiting the cohesiveness of such groups. For these reasons, as Ereshefsky noted, the biological species concept (BSC) proposed by Mayr (1970) cannot be applied to microbiology, since the presence of HGT makes microbial species open gene pools (Ereshefsky, 2010). So, reproductive isolation could be considered a mechanism for species definition, but it needs to be adapted to the different genetic backgrounds of the organisms taken into account (Ko, 2007). Similarly, the ecological species concept – in which a lineage occupies an adaptive zone which is only minimally different from that of any other lineage in its range and which evolves separately from all lineages (Van Valen, 1976) – was adapted to explain (genotypic and phenotypic) cohesion and divergence between species ("cohesive divergence") for asexuals. Such an explanation was offered by the Stable Ecotype Model, developed by Cohan (2002). According to this definition, species in the bacterial world may be understood as an evolutionary lineage bound by ecotype-periodic selection. Ecotypes are subject to neutral mutation and drift, which, along with periodic selection events, result in separate clusters of ecological and genetic diversity. Thus, coherence is maintained by eliminating diversity in a species that arises by mutation and deviates from a species' niche-specific adaptations. The species will vary following changes in its environment. These are two examples that illustrate why the mechanisms used to define species in the kingdom Animalia cannot be directly applied to microorganisms, but need to be revised and adapted to different molecular mechanisms. Thus, the difficulties in applying the notions used in the macroscopic world, together with the limited range of phenotypic traits, led microbiologists to use molecular markers in order to organize microorganisms into different classes. The development and application of DNA-based analyses promoted the use of genotypic traits to ensure a more accurate characterization of an organism. The DNA-DNA hybridization (DDH) of genomic DNA (Johnson and Ordal, 1968) was acknowledged to be the genotypic "gold standard" for the comparison of prokaryotes. A DDH similarity of approximately 70% served as the recommended demarcation to define bacterial species. This method proved to be pragmatic, operational, and universally applicable. A few years later, the *ad hoc* committee for the re-evaluation of the species definition in bacteriology suggested the adoption of techniques such as 16S rDNA sequence analyses, which established the major role of the relationships between these sequences in the definition of bacterial species (Stackebrandt, 2002). Because of some molecular characteristics of ribosomal sequences such as universality across taxa, the presence of conserved and variable regions, and a high barcoding gap, nucleotide sequences have been widely used in microbial taxonomy.

5.2.2 Efforts to find optimum criteria for the definition of microbial species

Ribosomal RNA sequence analysis has been employed for the identification of both *Prokaryota*, with the 16S gene, and for *microbial Eukarya*, such as yeast, for which ITS sequences are currently considered the standard barcode (Schoch, 2012). This means that the amount of divergence of such sequences is the criterion by which microbiologists divide the organisms into different species. Two recent works by Suárez (2016; 2020) have demonstrated that not even the use of molecular markers is enough to define microbial species, because this use does not take into consideration the kind of functional differentiation that could distinguish genetically similar organisms. In these articles, Suárez has shown that the different goals pursued by different disciplines require different concepts of biological species, even if this may lead to cross-classification. Indeed, as the author states "different properties are emphasized and therefore different cross-classifications can exist in perfect harmony" (Suárez, 2016, 91-105). Another aspect that, according to Suárez (2020), should be considered when trying to delimit microbial species is their role in holobionts. He reports an example demonstrating that the evolution of certain bat families could not be explained without considering the close relationship between the evolution of the bat genome and that of the microbiome that has functionally evolved in a specific way along with it. Thus, the use of rDNA sequences alone has been shown to be limiting for species definition, because they cannot describe every aspect of variability. According to Suárez, this is the reason why we should use different criteria that can fit different situations and research needs. The arguments adduced by Suárez support the pluralist approach to the species problem.

Another example that could be used for the same purposes is the metagenomic analysis of microbiota. The latter term is defined as the whole range of microorganisms that typically inhabit a particular environment, such as the soil, or a particular site or an organism (Pickrell, 2003). Microbiota are made up of a variety of species but act as an entity that fulfils specific functions. Human-associated microbiota, for example, play many roles, such as helping to digest food and produce vitamins. Moreover, they compete against pathogens and produce anti-inflammatory compounds. Such microbiota have also been shown to play a role in the formation and "education" of the immune system (Duperron, 2017). Furthermore, soil microbiota are important for the functioning of natural ecosystems. They provide nutrients by mineralizing organic matter, control organic carbon storage in the soil, suppress soil-borne plant pathogens, and, as a consequence, affect plant health and crop yield (Bonanomi et al. 2016; Aislabie et al., 2013). It was estimated that 80-90% of processes in the soil are reactions mediated by microbes (Nannipieri et al., 2003). Considering only the above two cases (gut and soil microbiota), we would like to emphasise that microbial biodiversity is not only a collection of different species but also a unit with peculiar functions. This creates a problem when trying to define microbial species, because it increases those aspects that should be taken into consideration for the correct description of biological diversity.

A taxonomy based on rDNA information is reducing the gap between the ontological and the epistemological conception of species, because differences in DNA sequences have become both the propriety defining the existence of groups that could be called species and an instrument to characterize such groups. Nathan (2019) has proposed replacing ontological stances with a sort of "metaphysical agnosticism": he avers that "[u]nless various epistemic, methodological, and conceptual preliminaries are clarified, we are not in a position to adequately address the metaphysical status of species, which is replete with controversial assumptions" (Nathan 2019, p. 8).

5.2.3 The use of the new mechanistic approach for the definition of microbial species

According to Nathan (2021, pp. 164-190), the new mechanistic approach has the merit of having shown that the concept of mechanism has a two-sided nature: on the one hand, mechanisms are natural kinds; on the other, they are a model-theoretical construction and a means of scientific representation. Therefore, a single definition of mechanism would be unrealistic because the levels of idealization and abstraction involved at the epistemic and ontological levels do not always go hand in hand. Mechanisms are central for constructing a scientific theory, although they are placeholders, indicators around which a theory is built. Placeholders can function as a frame when it "spells out an explanandum as a behavior, or range of behaviors, in need of explanation", or as a difference-maker, when it stands "for the mechanisms, broadly construed, which bring about the patterns of behavior specified by the frame, regardless of how well their nature and structure are understood" (Nathan, 2021, p. 18). By keeping the ontic and epistemic levels separate, the concept of species functions as a mechanism in the case of both eukaryotes and prokaryotes, albeit in different ways.

The reference to reality in each mechanistic representation is different. The "multiple model idealization" approach (Weisberg, 2013) provides valuable assistance here. Models are distinguished by their underlying structure (e.g., real physical entities representationally related to some abstract systems) and their interpretational capacity. Both actual reference points and imagined elements are part of the model, and the model's interpretation must explain their relationship and how the model represents phenomena. A good model is an adequate construct, but it must also have good representational skills. Considering that theories are epistemic products, multiple model idealizations can coexist and capture distinct and independent aspects of a complex system. Thus, complete knowledge of reality is impossible, but different levels of abstraction explain why an explanation also has ontic value (Glennan, 2017, pp. 59-86; Bechtel & Richardson, 2010) and why the identification of epistemic rules is so important in the definition of species (Galtier, 2018). Such an approach ensures the management of borderline cases, such as those of interspecific hybridization and polyploidy (Barrington et. al., 1989; Van Tuyl & Lim, 2003; Lafon-Placette et. al., 2016).

6. Conclusions

By the term "species" we can understand both the individual organisms that arise as products of speciation events and natural kinds used to classify and order the living world. In this sense, we could compare species to the human body, which is both an entity and a set of apparatuses that, in turn, are made up of different types of cells. Any given part of the body could be described according to its morphology, functionality, or location within the human frame. Similarly, species could be defined by considering the different proprieties of the elements they are made up of, such as metabolic pathways (Doolittle & Booth, 2017), geography (Van Valen, 1976), sexuality (Mayr, 1970), or genetic markers (Schoch et al., 2012). These different criteria have paved the way for the idea that the concept of "species" could be something like a "black box", something necessary for biology to work but impossible to define once and for all.

Section 2 has pointed out two main issues concerning the species problem:

1) at the epistemic level there is the variety of theoretical constraints imposed by the proposed definitions of species and the operational methods applied to the identification of species;

2) at the ontic level species denote various entities in the world, e.g. classes, populations, lineages, or other spatiotemporally limited entities.

These two main issues can rightly be said to constitute the ontic-epistemic origin of the species problem. In the section 3 we have shown that when it comes to the species problem, the realism-nominalism debate and the monism-pluralism one are conceptually independent, yet often intertwined. This crossing of two theoretical frameworks has not enhanced the clarity of the debate on the species problem, but rather led to various ontic and epistemic commitments being combined without proper distinctions, giving rise to a set of theoretical problems:

1) at the epistemic level:
    a. the criteria that allow the formation and usage of general concepts of entities (e.g., species treated as kinds or classes) starting from a multiplicity of individuals, or the criteria that allow the opposite operation, namely deriving individuals from general entities: both of these inferences must be explicated and justified in every explanation;
    b. the carve-up of the species is a theory-dependent problem: whether the species definition is interpreted within the realist or nominalist stance ultimately depends on explanatory choices.
2) at the ontic level:
    a. there are various kinds of species in the nature, and natural phenomena in themselves are highly complex;
    b. the boundaries between living species are often flexible and it seems impossible to fix them univocally; natural phenomena are not found to be sharply divided in themselves if one deals with the boundary issues.

Whether “the mechanistic translation” of the HPC theory of natural kinds makes it the decisive answer to the species problem remains highly dubious, as we have shown in section 4. Conflicts in the species debate do not arise only from the naïve realist assumption that species are just waiting to be discovered “in the world” – which is not actually the case – since these conflicts else emerge at the ontic and epistemic level. From an ontic point of view, it is unclear how the species is to be ontologically described, while from the epistemic point of view there is no agreement on the set of theoretical constraints to be applied indistinctly to all biological explanations. Does the new mechanistic project, then, shed any new light on the species problem? We have emphasized that the mechanistic analysis highlights the need to consider the epistemic and ontic dimensions of the species problem in close parallel. Abstractions, idealizations, and models are all necessary to clarify biological concepts, but above all, to make them applicable – i.e., useful to be translated into numbers and calculations. At the same time, numbers and calculations necessarily refer to objects. Although it is rather the modest conclusion, the mechanistic strategy is enlightening since it pays attention to how epistemic and ontic constraints are intertwined within scientific explanations and why we should temper our metaphysical implications in the case of the species problem.

In section 5 we have shown how this problem affects many living kingdoms: from Animalia to Prokaryotes and Fungi, which have different genetic backgrounds yet pose similar difficulties when it comes to formulate a unique definition of the species category. We have described how the controversy could be translated into the realism-antirealism question. On the one hand, considering the current debate in zoology, the two main positions are: a phylogenetic species concept, and the one that uses a “crude yardstick”. On the other hand, because of some characteristics proper to microorganisms that prevent the use of the common species concepts, microbiologists have long been using an epistemic approach. Indeed, DNA-based methods are the standard criteria for setting boundaries between both procaryotes and microbial eukaryotes (i.e., Fungi and Yeasts). In particular, the use of specific sequences, called barcodes, is widely used nowadays. Another point that we have explained in this section is that this procedure too has caused some perplexity, because it lacks the kind of functional information that could be useful for the correct assignment of organisms to its species. This problem entails the pluralism of species concepts, for which we can use different criteria depending on the particular classification we wish to produce. For example, a medical classification would consider pathogenic elements to distinguish between different organisms, whereas taxonomists usually classify organisms on the basis of ribosomal DNA sequences. The aim of this section was to observe how the theoretical problem of species is reflected by the specific scientific research. We concluded by affirming that the new mechanistic approach which considers the ontic dimension in close connection with the epistemic one could help deal with the species problem.

By describing the various species concepts and the debate surrounding them, we have demonstrated that the question of the reality of the species remains unsolvable if one considers univocal and definite solutions, as many scholars have reiterated. The concept of species is a necessary black box. The use of various approaches and methods remains vital. However, each approach and method enhances interconnected aspects, offering specific and circumscribed solutions. The neo mechanistic approach emphasizes this pluralism and suggests that the species problem should always be addressed by bearing in mind the dual track of epistemic and ontic levels. If, however, one considers all the conceptual and applicative elements involved in defining the concept of species, then to some extent it becomes possible to solve the same question: the concept of species has a dual, ontic-epistemic dimension, which demonstrates the close correlation between the methods of observation and analysis and the data themselves. It thus becomes revealing of the fact that any scientific theory is a single whole preceding its decomposition into separate elements, and whose concepts are understandable within a holistic approach that deserves further investigation.

Author contribution:

We began designing this article a few years ago during a winter school in biotechnology held at the University of Perugia in January 2020. Flavia Marcacci was responsible for the direction and organization of the project, Michal Oleksowicz contributed more to writing the philosophical analysis, and Angela Conti edited the biological part. However, all the content of the paper was conceived, discussed, and written together, and each author has intervened repetitively in all the sections. Thus, the authors share the full responsibility of the publication.

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