Individuating Genes as Types or Individuals: Philosophical Implications on Individuality, Kinds, and Gene Concepts

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Abstract

"What is a gene?" is an important philosophical question that has been asked over and over. This paper approaches this question by understanding it as the individuation problem of genes, because it implies the problem of identifying genes and identifying a gene presupposes individuating the gene. I argue that there are at least two levels of the individuation of genes. The transgenic technique can individuate "a gene" as an individual while the technique of gene mapping in classical genetics can only individuate "a gene" as a type or a kind. The two levels of individuation involve different techniques, different objects that are individuated, and different references of the term "gene". Based on the two levels of individuation, I discuss important philosophical implications including the relationship between individuality and individuation and that between individuals and kinds in experimental contexts. I also suggest a new gene conception, calling it "the transgenic conception of the gene."

Keywords: gene concept, individuality, individuation, experiment, classical genetics, transgenic technique

1. Introduction: what is a gene and why individuation matters

"What is a gene?" and its related questions have been asked over and over by philosophers, historians, and scientists of biology (Beurton, Falk, and Rheinberger 2000; Carlson 1991; Falk 1986, 2010; Gerstein et al. 2007; Griffths and Stotz 2006, 2013; Kitcher 1982, 1992; Pearson 2006; Stotz and Griffiths 2004; Snyder and Gerstein 2003; Waters 1994, 2007). Those questions are frequently embedded in discussions about the definition of the term "gene" and the gene concept. As a consequence, the phrase "a gene" in this question usually refers to a type of gene. However, should we use "a gene" to refer to an individual gene, i.e., a gene token? Could it in fact be this?

The question "what is a gene" explicitly implies the problem of identifying genes, and identifying a gene presupposes individuating the gene. In what ways are genes individuated and how do scientists individuate them? I call this *the individuation problem of genes*. This paper shall approach the problem from three different but related perspectives.

From the epistemic perspective, a concept of the gene provides at least a working definition, which by nature is a hypothesis, for scientific research. Any hypothesis of the gene may be in error and may be confirmed only by experimentally individuating particular tokens of some gene. From the semantic perspective, according to a Fregean philosophy of language, the concept of reference usually serves for proper names that refer to individuals or particulars. We may extend the concept of reference to general terms (e. g., "humankind" or "gene kind") for the case in which some token of a kind is presented, and so we use a general term to refer to the kind. This means that at least some token of a kind has to be individuated. This semantic perspective presupposes an ontological perspective: the existence of a kind should be presented or demonstrated by the existence of at least a token of the kind. In the case of the gene, the ontological requirement means that we have to individuate a token of some gene kind. All three perspectives indicate the key status of individuation for answering the question of what a gene is.

According to the literature of analytic metaphysics, "individuation" is understood in a metaphysical and an epistemic sense. In the epistemic sense, someone individuating an object "is to 'single out' that object as a distinct object of perception, thought, or linguistic reference." (Lowe 2005: 75) This epistemic sense presupposes the metaphysical sense, in which what 'individuates' an object "is whatever it is that makes it the single object that it is – whatever it is that makes it one object, distinct from others, and the very object that it is as opposed to any other thing." (Lowe 2005: 75) Bueno, Chen, and Fagan (2018) add a practical sense to the term, interpreting

"individuation" as a practical process through which an individual is produced. They characterize the relation between "individuation" and "individuals" as when "an individual emerges from a process of individuation in the metaphysical sense. Epistemic and practical individuation, then, are processes that aim to uncover stages of that metaphysical process." (Beuno, Chen, and Fagan 2018) The approach to the individuation of genes I adopt herein follows their characterization, especially by focusing on the process of epistemic and practical individuation. Reversely, the case I am investigating in this paper offer an illustration for the new sense of individuation.

Although philosophers have investigated concepts of the gene and its change by examining many cases in scientific practices, they have seldom considered the role that the transgenic technique developed in biotechnology may play in philosophical discussions. This paper explores experimental individuation of genes from the direction of that technique, considering the possibility that a gene is individuated as an individual in the relevant contexts.

This paper thus addresses two central questions: (Q1) In what sense, can we reasonably say that classical geneticists have individuated a gene? (Q2) Are there experiments that can individuate a gene as an individual? Some new questions such as the relationship between individuality and individuation will be derived from the answer to the two questions. This paper is thus structured in the following way.

In the second section, I review the literature about the concepts and references of genes. Section 3 argues that the answer to Q1 is that the geneticists individuate a gene as a type, because they used the chromosomal location technique. Section 4 argues that the answer to Q2 is the experiments that use the transgenic technique. The two answers indicate two different kinds of individuation: individuation of a type and individuation of an individual. This raises a new question about whether or not "individuation of a type" is a consistent phrase. In order to respond to this, section 5 discusses in what sense we individuate a type and compare between two kinds of individuation defined by two different kinds of experiments and techniques: the chromosomal locution of genes and the transgenic experiment. My argument thus involves the relationship between kind and individual in the context of experimentation. Given the new question, Section 6 argues that transgenic experiments can demonstrate a gene type by individuating its tokens, while gene mapping experiments in classical genetics only individuate gene types. Thus, a new gene conception, calling it "the transgenic conception of the gene," can be proposed. I further discuss the relationship among the classical gene concept, the molecular gene concept, and the transgenic conception. In the seventh section, I defend the thesis that practices of individuation in scientific investigations are prior to characteristics of individuality identified by traditionally metaphysical speculations.

2. Concepts and references of the gene

The rapid change of the gene concept has produced a large multitude of gene concepts that have bewildered scientists (Gerstein et. al. 2007; Pearson 2006; Stotz and Griffiths 2004). The confused situation has attracted many philosophers and scientists to provide clarifying analyses. Although scientists as well as philosophers have made endeavors to overcome the predicament, they are motivated differently. Scientists believe that they need a unified concept to help them conduct research and to communicate with each other, because, as developmental geneticist William Gelbert says, "it sometimes [is] very difficult to tell what someone means when they talk about genes because we don't share the same definition" (Pearson 2006: 401). Thus, most scientists seek to redefine the "gene" and tend to adopt a single preferred perspective on the gene concept, although they are well aware with the plurality of gene definitions (Wain et. al. 2002; Gerstein et. al. 2007).

Philosophers at different times have been interested in clarifying concepts of the gene and in investigating the patterns of associated conceptual change. In contrast to actual definitions used by working scientists, they often consider more abstract concepts of the gene that can guide several different definitions in the context of scientific research. Consequently, they conclude that it is almost impossible to find a unified concept of the gene, and hence they take different stances to respond to this situation (rf. Waters 2007). Some are gene skeptics (e.g., Kitcher 1992). Some take a dualistic position, such as Moss (2003), who distinguishes between Gene-P and Gene-D based on the fields in that gene concepts are applied. Some are pluralists, such as Griffiths and Stotz (2006, 2013), who differentiate between three senses of the gene: the instrumental gene, the nominal molecular gene, and the postgenomic molecular gene. Still others are both pluralists and pragmatists. Waters (2018) emphasizes that scientists do and should apply different gene concepts under various investigative contexts.

With some exceptions, few philosophers explore the reference problem of the term "gene". Although Fregean semantics holds that the sense/concept or intension of a name determines its reference or extension, the matter about how a sense determines the reference is not easily seen from the scientific context. The determination of a theoretical term's reference usually involves experimental procedures and techniques that should be investigated and analyzed. Weber (2005, ch.7) does impressive work by providing several reference-determining descriptions of the term "gene" in the history of genetics. Based on those descriptions and the analysis of *Drosophila* genetic practices, he suggests that the pattern of referential change for "gene" is a kind of

freely floating reference. He also argues that different gene concepts refer to *different* natural kinds, which are overlapping but not coextensive.[1] According to Weber, reference for "gene" is fixed in the following manner for classical and molecular genes.

> Reference of [classical] "gene" (2): Whatever (a) is located on a chromosome, (b) segregates according to Mendel's first law, (c) assorts independent of other genes according to Mendel's second law if these other genes are located on a different chromosome, (d) recombines by crossing-over, (e) complements alleles of other genes, and (f) undergoes mutations that cause phenotypic differences. (Weber 2005: 210)

> Reference of [molecular] "gene" (5): The class of DNA sequences that determine the linear sequence of amino acids in a protein. (Weber 2005: 212)

Both classical and molecular gene concepts do refer to natural objects, because, as Weber notes (2005: 210-211), some *tokens* satisfying the reference-determining descriptions are experimentally presented when using the concepts with the intention of referring to sets of entities in historical occasions. However, one should note that the experimented tokens in classical genetics seems to be only some organisms with specific phenotypes (say, fruit flies or other kinds of organisms) while the experimented tokens in molecular biology may be some DNA segments. This difference raises interesting problem: what tokens are individuated in different contexts of experiments?

Before moving to the next section, I want to clarify that the individuation problem of gene concept's tokens is not the issue of gene individuality as raised by Rosenberg (2006: 121-133).[2] He defends the gene individuality thesis in parallel to the species individuality thesis, but Reydon (2009) objects to his argument and defends the gene as a natural kind. This paper aims to discuss how a gene kind and its tokens are individuated rather than whether or not an allele such as *Hbf* (the human fetal hemoglobin gene) is an individual.

3. Chromosomal location of a gene

[1] Baetu (2011: 411) argues that "the referents of classical and molecular gene concepts are coextensive to a higher degree than admitted by Waters and Weber…" However, Baetu builds his argument in terms of Benzer's work on phage. In my view, he does not successfully refute Waters' and Weber's arguments, because the referential change occurred within the classical gene concept, as Weber cogently argues.

[2] Rosenberg uses "natural selection and the individuation of genes" as the title of the section in which he discusses the gene individuality thesis.

Weber's argument indicates that we may and should consider the reference of the classical gene concept independently of the molecular gene concept and others. Weber's reference-determining description of "gene" (2) indicates that the chromosomal location (or mapping) of genes plays a key role in determining referents. However, the question "what tokens are individuated and thus referred to?" does not be answered.

Classical geneticists in the early 20th century located and labeled some specific classical genes on some specific chromosomes. The earliest genetic map (see Figure 1) of *Drosophila melanogaster* (fruit fly) was depicted in 1915. Figure 1 shows that the gene (allele) pair of *Drosophila's* grey body and (mutant) yellow body is located at the first locus on the first chromosome. The second gene pair of red eyes and (mutant) white eyes is located below the grey body gene. The other genes are located below the first two in order. However, every gene is differently distant from the first gene and thus occupies *a single locus* without overlapping. Accordingly, are we able to say that the location of a gene individuates the gene? Before answering this question, it is necessary to discuss how classical geneticists locate a gene on a chromosome. In other words, what technique is used in the process of locating genes?

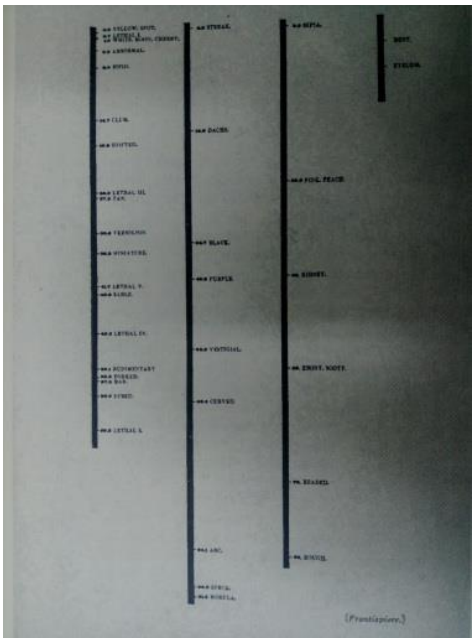

Fig. 1. Genetic map of *Drosophila* in 1915. Reproduced from Morgan, T. H. et. al. (1915).

Chromosomal location or mapping of genes is a well-known story (Darden 1991, Waters 2004, Weber 2005, 2006; Falk 2009). For the purpose of this paper, I introduce a very brief version. In the 1910s, Thomas Hunt Morgan's team developed a

technique to map the linear relations among factors (genes) in linkage groups, using Mendelian breeding data. Morgan and his team discovered that a pair of chromosomes may cross over with each other partially during the period of meiosis. Crossing over produces a specific ratio of the linked traits. Morgan believed that "the percentage of crossing over is an expression of the 'distance' of the factors from each other." (Morgan et.al. 1915: 61) Sturtevant then used percentages of linked characters that exhibited crossing over to calculate the relative positions of the factors to each other. This is the kernel technique for constructing genetic maps. By using genetic maps, Morgan's team determined the loci of many genes on the four chromosomes of *Drosophila*. Given the genetic maps, the classical geneticists assume that no other genes are located at the same position of a chromosome.[3] As a consequence, the single location of a gene actually indicates the individuality of genes.

Genetic maps by nature are diagrammatic models for the actual loci of genes in chromosomes. They are inferences from the statistical data of breeding experiments. Models represent the general. When we say that the location of a gene in a genetic map represents the locus of a classical gene on a chromosome, we really mean that it represents the locus of a type of classical gene on an identical type of chromosome in a cell within a kind of organism. Of course, this implies that a token of a type of classical gene on a token of a type of chromosome can be cognitively identified and discerned, because we can distinguish it from the tokens of the other genes. As a result, we can also count genes within cells. The located genes thus satisfy the two traditional characteristics of individuality: distinguishability and countability.[4]

If all chromosomes were stick-shaped substances of uniform material without complicated structure, then the chromosomal location of classical genes would be able to genuinely individuate them. According to molecular biology, however, chromosomes are a long chain of double helix DNA molecules that curl themselves up in twisted shapes. In such a case, we cannot delineate a located classical gene or depict its contour or boundary, because the chromosomal locus at which the gene is located includes a twisted part of the long DNA molecule. Even by invoking the knowledge from molecular biology, one would still be puzzled by the problem of defining the molecular gene.

4. Individuating molecular genes as individuals

Ever since the era of molecular biology, the continuously accumulating knowledge of genetics has not solved the individuation problem of genes. Instead, it

[3] Of course, a full story is more complicated. For the simplifying purpose, I skip the relevant discussion about gene mutation.

[4] The implications of using these criteria will be discussed in the sixth section.

has brought more troubles about the definition of the gene concept. Is a gene "a sequence of DNA for encoding and producing a polypeptide"? Should we include the start and stop codons (i. e., the regulation problem)? Should we count those introns deleted during the process of transcription into the investigated gene (i.e., the splicing problem)? The difficulty in defining the molecular gene concept directly contributes to the impediment of individuating a gene.

Many gene sequencing projects have been conducted during the genomic era. Scientists do not identify a DNA sequence as a gene and discern the gene from others by using gene sequencing *per se*, because it offers only syntactical orders of genetic codes. Gene annotation, which is used to infer what those annotated sequences do, has been developed to offer *senses* or *intensions* for them. However, the impediment of discerning genes remains, because the definition of the gene is still vague and confusing (rf. Baetu 2012; Gerstein et. al. 2007; Griffiths and Stotz 2013, ch. 4). In fact, gene annotation is based on several assumptions, by which scientists infer that a few sequences may be genes that contribute to phenotypes or functions. Those assumptions need to be confirmed by experimental investigations. Many techniques such as directed deletion, point mutation making, gene silencing, and transgenesis in reverse genetics have been developed to determine what a gene is and what it does (Gilchrist and Haughn 2010).

I argue that the transgenic technique is a very definite and powerful way to individuate a gene. It can even individuate molecular genes as individuals without a clear boundary of a gene or a clear definition of the gene, although the technique is limited.[5] How does the transgenic technique do this? What conditions of individuality allow the technique to individuate a gene as an individual?

Chen (2016) proposes a conception of experimental individuality with three attendant criteria (separability, manipulability, and maintainability of structural unity) and argues that the first experiment of bacteria transformation individuated an antibiotic resistance gene by satisfying the three criteria.[6] Below I reiterate this story in brief.

Stanley Cohen and Herbert Boyer combined DNA of *Escherichia coli* (*E. coli*) in 1973 and 1974 by transferring two different DNA segments encoding proteins for ampicillin and tetracycline resistance into *E. coli*, thereby realizing the transformation of this bacterium (Cohen et. al. 1973; Chang and Cohen 1974). Both DNA segments are called an "antibiotic resistance gene." Cohen and Boyer used small circular

[5] The technique cannot be applied in many occasions because of technological difficulties. It should not be applied to humankind due to ethics consideration. In addition, many gene-modification organisms produced by using the technique may involve ethical issues.

[6] Chen (2016) uses the creation of Bose-Einstein condensates in physical experiments as the other example. Chen's intent is to argue that biological entities and physical entities in laboratories share the same criteria of experimental individuality.

plasmids (extrachromosomal pieces of DNA) as vectors to transfer a foreign DNA segment into a bacterial cell. The plasmids were made by cutting out a (supposed) antibiotic resistance gene from other bacteria with the restriction enzyme *EcoRI*, linking the segment into a plasmid by using another enzyme, DNA ligase. The scientists then transferred the plasmid into an *E. coli* cell without the ability to resist antibiotics. The result, a modified *E. coli* cell, was able to resist antibiotics and contained the antibiotic resistance gene. In that experiment, the antibiotic gene was separated from its original bacteria and then was manipulated (i.e., linked and transferred). Its structural unity was not broken down, hence allowing it to be expressed in the other kind of bacteria. Scientists thus identify it as a gene, an individual biological entity, because the separated, manipulated, and maintained antibiotic gene was naturally separable, manipulable, and maintainable. The photos in Figure 2 show that scientists worked with a single DNA segment, as indicated by (b) in [A] and [B].

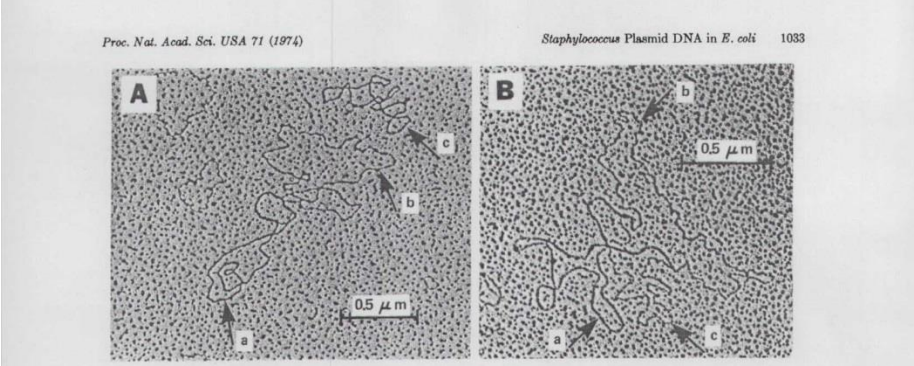

FIG. 4. (*A*) Heteroduplex of pSC101/pSC112. The region of homology is indicated by (*a*). The single-stranded loop (*b*) contains the DNA contribution of pI258 to the pSC112 hybrid plasmid. (*c*) Double-stranded molecule of pSC101 serving as internal standard for contour-length measurements. (*B*) Heteroduplex of pI258/pSC112. (*a*) Double-stranded region of homology (i.e., the segment of both plasmids containing fragment I of pI258). (*b*) Single-stranded region containing the *Eco*RI fragments of pI258 that are absent in pSC112. (*c*) Single-stranded region containing the DNA contribution of pSC101 to pSC112.

Fig. 2. Two pictures of plasmids in bacterial transformation. Reproduced from Chang and Cohen (1974).

I next interpret the performance of the technique used in transgenic experiments as the general process of individuating transgenes. The process has five stages.

(1) Use restriction enzymes to cleave specific segments from recognition sites of long DNA chains. A specific restriction enzyme can cut away a specific DNA segment at a specific site.

(2) Link the cleaved segment of DNA to a plasmid vector by using DNA ligase. The vector is a circular DNA that may come from a wild type of virus.

(3) Incorporate the DNA segment in the vector into the genome of another organism by injecting the plasmid vector to a cell of the target organism. Of course,

they may fail when the intended feature is not expressed.

(4) Make copies of DNA segments by cloning the cell containing the transferred segment of DNA. The aim of DNA cloning is to copy a segment of interest (or a gene) from an organism and produce many copies.

(5) Observe the expression of the novel feature that the target organism does not typically have. If a DNA segment cut from an original organism is successfully pasted into a cell of a target organism and the target organism expresses the intended feature that the original organism has, then one concludes that the segment is a gene.

The first stage corresponds to the separation condition, the second, the third, and the fourth stages to the manipulation condition, and the fifth stage to the maintenance condition. Accordingly, one can easily see that those cut, linked, transferred, pasted, and copied genes are particulars – individuals, because they satisfy the three criteria of experimental individuality that indicates their *singularity* and *particularity*. In other words, a single segment of DNA maintains its structural unity when being separated and manipulated. This is so, because cutting a gene from an original organism is in fact separating it from its environment and because transferring, pasting and copying a gene is manipulating it. If the gene does express the intended feature in a target organism, then this condition indicates that the unity of its chemical and informational structure has been maintained.

5. Two kinds of individuation of genes

The previous discussion indicates that two different objects have been individuated in different experimental and theoretical contexts. In the context of classical genetics, scientists used breeding experiments and theoretical inferences to locate a gene at some locus on a chromosome. They would individuate genes as types if they assume that no other genes could coexist at the same locus. If one interprets the meaning of "individuation" as "only individuals can be individuated," then the phrase "individuating genes as types" sounds unreasonable. Is it better to say "unitization of genes" rather than "individuation of genes"?

It is quite right to say classical geneticists *unitize* genes as types. In a sense, however, we may reasonably say that we individuate a gene as a type, because the type has tokens or members that are distinguishable and countable individuals. Classical geneticists suppose that all types of genes have corpuscular members, i.e., substantive individuals. In such a sense, talking of "individuating genes as types" is reasonable. If no distinguishable and countable members or samples of a kind can be identified, then the kind cannot be individuated. In other words, we cannot individuate

such a kind as water or air that is expressed by “mass” nouns at the macroscopic level, although we can individuate a sample of water by using a container or individuate a water molecule by specific technique at the molecular level. For the cases of experiments using the transgenic technique, molecular biologists physically individuate *singular and particular* gene tokens. Thus, we claim that scientists experimentally individuate genes as individuals in such a context.

In consequence, two different sets of criteria for individuality are presupposed. Experiments using the location technique have individuated a type whose tokens or members are countable individuals rather than matter referred to by mass nouns. In such experimental contexts, we emphasize distinguishability and countability as the indexing features of individuals. Experiments using the transgenic technique individuate singular and particular individuals – gene tokens. For these experimental contexts, we emphasize singularity and particularity of individuals in contrast to universality of types or kinds. We assure the particularity and singularity of the individuals through the realization of experimental individuality, namely, the joint realization of separability, manipulability, and maintainability of structural unity. At this point, more philosophical implications will be discussed in next section.

The two individuated targets indicate two different referential levels of the term “gene” in the literature. As we have seen, when many philosophers and scientists ask “what is a gene,” they really refer to a type of gene in conjunction with discussing the gene concept or the definition of “gene.” Similarly, in some contexts of scientific investigation, scientists use “a gene” to refer to a type of gene as the phrase “chromosomal location of a gene”. In the context of transgenic experiments, however, “a gene” is used to refer to a genuine individual – a single and particular gene token, because scientists have worked with particular objects that maintain their structural unity when being separated and manipulated in the process of experimenting.

The two referential levels indicate two different kinds or levels of experimental individuation, which are realized by two different techniques: the chromosomal location technique and the transgenic technique. Although the two techniques aim to the same target (i.e., genes or types of genes), they physically experiment and manipulate different objects. Experiments using the chromosomal location technique indirectly identify loci of genes by manipulating organisms that contain chromosomes with genes in breeding, while experiments using the transgenic technique directly manipulate DNA segments. Therefore, classical geneticists can only cognitively discern gene types by identifying their loci without practically interacting with gene tokens; they really practically interact with organismal individuals that contain different types of genes. Reversely, molecular biologists can practically interact with gene tokens and then cognitively infer out the existence of a gene type.

6. Gene concepts and individuation

One may still wonder: Can the location technique individuate a singular and particular gene in the sense of individuating entities as individuals? The answer is obviously negative, because that technique cannot separate and manipulate a gene token and maintain its structural unity. On the contrary, one may ask: Can the transgenic technique individuate a type of gene? Here the answer is less clear. In the sense that scientists suppose that a token of a gene has been physically individuated in transgenic experiments, we are allowed to say that the technique also individuates a type of gene. However, scientists are not fully sure that the transgenic technique on a posited gene can be always successfully applied to another individual of the same organism. In fact, the probability of failure is quite high. Unless the experimental individuation of particular tokens can be performed repeatedly and stably, then one can say that the gene tokens indicate a general type of gene and that the type has been identified. However, the object individuated by the technique is not a type of gene, because the technique always requires manipulating particular segments of DNA -- gene tokens. If a kind of transgenic experiment with a specific transgene has been stably repeated, then a type of gene has been discovered by experimentally individuating its tokens in performing such an experiment.

Since transgenic experiments may be successfully and stably performed by using different transgenes, one can extract a special conception of the gene that is characterized by the transgenic technique. I call this "the transgenic conception of the gene," in which *a gene is a transferrable DNA sequence which is able to express a phenotype/function on another kind of organisms*. Of course, this does not imply that those technically untransferrable DNA sequences are not genes, given the fact that the number of transgenes is relatively few to the number of genes located at chromosomes. This is so because scientists do not always find the precise site of a gene (type) and available restriction enzymes to cut the DNA segment of the gene. Thus, the extension of the transgenic conception of the gene is not equivalent to that of the classical gene concept. Due to the limited number of transgenes, the transgenic conception is not yet co-extensional with the molecular gene concept. To be precise, the extension of the former is included within the extension of the latter, because all transgenes are molecular genes but not all molecular genes can be transplanted. In addition, the intension of the transgenic conception is implied in the intension of the molecular gene concept, because the technique was developed from molecular biology. As a consequence, the transgenic conception can be viewed as a *sub-conception* of the molecular gene concept. Nevertheless, we have a conception

derived from scientific practices.

7. The priority of individuation to individuality

Bueno, Chen, and Fagan (2018) promote an approach by which investigating processes of individuation in scientific practices is prior to metaphysical speculation on criteria of individuality. This paper obviously follows the approach. However, this does not mean that we do not need any criterion of individuality in identifying any individual in scientific practices. Rather, criteria of individuality are implied in or extracted from procedures of scientific practices, as the three conditions of experimental individuality are extracted from experimental practices (Chen 2016). Criteria of individuality based on scientific practices may or may not conflict with criteria from metaphysical theories. Considering the relationship between practical criteria and speculative criteria will help us understand practical individuation more deeply.

The metaphysical tradition has identified at least six characteristics or indexing features of individuality in general: particularity, distinguishability, countability, delineability, unity, and persistence (Pradeu 2012: 228-229; Chen 2016: 351).[7] Recently, some philosophers argues that all biological entities are processes (Dupré 2018, Nicholson and Dupré 2018, Pemberton 2018), so I would like to add processuality to the list. Indeed, I believe that all biological individuals pass through a life, i.e., a process (see also Chen 2018), therefore, processuality is a central characteristic of biological individuality. Those characteristics, originally come from metaphysical speculation, can singly, jointly, or collectively serve as epistemic criteria of individuality.

In the context of scientific practices, they are the outcomes from rather than preconditions for the realization of individuation. For example, individuating genes as individuals in the context of transgenic experiments indicates that the separated, manipulated, and maintained genes are particular and singular tokens. As the experimental individuation of gene tokens is realized, those tokens are also distinguishable, countable, unitary, persistent, and passing through a process, because particular and concrete individuals are being separated, manipulated, and maintained. The practices of separation and manipulation indicate epistemic particularity,

[7] Characteristics of individuality can serve as criteria of individuality and thus be involved in a theory of individuation. Bueno, Chen, and Fagan (2018) identify six theories of individuation in traditionally analytic metaphysics. A theory of individuation in the metaphysical sense involves not only "a theoretic construction of the nature of individuality and its attendant criteria," but also other metaphysical concepts such as "property, trope, universal, particular, substance, substratum, time, space, sort or kind." (p. 3) For my purpose, I will discuss only characteristics of individuality rather than any theory of individuation.

distinguishability, and countability. The practice of maintenance of structural unity indicates the unity, persistence, and processuality of the maintained gene token. However, all of the three practices would not indicate the delineation of a gene token, because the spatial boundary of the manipulated gene does not and cannot be delineated. Of course, this point does not mean that delineation is not a characteristic of individuality, but rather that it is not applicable to this case.

Individuating genes as types in classical genetics indicates that the individuated types of genes contain distinguishable and countable tokens, because the individuation is the location of a gene at a chromosome in a diagrammatic model. Supposing that the loci of different genes do not overlap, then the special locus of a gene is thus distinguishable from the locus of another gene. As a consequence, a gene token at a chromosome in a cell of a kind of organism is thus distinguishable from another token of the identical type of gene. All gene types located at chromosomes are countable. Supposing that every organism contains a token of a specific type of gene, then tokens of that gene type are countable. However, chromosomal location of genes does not indicate particular and singular gene tokens, because the individuated objects are only types of genes. As I have argued, the kind of individuation practice did not touch down the manipulation of individuals and remained in the cognitive level which focuses on gene types in general.

Although the concept of individuation can be reasonably applied to a kind whose members are individuals, all characteristics of individuality are not applicable. One cannot apply particularity, delineation, unity, and processuality to gene types, because a gene type is, in principle, universal, occupying multiple spaces, not cohesive, replicable, and non-processual. However, distinguishability and countability can be adequately applied to gene types, because one can distinguish one gene type from another gene type and count gene types when the chromosomal location is realized. In this case, thus, both distinguishability and countability cannot sufficiently demonstrate that the individuated objects are individuals. On the other hand, in the case of transgenic experiments, we can derive particularity, unity, and processuality from the three conditions of experimental individuation (separation, manipulation, and maintenance of structural unity). As a consequence, characteristics of individuality are derived from individuation; they are outcomes of practical individuation.

8. Conclusion

In this paper, I argue that there are at least two kinds of experimental individuation of genes. Scientists individuate genes as types in classical genetics and

individuate genes as tokens in transgenic experiments. Individuating a gene as a type or individuating a gene as an individual depends on the technique used in experimentation. I argue that characteristics of individuality identified in traditional metaphysics are not presupposed by individuation. Rather, they are outcomes or products derived from practical individuation in scientific experiments. I further argue that different kinds of experimental individuation presuppose different concepts of the gene: the classical gene concept and the transgenic conception of the gene. I argue that the transgenic conception can be viewed as a sub-conception of the molecular gene concept. An outstanding problem remains. Whether we can unify different concepts of the gene by integrating different experimental techniques, such as the chromosomal location technique, the technique of genetic sequencing, the techniques in reverse genetics, and the transgenic technique. Future analyses can approach this and other related questions in light of our new understanding of how classical geneticists individuated genes and the role experimental techniques play in identifying a gene as an individual.

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