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Have you ever tried to get all your friends and family to agree on a single definition of "love"?

Talk about different points of view! Even if you come to some kind of consensus, it probably won't satisfy everyone. Besides, the more experience you get and the more you get to know yourself (and others), the more complex your take on love can become. Well, scientists have a similar problem with the concept "gene".

Although geneticists all agree that a gene is the functional unit of heredity, they're not unanimous about what exactly makes up that unit. The definition of "gene" can change depending on the circumstance. On our website, we've tried to write the most encompassing definition in our glossary. But how we've defined the term may not fit the bill for everybody.

Here's the problem. Very (very) simply speaking, a gene is a unit of heredity. But we're going to have to follow a complex route to find more accurate definition.

Heading Back to Classics

Classical genetics studies the inheritance patterns to yield DNA information for characteristics. This kind of analysis is rooted in the old 19th century experiments Gregor Mendel did with peas. Cross-breeding peas gave him (and us) a lot of information about inheritance patterns.

In crossing a red, wrinkled plant with a white, smooth plant, you might find that all the "children" were pink and wrinkled. Therefore, you can safely conclude that wrinkled is dominant to smooth because it covered up the smooth contribution. Interestingly, red does not completely cover up white because the red was diluted to pink.

Mendel then crossed the pink and wrinkled siblings. This resulted in a variety of red, pink, and white offspring; and as well, each colour was sometimes smooth and other times wrinkled.

That the texture of the plant was not inherited with a particular colour tells us that colour and texture are independent - and therefore different genes. Mendel did this kind of experiment with every type of physical characteristic possible on a pea plant.

Classical Definition

Classical genetic analysis is usually the starting point when you are trying to figure out genetic contributions to various disorders. By analyzing family histories, geneticists can see the pattern of inheritance.

However, we begin to run into problems with the classical definition. Firstly, human traits are not usually things like wrinkled or smooth skin at birth. (A huge proportion of babies are born pink and wrinkled - but that's a whole other story.) The human inherited traits we study are very complex - like diseases, intelligence, and personality.

Secondly, classical analysis tended to lump genes and the defects that cause disease together. For example, when looking at a family history from this classical perspective, we say that an affected person has the "gene for" a particular condition. But really, we all have the same genes. The affected individual happens to have a

derail any possibility of a clear definition.

The Gene Seen Today

The Human Genome Project has enabled us to list all the 3 billion base pairs of nucleotides in our DNA. This is a truly amazing accomplishment, one of the greatest scientific achievements of this new century.

But there's still a lot of work needed to figure out how this immense list is broken up into functional units of inheritance (genes) that help determine, among many other things, our appearance, metabolic function and disposure to disease. It's a big challenge for us researchers to discover where the genes are, let alone figure out what stunningly complex work they do.

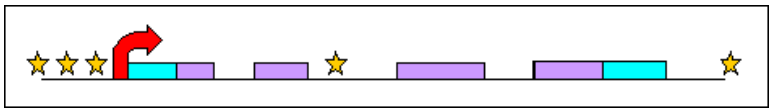
In fact, this whole discovery process is kind of like trying to interpret a book written in a totally unknown language. We have to determine the spacing between the words, what makes up phrases and sentences (as well as what the words themselves mean) - sometimes right from square one.

While on the gene trail, some of us researchers will call a 'phrase' or 'sentence' we discover a single gene; others will say that this very same phrase or sentence is made up of two or three genes. And so it goes with science: the more you find out, the more there is to learn and the more you have to argue about!

These days, in addition to clinicians working from phenotype to determine genotype, molecular geneticists examine DNA (the substance of the genotype) to figure out physical characteristics (the phenotype). Despite this different approach, the same terminology was used - further stirring up differences in opinions concerning definitions.

Initially, the genotype-first approach to genetics didn't cause problems because geneticists were studying simple traits with very high penetrance. But as information about gene structure increased, researchers tackled more and more complex traits. Unfortunately, they continued to use the old words to describe very new and different things, further complicating our elusive definition.

One Gene = One Protein?



In our diagram above, the boxes represent exons - parts of the DNA that will be transcribed and make it into the messenger RNA. The purple parts of the boxes are the specific bits that will be translated from the messenger RNA into protein. The aqua blue parts are the un-translated regions of mRNA. The red arrow signals the start of transcription and the promoter. The gold stars represent binding sites on the DNA or RNA where the bound protein helps with expression or translation.

If we define a gene as "the part of the DNA that leads to a protein product", what about the introns? In the protein-production process, they are spliced out and as far as we know, cast aside. As further evidence that introns might be useless in human DNA, bacterial genes don't have them so they aren't essential to make proteins. But generally, introns are included as parts of a gene because they are like the all important spaces in text.

Protein Problems

Another obstacle in defining a gene is something called alternative splicing. A single gene may produce more than one functional protein. Adding or deleting an exon can radically change the type and function of proteins produced by the gene. Two products transcribed by one and the same gene may have two completely different roles in the cell. So is the underlying sequence defined as one gene or two?

Well, it depends on your point of view. If you see the world from the DNA perspective, the sequence probably looks like one gene. But if you see the very same world from the perspective of an expert in cell biology, what

not part of the coding sequence, but the gene needs transcription factors at the promoter before it is can be expressed. Another analogy: if a gene is like a car, the promoter is like the ignition key. Most people would agree that the key is not part of the car but it is required to make it function. There can be mutations in a promoter sequence so that a gene is not expressed.

To continue with the car analogy, enhancers are like the factory extras. They can ramp up transcription (like a turbo engine); respond to the environment quickly (air conditioning cools car faster than opening window); and they are involved in cell-specific transcription (navigational system for direction). You don't need the extras to drive your car, but some may feel that a car without extras is not worth driving.

There is no real consensus on the function(s) of extra sequences in a gene. Some researchers argue that a mutated enhancer could reduce the amount of functional product below the accepted level leading to disease. Others say that the gene itself is fine but its regulation is altered.

Complexity: that's what we're faced with when we study the world. Someone once said that 'Nature loves to hide'. Those of us in search of her fundamental laws certainly agree. And so does the young geneticist when she tries to give a clear and definitive answer to the question, "Say, what are genes, anyway?"

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