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## De-Extinction and the Conception of Species

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# De-extinction and the Conception of Species

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## Abstract

Developments in genetic engineering may soon allow biologists to clone organisms from extinct species. The process, dubbed “de-extinction,” has been publicized as a means to bring extinct species back to life. For theorists and philosophers of biology, the process also suggests a thought experiment for the ongoing “species problem”: given a species concept, would a clone be classified in the extinct species? Previous analyses have answered this question in the context of specific de-extinction technologies or particular species concepts. The thought experiment is given more comprehensive treatment here. Given the products of three de-extinction technologies, twenty-two species concepts are “tested” to see which are consistent with the idea that species may be resurrected. The ensuing discussion considers whether or not de-extinction is a conceptually coherent research program and, if so, whether or not its development may contribute to a resolution of the species problem. Ultimately, theorists must face a choice: they may revise their commitments to species concepts (if those concepts are inconsistent with de-extinction) or they may recognize de-extinction as a means to make progress in the species problem.

## 1. Introduction: A thought experiment

Charles Lyell once speculated that dinosaurs ‘might reappear in the woods, and the ichthyosaur in the sea, while the pterodactyle might flit again through the umbrageous groves of tree ferns’ (quoted in Rudwick 1975, 558). Fellow geologist Henry De la Beche lampooned Lyell’s claim in a cartoon titled “Awful Changes,” wherein a bespectacled Professor Ichthyosaur presents his reptilian students with false ideas about long-extinct humans. Darwin (1859) and later Darwinians (Hull 1978; Kitcher 1984; Ruse 1986) received Lyell’s idea in the same spirit as De la Beche: they dismissed the idea that extinct species might return as science fiction rather than potential science fact.

Lyell’s idea may nevertheless be productive: science fiction can be a useful philosophical tool for conceptual analysis. Exploring the logical implications of resurrecting extinct species gives us an opportunity to analyze concepts of biological theory. The purpose of this essay is to engage in a thought experiment about the process that has come to be known as de-extinction.

Resurrection biologists—researchers engaged in de-extinction efforts, through cloning organisms from extinct species—hope to make fact out of what was previously science fiction. Resurrection biologists treat extinction as a contingent technological problem. Through a combination of husbandry, genetic engineering, and ecological manipulation, these biologists hope to restore extinct species (Zimmer 2013). Extinct species currently targeted for resurrection include the woolly mammoth (*Mammuthus primigenius*), the passenger pigeon (*Ectopistes migratorius*), and the Tasmanian tiger (*Thylacinus cynocephalus*) (Greer 2009; Archer 2013; Brand 2015).

Despite some early successes (Folch *et al* 2009; Pina-Aguilar *et al* 2009; Archer 2013), this new frontier in the life sciences has inspired the same sort of skepticism that Lyell faced. Delord (2015) suggests one conceptual difficulty with resurrection biology: the species concepts most obviously consistent with the return of extinct species seem inconsistent with modern biological theory (27-28). Slater & Clatterbuck (2018) argue that metaphysical objections of this sort are largely overstated, but they admit that the conceptual viability of de-extinction is logically dependent on a range of metaphysical commitments. To date, however, there has not been a comprehensive analysis of the logical relations between de-extinction practices and metaphysical concepts in biology. The thought experiment given below will give such an analysis by “testing” the consistency of resurrection biology with biological theory.

This test is of timely importance. Not only does it give an opportunity for theory to catch up with emerging technologies; it also gives an opportunity for more informed normative judgment. Researchers have already spent tens of millions of dollars developing de-extinction technologies and if viable populations are to be produced the price will increase by orders of magnitude (Greer 2009). In light of these fast-mounting costs, theorists have more vocally questioned the value of de-extinction projects (Cohen 2014; Diehm 2015; Jebari 2016; Blockstein forthcoming). Further consideration of whether or not de-extinction *should* happen is predicated on belief that de-extinction *could* happen, but analyses such as Delord’s suggest that there are conceptual reasons to doubt the latter belief.

The goal of this essay is to analyze the conceptual frameworks available to resurrection biologists and philosophers of biology. I will do so through a rigorous thought experiment. I will describe that experiment's "materials"—i.e., the products of resurrection biology that serve as the subjects of the experiment—in section two. In section three I will describe the methods by which these "test" subjects will be classified by categorizing species concepts. I will then, in section four, summarize the "test" results for species concepts. Finally, in section five I will note some patterns that emerge from my results and suggest how these conclusions may be applied in future research.

Philosophers can be poor forecasters of scientific progress and so I will not address the practical or technological questions of whether or not biologists can clone organisms from extinct species. Neither will I attempt any broader resolution of the so-called species problem. I intend to provide a comprehensive survey the intellectual landscape, considering the full range of practices in resurrection biology and an exhaustive list of species concepts. This work therefore complements earlier analyses that focused on a narrower range of concepts or did not distinguish between different methods of de-extinction (e.g. Delord 2015, Slater & Clatterbuck 2018).

## **2. Materials: The three "mammoth"**

Attempts to resurrect extinct species may take one of several forms: "back-breeding," genomic transfer, and direct gene editing. While the first method is the most easily practicable, the latter genomic technologies are better publicized (Zimmer 2013). By

understanding the products of each process, we can determine the consistency of these processes with different species concepts.

Resurrection biology's earliest attempts took the form of "back-breeding" (Oksanen & Siipi 2014). Through well-practiced methods of husbandry, skilled breeders may cross individuals from extant lineages towards the goal of replicating phenotypes, and perhaps even genotypes, of organisms from closely related extinct lineages. This method is structurally identical to other forms of artificial selection, but with one key difference: instead of perpetuating existing breeds or creating new ones, back-breeding is intended to produce new members of extinct breeds. Conservationists are now debating the practicability of this technique, also known as "lineage fusion," in resurrecting extinct subspecies of Galápagos tortoises (Poulakakis *et al* 2008; Garrick *et al* 2014).

Genomic transfer methods were popularized at the turn of the millennium by works of fiction such as *Jurassic Park* and reporting on the cloned sheep Dolly, both of which highlight the genomic transfer method known as somatic cell nuclear transfer (SCNT) (Zimmer 2013).<sup>1</sup> SCNT begins with the cultivation of somatic cell's nucleus from a donor organism. That nucleus, including its full complement of genetic material, is then inserted into a mature enucleated egg. After the embryo is implanted into a surrogate mother and

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<sup>1</sup> A second form of genomic transfer—primordial germ cell transplantation (PGCT)—is more appropriate for organisms from which unfertilized eggs are difficult to obtain, such as birds and fish (Simkiss, *et al.* 1987; Shapiro 2015). This process has already produced chickens (Chang, *et al.* 1997) and zebrafish (Saito, *et al.* 2010) and may be an appropriate means of resurrecting extinct fish or fowl; however, it is technically not considered *cloning*, which is a term reserved for SCNT. One may consider PCGT rather than SCNT in the discussion below without altering the conceptual inferences noted.

carried to term, the result is an organism whose somatic cell nuclear genotype matches that of the original donor (Wilmut, *et al.* 1999).<sup>2</sup>

Genomic transfer has already been a qualified success. Spanish geneticists succeeded in using SCNT to engineer a viable clone from a member of the extinct subspecies *Capra pyrenaica pyrenaica*, although the clone died of respiratory failure less than a minute after coming to term (Folch *et al.* 2009; Pina-Aguilar *et al.* 2009). SCNT has also been recommended as a means of resurrecting species such as gastric brooding frogs (*Rheobatrachus silus*) (Archer 2013), woolly mammoths (*Mammuthus primigenius*) (Loi, *et al.* 2011), and Tasmanian tigers (*Thylacinus cynocephalus*) (Greer 2009).

I will call the last method of de-extinction “direct gene editing.” The primary difference between genomic transfer and direct gene editing is the genome’s origin: the material basis used in genomic transfer is from the target species, but the material basis used in direct gene editing is from a sister taxon. Assuming that genomic differences between the extinct species and its sister taxon can be identified, the genetic material from a donor organism in the sister taxon would be edited to match the extinct species’ genome. Following this genome editing, the process resembles genomic transfer: the edited genome is inserted into an enucleated egg, which is in turn implanted into the surrogate mother.

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<sup>2</sup> There may still be genetic dissimilarities between donors and clones produced by SCNT. Since mitochondria—which carry their own DNA—are situated outside the cellular nucleus, the success of SCNT does not imply that clones will carry the same mitochondrial DNA as their genetic donors. Furthermore, immune cell genes differentiate during ontogeny in response to the individual organism’s environment and so a clone’s leukocyte DNA will differ from its genetic donor’s (Russell, *et al.* 2008, 976-989). Nevertheless, the genetic similarity between donor and clone will be the highest degree achievable by any means other than mitosis or parthenogenesis.



Efforts are currently under way to recreate a passenger pigeon (*Ectopistes migratorius*) by editing genetic material from the band-tailed pigeon (*Patagioenas fasciata*) (Zimmer 2013; Shapiro 2015). An Asian elephant (*Elephas maximus*) genome might serve as a template for resurrecting the woolly mammoth if genomic transfer from preserved tissues fails (Shapiro 2015).

Each of these methods of resurrection biology faces obstacles and limitations. Back-breeding is only practical for resurrecting extinct taxa below the species category: resurrecting species-level taxa requires cross-breeding organisms from different species that share a common ancestor with the target species, but doing so is unlikely to produce fertile offspring. Furthermore, artificial selection within a single species towards replication of a sister taxon probably requires macroevolutionary timescales. Genomic transfer methods require viable cell nuclei from organisms in the extinct species, which may not be practical for species that went extinct before the development of sophisticated conservation tools<sup>3</sup>. SCNT is viable only for extinct taxa whose developmental environments were sufficiently similar to those of extant surrogates. Direct gene editing assumes antecedent knowledge of the extinct taxon's genome.

Overcoming these obstacles is contingent on the state of our technological art. The production of a new organism that is genetically or phenotypically identical with an organism from an extinct species remains consistent with current biological theory

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<sup>3</sup> Kato, *et al.* (2009) recovered viable mammoth cell nuclei. This particular case depended on discovery of a frozen partial carcass whose tissues had not degraded before freezing. Such discoveries are certainly extraordinary. In any event, the preservation of intact genetic material from extinct species requires a highly contingent chain of events.

(Zimmer 2013; Shapiro 2015). One may doubt that efforts to clone organisms from extinct species will succeed, but success remains a theoretical possibility.

Bearing this in mind, we may imagine products of three attempts to resurrect (say) *M. primigenius*. Let's name the resulting organisms Backbreedagus, Nucleartransferagus, and Geneditagus. Backbreedagus will be the product of back-breeding Asian elephant lineages; Nucleartransferagus is the product of SCNT from the intact nuclear DNA of well-preserved woolly mammoth remains implanted into an Asian elephant<sup>4</sup>; Geneditagus is the product of an edited Asian elephant genome carried to term by a member of that species. We will assume that Backbreedagus, Nucleartransferagus, and Geneditagus are all phenotypically identical with extinct mammoths and that each is as genotypically similar to those mammoths as their respective cloning methods allow<sup>5</sup>.

The success of resurrection *per se* depends (in part) on whether any of the three organisms can be classified as a member of *M. primigenius*. The standards for classifying Backbreedagus, Nucleartransferagus, and Geneditagus are established by some species concept.

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<sup>4</sup> Between the two genomic transfer methods, SCNT seems more appropriate for mammals given the relative ease with which biologists may culture mature unfertilized mammalian egg cells. By contrast, PCGT is designed to overcome distinctive difficulties posed by avian cloning (Shapiro 2015; *cf.* Wilmut, *et al.* 1999). If necessary, we can imagine Nucleartransferagus as the product of PCGT without changing the outcomes of our thought experiment. The "material" remains the same: a clone carrying genetic material cultured directly from the cells of an organism belonging to an extinct species.

<sup>5</sup> It is unlikely that back-breeding or direct gene editing would actually produce either phenotypic or genotypic identity with extinct species (see note 2). However, such identity is not logically impossible. Assuming near-complete similarity *ex hypothesi* is a useful control for our thought experiment.

### 3. Methods: A taxonomy of species concepts

There are two relevant questions at hand. First: can Backbreedagus, Nucleartransferagus, or Geneditagus be classified as members of the species *M. primigenius*? Second: would their classification in the species be sufficient to resurrect *M. primigenius*?

These questions track with the two ways one might interpret the broader question, “What is a species?” The first question—can the clones be classified in the extinct species—asks which properties attributable to organisms are necessary or sufficient to classify an organism within a species. This is a question about the *species taxon*. The second question—would the species be resurrected by production of clones—asks about a property that may or may not be attributable to species themselves, i.e., to populations or lineages rather than to particular organisms. This is question about the *species category* (Mayr 1962; Devitt 2008; Ereshefsky 2010).

Species concepts are the tools with which philosophers of biology answer species category or species taxon questions. The species problem is ultimately a debate over which of these tools, if any, is the one best suited to answering all conceptual questions about species (Kitcher 1984; Ereshefsky 2010).

One reason that the species problem has been so intractable may be that theorists cannot agree on the number of concepts up for debate. In a comprehensive summary, Mayden (1997) lists twenty-two concepts; Wilkins (2011) argues that the number may be reduced to seven (if we focus on basic patterns of organization) or increased to twenty seven (if we focus on semantic differences). Okasha (2002) argues that there are basically four species concept categories, regardless of the total number of particular concepts.

For ease of analysis, I will develop a taxonomy of species concepts useful for classifying the three clones named in the last section. Species concepts can be sorted along two dimensions: by broad views of the species category and by broad views of the species taxon. This sorting will ultimately give us three species concept categories.

The first dimension along which we can sort species concepts focuses on a question about the species category: are species individuals or classes?

According to Ereshefsky (2010), the view that species are individuals is the predominant view of the species category. To say that a species is an individual is to say that speciation and extinction establish spatiotemporal boundaries within which the species exists and between which the species has some kind of material continuity (Hull 1978). Different species concepts suggest different standards of material continuity<sup>6</sup>. To say that a species is an individual, then, is to say that it is an entity that comes into being with a speciation event, goes out of existence with extinction, and is unified in space and time between those events. Such a view is appealing to evolutionary theorists because it gives a way to maintain a species' identity across time even if properties of the species' members change as a result of microevolution.<sup>7</sup> By contrast, Grene (1990) argues that the "individuality thesis" is inconsistent with the theory of natural selection, which holds that

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<sup>6</sup> Godfrey-Smith (2011), for example, describes material continuity as a sequence of materially overlapping replicators that occasionally pass through 'bottlenecks' that distinguish one individual from the last or the next. See also Griesemer (2000) and Piotrowska (2018).

<sup>7</sup> Standards of biological individuality are more stringent than standards of individuality *simpliciter*. Gracia (1988, 28) elaborates standards of general individuality, but these are consistent with the possibility of spatiotemporally disjointed 'scattered objects' (Cartwright 1999). Biological individuals, by contrast, require spatiotemporal continuity (Ghiselin 1974; Hull 1978; Griesemer 2000; cf. Godfrey-Smith 2011; Piotrowska 2018).

populations evolve and individuals do not. The alternative is to view species as classes, which need neither spatiotemporal boundaries nor material continuity (Kitcher 1984).

We may categorize species concepts along a second dimension that distinguishes answers to a species taxon question. What is the appropriate temporal relation between organisms classified in the same species?

Theorists may consider species as synchronic (i.e., wholly present at a particular time) or as diachronic (i.e., spread across an extended period of time). A theorist's position along this dimension depends on their view of the conspecificity relation. For those who favor synchronic concepts, conspecificity is an intransitive relation: the conspecificity of organisms A and B and of organisms B and C would not imply the conspecificity of organisms A and C.<sup>8</sup> For those who favor diachronic concepts, species membership is transitive within certain boundaries established by the particular species concept. Some diachronic concepts (e.g., the Successional Species Concept) are synchronic concepts (e.g., the Biological Species Concept) modified to allow transitivity of conspecificity (Mayden 1997).

There may be practical importance in this distinction. For example, if theorists intend to test species membership by observation of some interaction between species members then the different members of a species must live within roughly the same

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<sup>8</sup> Mayr (1982) argues that species identity across time is 'irrelevant' given our inability to test conspecificity along that dimension (286). Ring species provide a spatial analog for the potential intransitivity of species membership across time. These species 'consist of chains of populations' in which consecutive links satisfy conditions for conspecificity with their neighbors, but populations separated by multiple links do not (Sterelny & Griffith 1999, 189). If we consider a chain of populations across space to be analogous with a lineage of populations across time, then we may recognize what motivates theorists such as Mayr to deny the transitivity of conspecificity.

timeframe; observation of interactions between long-dead woolly mammoths and modern organisms—including clones—is impossible (*cf.* Stamos 2001). The synchronic-diachronic dimension is therefore an important one for our thought experiment.

I therefore propose sorting species concepts into three broad categories. The categories, determined by concepts' positions along the individual-class and synchronic-diachronic dimensions, are as follows: *diachronic individual*, *synchronic class*, and *diachronic class* concepts<sup>9</sup>. Readers interested in the sorting criteria for particular species concepts may turn to an appendix provided at the end of this essay.

We must clarify one additional point before we can answer the two questions that opened this section. What does it mean to say that *M. primigenius* is extinct? Delord (2014) distinguishes “demographic” and “final” senses of the term “extinct.”<sup>10</sup> Demographic extinction follows the death of all organisms in a species; however, the means for perpetuating the species—intact genetic material, for example—may survive. A species is extinct in Delord’s “final” sense only when all means of perpetuating the species have totally disappeared.

*M. primigenius* is certainly extinct in the demographic sense of the term “extinct,” but to say that the species is extinct in the second sense would beg the question against de-

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<sup>9</sup> The fourth possible category implied by my two dimensions—*synchronic individual* concepts—is an empty set. Individuals are diachronic by definition given that they are defined by different historical events (Hull 1978).

<sup>10</sup> Delord also describes “functional” senses of the term, wherein a species may have living members that are unable to perpetuate the species’ lineage. I exclude this sense of the term “extinct” from the discussion above because it does not seem relevant to de-extinction *per se*, which is intended to resurrect species whose members are all currently dead. Efforts to mitigate or reverse the effects of functional extinction are more properly the domain of conservation biology (Tilman, *et al.* 1994).

extinction. After all, de-extinction is a means of perpetuating extinct species; if it is a viable means of perpetuation, then no candidate for de-extinction would be extinct in the “final” sense. To assume that *M. primigenius* is extinct—as we must assume if we consider the species to be a candidate for *de*-extinction—is therefore to imply that all members of the species have disappeared, even if there is theoretically still some means for perpetuating the species. Conversely, to claim that *M. primigenius* has been resurrected through de-extinction would require not only that a clone of an organism from the species has been produced, but also that the species is once again extant because of the clone’s production (*cf.* Siipi & Finkelman 2016).<sup>11</sup>

This clarification implies a methodology for our thought experiment. For each species concept, we will ask first if the concept would classify Backbreedagus, Nucleartransferagus, or Geneditagus as a member of the species *M. primigenius*. If so, we will then ask if the classification of one of those clones in *M. primigenius* would be sufficient to resurrect the species. If the goal of resurrection biologists is to reverse demographic extinction, then it must be the case that the extinct species is revived because a new member of the species has been created. It follows, then, that concepts that are consistent with de-extinction will offer affirmative answers to both of the questions we’ve asked.

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<sup>11</sup> Another way to distinguish “demographic” and “final” senses of distinction would be to consider “demographic” extinction a *biological* sense of the term and “final” extinction an *informational* sense of the term. Again: de-extinction must assume the biological sense of extinction. After all, if a species can be resurrected at all then the information necessary for its resurrection must be intact, i.e., the species cannot be extinct in the informational sense *ex hypothesi*.

#### 4. Results: Which concepts allow resurrection?

Let us assume the following facts: first, that the species *M. primigenius* is extinct; second, that resurrection biologists have engineered organisms genetically or phenotypically identical with members *M. primigenius*. Which species concepts are consistent with the claim that *M. primigenius* is resurrected through those cloned organisms?

Given these assumptions, we would find the following results:

Diachronic individual concepts are generally inconsistent with back-breeding. This can be demonstrated by a *reductio* argument. Assume that Backbreedagus, the product of selective breeding between elephants classified in the species *E. maximus*, is classified as a member of the species *M. primigenius*. By the standards of diachronic individual concepts, *M. primigenius* is therefore a lineage with one terminal endpoint defined by the species' origin and another endpoint instantiated by Backbreedagus. As noted above (see *supra* notes 6 and 7), biological individuals are materially integrated; given that Backbreedagus is the product of artificial selection in the *E. maximus* line, any material integration between Backbreedagus and other members of *M. primigenius* would have to be mediated through ancestors in the *E. maximus* lineage back to the divergence point between the genera *Elephas* and *Mammuthus*. Consequently, Backbreedagus' direct ancestors—members of the *E. maximus* lineage—would be materially integrated with a *M. primigenius* lineage and so should be classified in that species. However, we have stipulated that *M. primigenius* is extinct before Backbreedagus is produced. Absent some reasonable account of backward causation, we therefore have just as much reason to infer that Backbreedagus' ancestors are part of *M. primigenius* as we have to conclude that they are not.



Given appropriate accounts of inheritance and reproduction, it is not impossible that a biological lineage could cross the phylogenetic gap between genera, as would be required here. Piotrowska (2018) argues that spatio-temporally “gappy” lineages of this sort are possible even when material overlap within a lineage is necessary. The problem in Backbreedagus’ case is that all of the putative new mammoth’s material inheritance has its origin in elephants classified in a different genera; the overlap between Backbreedagus and earlier mammoths is formal, not material. Following Gunn (1999) and Griesemer (2000), Piotrowska admits that formal similarity is insufficient for material integration of biological individuals. Resurrection biologists adhering to diachronic individual concepts must therefore turn to some method of de-extinction other than back-breeding.

Gene editing does no better by the standards of diachronic individual concepts. The same logic given above implies that Geneditagus cannot be classified as a member of *M. primigenius* if the species is a diachronic individual. In purely material terms, the only difference between Geneditagus and Backbreedagus is that direct manipulation of the *E. maximus* genome allowed resurrection biologists to reproduce the mammoth phenotype and genotype in a single generation, whereas achieving the same result in Backbreedagus required several generations. Regardless of the number of intervening generations, it is still the case that Geneditagus’ immediate ancestors are not members of *M. primigenius*, but the logic of diachronic individual concepts would require otherwise. As Piotrowska argues, this is another case of formal rather than material overlap.

Alone among de-extinction technologies, SCNT may provide the material overlap required by theorists endorsing diachronic individual concepts (Piotrowska 2018).

Depending on the particular concept's standards for material continuity, diachronic individual concepts may be consistent with de-extinction by genomic transfer. Some diachronic individual concepts (e.g. the Hennigian Species Concept or the Reproductive Competition Concept) cast the concept of material cohesion in terms of interactions between different members of the species; since Nucleartransferagus cannot interact with past mammoths, she would not be classified as a mammoth by these concept's standards. The other diachronic individual concepts cast the concept of material cohesion in terms of descent or shared ancestry; Nucleartransferagus may meet this standard for classification as a member of *M. primigenius*, but only given an appropriate understanding of descent. Even given that understanding, the clone's classification as a member of the species would only resurrect the species given an appropriate understanding of individuality (see section 5).

Synchronic class concepts are inconsistent with all forms of de-extinction. All synchronic class concepts hold that all members of a species are contemporaneous, by definition. The two relevant senses of the term "extinct" given above—demographic and final—both imply that an extinct species is one whose members are not currently alive. If *M. primigenius* has been extinct, then, it follows that there is a temporal gap between earlier members of *M. primigenius* and any clone produced through de-extinction techniques. Since the clones are not contemporaneous with earlier members of *M. primigenius*, they cannot be classified as members of that species<sup>12</sup>.

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<sup>12</sup> One might argue that synchronic class concepts do not address the issue of de-extinction at all because the concepts' intended use is operational and the suggested test for is practically impossible for *M. primigenius*. However, the intentions of theorists are

Diachronic class concepts may allow that Backbreedagus, Nucleartransferagus, or Geneditagus are classifiable as members of *M. primigenius*. Since diachronic classes may be scattered in space or time, the temporal gap separating Backbreedagus, Nucleartransferagus, and Geneditagus from earlier members of *M. primigenius* does not preclude classifying the clones within that species. Classes are wholly instantiated in constituent individuals, and so classifying any one of the three clones as a member of *M. primigenius* would be sufficient for the resurrection of that species (*cf.* Kitcher 1984).

Most diachronic class concepts diagnose species membership on the basis of some relevant degree of similarity between species members; all forms of de-extinction are consistent with those concepts. Two diachronic class concepts—the Composite Species Concept and the Successional Species Concept—add the membership requirement that shared similarities within a species must be explained by a common cause. Backbreedagus and Geneditagus may not meet this additional requirement for membership in *M. primigenius*: their similarities to earlier mammoths are explained by human intervention that does not also explain similarities between earlier mammoths. Nucleartransferagus does meet the higher membership standards of these two concepts: her similarities to earlier mammoths would be explained by genetic material from an earlier mammoth.

To summarize the results of our thought experiment: De-extinction through backbreeding is consistent only with some diachronic class concepts. De-extinction through genomic transfer is certainly consistent with all diachronic class concepts and may be

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irrelevant to the concepts' given standards for species membership; since our clones do not coexist with other members of the extinct species *in fact*, it follows that the clones cannot be classified in the extinct species (*cf.* Mayr 1962). See further discussion in the Appendix.

consistent with some diachronic individual concepts. De-extinction through direct gene editing is consistent only with some diachronic class concepts. Readers interested in details for particular species concepts may consult the appendix following the next section of this essay.

## 5. Discussion and conclusions

The claim that the goals of de-extinction can be accomplished—i.e., to say that *M. primigenius* can return from extinction because resurrection biologists cloned a member of that species—has metaphysical implications for the persistence conditions of species. Our thought experiment makes those implications explicit.

What follows then? That depends on the purpose for which one conducts our thought experiment. One may intend to assess the conceptual viability of de-extinction given current views of species. Alternately, one may intend to reform our current views of species given the potential success of de-extinction. I will consider these approaches in turn.

The most popular contemporary views of species are the Biological, Ecological, and Phylogenetic Species concepts (Ereshefsky 2010). These concepts fall into our synchronic class concept and diachronic individual concept categories, respectively. Two of the three methods of de-extinction (back-breeding and direct gene editing) are certainly inconsistent with all concepts in both categories and the third method (genomic transfer) may or may not be consistent only with concepts in the diachronic individual category. By contrast, diachronic class concepts are currently unpopular among biological theorists (Ibid), but these concepts offer greater consistency with the logic of all de-extinction methods. If one

assumes that current understanding of species should drive the development of de-extinction methods, then, it likely follows that resurrection biology *per se* should be considered a fool's errand.

This conclusion only follows, however, if we take the goal of resurrection biologists to be the literal revival of extinct species. I have taken resurrection biologists at their word and assumed this to be the case (see, e.g., Archer 2013 or Brand 2015; *cf.* Zimmer 2013). Nevertheless, we can imagine that resurrection biologists might be satisfied with *duplication* rather than genuine revival: their goal might be to produce clones that are phenotypically or genotypically similar to earlier mammoths, even though the clones are classified as members of some different species. There is still some value in accomplishing such a goal. For example, Shapiro suggests that clones could serve as proxies for extinct keystone species, replacing members of the extinct species in ecosystems that might collapse otherwise (2015, 26-30). There is also some value in pursuing the development of de-extinction technology even if that technology can only produce facsimiles. Pina-Aguilar, *et al.* (2009) and Hooper (2013) suggest that mature de-extinction methods might complement other conservation efforts, serving as a last resort for species near extinction (*cf.* Diehm 2015). Finally, one may find aesthetic value in facsimiles—after all, zoos and aquariums offer that value even though their presentations of nature are mere representations (Zimmer 2013).

If Backbreedagus, Nucleartransferagus, or Geneditagus aren't members of the species *M. primigenius*, then what are they? A theorist must commit to a species concept in order to answer that question. Diachronic individual concepts might classify the clones as

Asian elephants—if unusual ones—following the logic that species are materially integrated from one generation to the next and like produces like. Synchronic class concepts might classify the clones as monsters of a sort, i.e., organisms that cannot be classified as members of any species. Alternatively, the clones might be classified as members of some new taxon. That latter suggestion would depend on the number of clones produced or their causal interactions with other organisms.

On the other hand, the presumption that de-extinction must be theoretically viable would prompt some revision of current attitudes toward species concepts in light of the thought experiment's results. If one thinks it absurd that a mammoth clone would not be a mammoth, then I would suggest the following directions for future philosophical development.

Recall that the classification of Nucleartransferagus by the standards of diachronic individual concepts depends on specification of two terms: “descent” and “individual.” Theorists have devoted considerable attention to defining the latter term in the context of evolutionary theory. If de-extinction is viable *ex hypothesi*, then we might alter current conceptions of biological individuality: rather than requiring spatiotemporal continuity between defining events, we might allow that species-individuals could have spatiotemporal gaps between parts (*cf.* Cartwright 1999). Along similar lines, the possibility that inheritance of genetic information might be mediated by human intervention should prompt re-examination of our understanding of descent. Current conceptions of descent tend to require some form of material overlap in inheritance (Griesemer 2000; *cf.* Piotrowska 2018), but the concept could be broadened to

accommodate inheritance of genetic information without material propagation—for example, by transfer of information from a computer database to an engineered genome (*cf.* Gunn 1999; Godfrey Smith 2015).

The idea that genetic information can be propagated without material continuity might initially suggest a problematically dualistic view; to be sure, similar concerns dissuaded theorists away from diachronic class concepts—and towards synchronic class concepts—following the neo-Darwinian synthesis (Hull 1965). The viability of de-extinction would suggest that such concerns were only contingently problematic. There were no previous means by which an organism could propagate its genetic information without being materially continuous with the next generation, but de-extinction technologies now provide those means. Species have heretofore been historically situated biological entities, but the development of cloning methods described above could mean that species no longer need to be so spatiotemporally restricted. If so, then current preferences for synchronic class concepts over diachronic class concepts would be less justified.

A further possibility is that the clones might be classified as mammoths, but the species *M. primigenius* nevertheless remains extinct—i.e., *M. primigenius* is an extinct species with new living members (*cf.* Siipi & Finkelman 2016). Such a possibility is not necessarily far-fetched: there are functional senses of the term “extinct” that allow for such a possibility (see note 10). This could be a valid response for theorists who endorse synchronic class concepts, which may be inconsistent with de-extinction only because of spatiotemporal separation between mammoths and their clones. Demographic extinction

already allows that a species may be extinct even though some means for propagating the species persists; in that sense, the clones in our thought experiment might be little different from isolated genomes or genetic information.

These are only a few suggestions for how biological theory might change to accommodate de-extinction. I have no doubt that there are many more possibilities than I can list here; the few listed above are only those explicitly suggested by the results of the foregoing thought experiment. In any event, theorists looking for some way to drive progress in debate over the species problem should consider this experiment and its results.

Perhaps the mammoth clones are, in fact, coming. That is an empirical question. The question of whether or not the arrival of those clones will signal the return of a once-extinct species, however, is not empirical. Philosophical commitments are relevant in the growing discussion of de-extinction. This work should make that relevance clear.

## **Appendix: Species Concepts and Particular Results**

I follow Mayden (1997) by considering the following twenty-one species concepts. My goal is comprehensiveness without irrelevancy or redundancy; I have therefore included only concepts that have distinctive definitions and excluded concepts that apply only to asexual organisms. In particular: I have excluded the Agamospecies Concept, which supplements the Biological concept for clonal and asexual lines; Mayden's "Non-dimensional" concept, which corresponds with my synchronic class category; and three variations of the



Phylogenetic concept that differ in member diagnosis, but not in species definition (Ibid, 403-408).

I have sorted the twenty-one concepts into their appropriate categories for ease of reference. Note that concepts may share the same species taxon criteria, but differ in their species category commitments (e.g., GCC and GSC; BSC and HSC).

### Individual Concepts

As noted in section 4, no diachronic individual concept is consistent with de-extinction via back-breeding or direct gene editing. I therefore consider only the classification of Nucleartransferagus with respect to the concepts below.

1. Cladistic (CISC): Species membership is defined by common descent from a single speciation event and, in the case of extinct species, elimination by a shared cause. Given that last stipulation, Nucleartransferagus would not be classifiable as a part of *M. primigenius* because that species went extinct at the end of the Pleistocene (see discussion of different senses of the term “extinct” in Section III above).
2. Cohesion (CSC): Membership is determined by cohesion mechanisms intrinsic to the species lineage, such as those that limit gene flow or genetic drift. If a lineage can have material overlap through spatiotemporal gaps, as Piotrowska (2018) argues, then Nucleartransferagus might be classifiable as a part of *M. primigenius*: the clone may develop as earlier mammoths did and perpetuate their genetic information, which would presumably limit gene flow or genetic drift as with earlier mammoths. If spatiotemporal continuity is necessary for material overlap in a biological lineage,

then Nucleartransferagus could not be classified as a part of *M. primigenius*, since the lineage would have its terminal endpoint before the clone's creation.

3. Diagnosable Phylogeny (DPSC): Membership is determined by overall genetic similarity between organisms descended from a single speciation event, forming the smallest individual lineages that participate in evolutionary processes.  
  
Nucleartransferagus could be classified as a part of *M. primigenius* given that her genetic similarity to earlier mammoths is a result of inheritance from nuclear DNA materially connected with the mammoths' speciation event.
4. Evolutionary (ESC): Organisms' shared evolutionary origins, selective pressures, and ultimate fate determine membership. Given that her nuclear DNA was produced as a material result of natural selection on earlier mammoths, Nucleartransferagus might be classifiable as a part of *M. primigenius* if current selective pressures are similar to those that earlier mammoths faced.
5. Genealogical Concordance (GCC): Membership is determined by the presence or absence of particular genetic markers. Nucleartransferagus must share the genetic markers relevant to *M. primigenius* since her nuclear DNA is taken from a member of that species, and so she must be classifiable as a part of the species.
6. Hennigian (HSC): Membership is determined by interbreeding between organisms, as limited by intrinsic or extrinsic reproductive isolating mechanisms.  
  
Nucleartransferagus cannot interbreed with extinct mammoths, and so she would not be classifiable as a part of the species *M. primigenius*.
7. Internodal (ISC): Membership is determined by organisms' position between nodes on a phylogenetic tree. While Nucleartransferagus' genome was taken from a

mammoth, her parentage is in the *E. maximus* line. Given that this concept's standards for species membership are the organism's position on the phylogenetic tree, but not the genome's position, it should follow that Nucleartransferagus is not classifiable as a part of *M. primigenius*.

8. Phylogenetic (PSC): Membership is determined by common descent from a shared ancestor, but excludes members of descendent species. Assuming that Nucleartransferagus bears the appropriate relation of "descent" from ancestral mammoths (see section 5), it would follow that she is classifiable as a part of *M. primigenius*.
9. Polythetic (PtSC): Membership is determined by common descent from a shared ancestor, as diagnosed by statistically covariant traits. Nucleartransferagus shares her traits with earlier mammoths and her similarity to those mammoths is explained by a genome materially inherited from earlier mammoths, and so she should be classifiable as a part of the species *M. primigenius*.
10. Reproductive Competition (RCC): Membership is determined by organisms' competition for the same resources. Nucleartransferagus cannot compete for resources with dead mammoths, nor does she compete vicariously for those resources through competition with organisms that did in fact engage in such competition; consequently, she could not be classifiable as a part of the species *M. primigenius*.

## Synchronic Class Concepts

As noted above, all synchronic class concepts are inconsistent with de-extinction. Again, any of the three clones may satisfy species taxon criteria, but the nature of the species category in these concepts excludes organisms created after the species' extinction. Such exclusion may seem trivial, but it is in fact a designed feature of synchronic class concepts. These concepts play an operational role in biological theory; each has been suggested as a means of testing species membership (*cf.* Mayden 1997; Stamos 2003). Although (say) Nucleartransferagus could potentially reproduce with earlier mammoths, '*unrealized* potentialities don't count' in operational concepts (Hull 1965, 209-210; see also footnote 8).

11. Biological (BSC): Membership is determined by interbreeding between organisms, as limited by intrinsic or extrinsic reproductive isolating mechanisms.
12. Ecological (EcSC): Membership is determined by interbreeding between organisms, as limited by extrinsic reproductive isolating mechanisms or "adaptive zones."
13. Genetic (GSC): Membership is determined by the presence or absence of particular genetic markers.
14. Genotypic Cluster Definition (GCDC): Membership is determined by overall multivariate genetic similarity between organisms.
15. Recognition (RSC): Membership is determined by the presence or absence of traits associated with reproduction, and particularly those through which organisms in the species recognize intraspecific mates and exclude members of other species.

### Diachronic Class Concepts

Thought experiment results for individual concepts are given for each concept.

16. Composite (CpSC): Membership is determined by the presence or absence of traits either fixed or lost in the population by a shared speciation event.
- Nucleartransferagus would qualify as a mammoth by this criterion since her genetic material is materially continuous with earlier mammoths. Neither Backbreedagus nor Geneditagus would be classified as members of *M. primigenius*: while both share traits with earlier mammoths, neither bears traits caused by a speciation event shared with all and only earlier mammoths. Both are materially descended from Asian elephants, and so any traits that haven't been directly manipulated by resurrection biologists would be fixed by the evolution of that group.
17. Evolutionary Significant Unit (ESUC): Membership is determined by interbreeding between organisms, as that interbreeding contributes to the "evolutionary legacy" of the population. If "interbreeding" requires actual interbreeding, then none of the clones meet criteria for classification as members of *M. primigenius*; if potential for interbreeding is sufficient, then all three would satisfy those criteria.
18. Morphological (MSC): Membership is determined by overall morphological similarity. All three clones would be classified as members of *M. primigenius* since each is as morphologically similar as possible to earlier mammoths *ex hypothesi*.
19. Phenetic (PhSC): Membership is determined by overall similarity, including morphological, genetic, and ecological traits. All three clones would be classified in *M. primigenius* since each of the three would be more similar to earlier mammoths than they would be to any other organisms, again *ex hypothesi*.
20. Successional (SSC): Membership is determined by interbreeding between organisms, as limited by intrinsic or extrinsic reproductive isolating mechanisms.

Nucleartransferagus and Geneditagus would both be classified as members of *M. primigenius* given that their overall genetic similarity to earlier mammoths would make them capable of interbreeding, if only potentially. Backbreedagus should not be classified as a member *M. primigenius*: while she might be capable of interbreeding with earlier mammoths, she should also be capable of interbreeding with her immediate ancestors in the species *E. maximus*. This follows from the fact that her genotype and phenotype should be only incrementally different from those immediate ancestors; after all, Backbreedagus is a product of selection processes. Members of *E. maximus* are not classifiable as members of *M. primigenius*, thus implying a *reductio ad absurdum*.

21. Taxonomic (TSC): Membership is determined by the diagnosis of well-qualified taxonomists. Depending on the goals, methods, or whims of individual taxonomists, any of the three clones could be classified in *M. primigenius*; however, that classification would not be a necessary consequence of the concept.

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