An Introduction to Evolutionary Biology

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Benefits of sex

Hi, in our last discussion, we realized that there are many potential costs to sexual reproduction. And yet, it turns out that sexual reproduction is extremely ubiquitous and widespread in the living world. So, that led us to ask the question of what the benefits of sexual reproduction are. As I said, several theories have been put forward. So, in this particular discussion, we are going to discuss three of those. Now, the first and most important one that comes straight to your mind when you think about the benefits of sex.

It is in terms of the generation of novel genotypes. Why is that so? That is because, remember, whenever there is crossing over happening during meiosis, Then alleles are actually coming together in all kinds of new combinations. And therefore, whenever there is epistatic variation occurring, that is variation due to the identity of the alleles at various loci, Then all these new combinations are going to throw up all kinds of variations, you know. At the phenotypic level on which natural selection can then potentially act.

However, if you think about it a little more closely, you realize that this is actually a double-edged sword. Why is that? Because the same recombination can bring these alleles into favorable combinations, They can also break the same favorable combinations later, right? Now, therefore, when particularly let us say you have a very very stable environment wherein you have ended up getting A nice, beneficial combination that is increasing fitness; you do not really want that thing to be broken down. If that combination gets broken down, then obviously after some time it is not there; therefore, you know retaining that combination becomes very, very important. Now, that means that under a stable environment, this thing, the generation of novel genotypes due to recombination, That perhaps is not going to be a potent force in terms of the maintenance of sexual reproduction. However, what really happens if the environment is not stable? What happens if the environment is fluctuating, or what happens if you know the environment is changing constantly? Not necessarily fluctuating, but changing in a particular direction.

Under all those situations, the ability to continuously generate new variations, Even if some of the old beneficial variations might get lost, that might end up being a favorite trait. And there is one particular condition in which it can really become a favorite trait. And that one particular condition is in the context of what is known as the Red Queen hypothesis. What is that? So, we know that we are always surrounded by all kinds of pathogens and parasites. Not only us; you know all organisms are surrounded by pathogens and parasites.

Now, these pathogens and parasites typically have a very short generation time, which allows them to evolve extremely fast. And because of that, they typically end up evolving very, very fast to be able to invade or infect. Or, you know, use what is the most common genotype, right? And this, basically, allows them to specialize very quickly on the common host genotypes. Now, if that happens, and you have a genotype in the host that is relatively rare, then it can escape the infection. by the specialized parasites and if they can escape the infection, the fitness of that rare genotype is going to go up.

And because recombination is continuously creating rare allelic combinations, therefore, This can become a mechanism by which a host can co-evolve alongside its enemies. So, basically, what is happening is that, let us say, you have lots of host genotypes. Some of which are very, very common; others are not so common. And now you have the pathogen; the pathogen is evolving extremely fast, much faster than the host. Therefore, it is becoming specialized to whichever is the common genotype.

And now, if the host has a mechanism by which it can generate rare genotypes, Then the pathogens will not be able to invade them as easily. Therefore, that mechanism of creating a rare genotype is what will be favored, and recombination is one such mechanism. So, this overall picture was proposed by this evolutionary biologist called Leigh Van Valen in 1973. To be fair, he explained it; he proposed it to explain the phenomena of coevolution. When two or more species are evolving, you know they are doing so in response to each other.

He did not propose it in the context of sex. However, very soon people figured out that this is a very nice potential explanation for the phenomenon of sexual reproduction. And they called it the Red Queen hypothesis. Now, why did they call it the Red Queen hypothesis? This is named after the character of the Red Queen in Lewis Carroll's book "Through the Looking Glass." Now, in that book, there is a character who very famously tells Alice, the main protagonist of the series, You know now, here you see, it takes all the running you do to keep in the same place.

It is a metaphor to explain the fact that in co-evolution, two species are evolving as fast as they can. and as much as they can, simply not to fall behind the other species. So, it is not that one is able to completely outweigh the other; you know it is like an arms race. Country one you know makes weapons, and country two now has to make something better. Once it has made something better, country one has to make something even better, and so on and so forth.

So, the relative position does not really change except that you keep making more and more advanced weaponry. So, the same thing is happening over here; both of the co-evolving species are evolving as fast as they can. Yet they are not really able to conclusively defeat the other species. So, the statement of the Red Queen hypothesis is that sexual reproduction in hosts is selected. Due to the co-evolutionary interaction between hosts and parasites to reduce infection risks.

Now, of course, you can see that this is a, you know, multi-step hypothesis. It is not a simple "you know A, therefore B" kind of thing. So, because the reasoning is multi-step, therefore, Each component of this reasoning chain has been validated extremely thoroughly in the literature. So, this is a very well-studied hypothesis. So, instead of giving you one or two validations, what I will do is show you what the various steps in the reasoning are.

And I will also tell you where the validations have happened, and I am also going to give you references. You can go and check them out on your own. I mean most of these steps have been validated multiple times in multiple systems. So, the total number of references is unmanageably high, but what is more important for us is to It is to understand what the various steps are and whether they have been validated or not. So, here are the various observations.

So, the first thing is, I mean, these are the references where you will find the primary references to all these things. So, the first thing is that it shows that this particular hypothesis assumes that if you have sexual reproduction, It is beneficial in the presence of parasites, which tells you that if there are no parasites, asexual is what should be favored and if there are parasites, sexual should be favored. And that is precisely what we see in nature; obviously, there are some places where there are more parasites. In some places, there are fewer parasites. Wherever there are fewer parasites, the asexual reproduction mode dominates whereas if there are more parasites, the sexual ones dominate. So, it suggests that asexuals eliminate sexuals, whereas, where parasite mediated selection is weak. Second thing is that for this entire thing to happen, the parasites need to be able to specialize, Because if the parasite is, you know, able to infect all the species, all the hosts, irrespective of the host genotype, Then this entire thing does not work; the entire Red Queen hypothesis does not work. So, this will work if the parasite is able to, you know, figure out the most common genotype and is able to specialize for it. and turns out that parasites in many cases it has been shown can indeed do that.

And not only that, not only can the parasite specialize, it can specialize against the common host genotype. That is also very, very important. And many experiments, you know, lab experiments as well as field work for a wide range of taxa, have explicitly shown. That parasites can not only specialize; they will specialize against the common host genotype. Then the fourth point is that you know when the parasite specializes, it should be able to specialize in a way that it can exploit the features of the common genotype, right? In other words, it is not just simple growth; it should be able to take care of something that the host has evolved.

In a variety of microbes, plants, and animals, it has been shown that the parasites are capable of doing that. And fifthly, it has been shown that when you have, you know, hermaphroditic worms, like earthworms. where the males and females are present in the same body, in all those cases, When you expose such hermaphrodites to pathogens, virulent pathogens, then, evolutionarily speaking, The rate of outcrossing increases. Outcrossing is the lack of selfing, where you use the males of one organism, explicitly. Sorry, the male gametes of one organism are fertilized by the female gametes of the other, and vice versa.

So, in all those cases where hermaphrodites are exposed to pathogens, that is where the rate of outcrossing goes up. And not only this, these outcrossed offspring are actually more resistant than the self-fertilized offspring. which basically means that this outcrossing is actually helping the host to fight the infection from the pathogens again, Much more than the self-fertilized offspring. So, the main mechanism by which sex is going to lead to resistance to infection is what is being proven here. And finally, it has been shown in flower beetles, Tribolium, that if you have antagonistic coevolution, which means that where you have a pathogen and a host, and the pathogen is actually harming the host, they are coevolving.

In those cases, the rate of recombination itself can increase in these organisms. So, all these are various chains, you know, or links in the chain of reasoning for the Red Queen hypothesis. Individually, each one of them has been very nicely validated. So, that is what I am saying: almost every aspect has been very well validated in some system or another.

But if that is the case, that means the problem is solved; we know what is happening, and it turns out that it is not that easy.

Why is it not that easy? That is because, although there are many cases where things have been supported, There are a few empirical examples where the various chains of the links of the Red Queen hypothesis. They have not been supported; in other words, the support is not universal. And therefore, today scientists think that although the Red Queen hypothesis by itself is fine, Having sex does help organisms combat infection. But it is not sufficient to explain the maintenance of sexual reproduction under all conditions. So, this is very nicely put by Sarah Otto and S. Nuismer when they say, "I mean," After a very long theoretical analysis and with some experimental data as well, I mean the analysis of other people's experimental data that we conclude that Although the Red Queen favors sex under certain circumstances, it alone does not account for the ubiquity of sex. So, it is not a necessary condition for sure, and I mean when it happens, it will explain sex. But there are so many conditions where you do not even expect this to be the primary reason. Great. So, what else do we have? So, this leads us to our second hypothesis; but before we get to that second hypothesis, We have to understand a very major problem that occurs in the context of asexual reproduction.

What is it? So, remember that deleterious mutations always appear in a population. I mean, mutations are always appearing in a population. As we discussed when we were talking about mutation, most non-neutral mutations are actually deleterious. So, deleterious mutations are always cropping up. Now, when these mutations are cropping up in an asexual population, remember there is no recombination happening in it, right? Now, because there is no recombination happening, the healthiest individuals are the ones.

Which have the fewest harmful mutations in their genomes. So, suppose you have an individual who has no harmful mutation, and you consider the fitness of that individual to be 1. then obviously all the individuals which have 1, 2, 3, 4, whatever number of harmful mutations, their fitness will be less than that of the one which has 0 harmful mutation. So, this extra, this reduction in fitness is what is known as the genetic load. So, if you are talking about the healthiest individual, as I am pointing out here, These are the ones that have the fewest harmful mutations and therefore, technically speaking, These are the ones that are the least loaded among all the genotypes present in the asexual population.

Now, because of this, if there is genetic drift also happening in the population, then this least loaded class. Although selection is favoring it because it has the highest fitness, remember fitness. Sorry, selection and drift are always working in tandem or sometimes opposing each other. Therefore, the least loaded class can be completely lost, particularly when the population size is small. And in that case, other less fit individuals can end up surviving in the population.

When that happens, what is the consequence of that, you know? Once a least loaded class is lost, there is no other way of naturally restoring this within a class except back mutation, of course. There is no other way to naturally restore this least loaded class in the absence of recombination. This process is irreversible. So, what is the outcome of this? The outcome of this is what you can think of in terms of instruments very often used in autos by auto mechanics and others. What is known as a ratchet? So, what is a ratchet? A ratchet is something that you will be using to turn a nut or a socket in one direction.

But you will not be able to turn it in the other direction, right? So, a ratchet mechanism is a mechanism that only turns in one direction and not the other. So, you have what we discussed on the previous slide. This is technically known as Muller's ratchet, which is a process by which The absence of recombination leads to an irreversible accumulation of deleterious mutations in a population. Why is that? Because if you do not have recombination, then harmful mutations accumulate. And if the least loaded class gets, you know, wiped out, there is no way of going back.

So, the accumulation of mutations becomes an irreversible process in an asexual population. So, of course, big examples of this are bacteria, but a very human-centric example is the human Y chromosome. Remember, we have X and Y chromosomes; the females are XX, and the males are XY in humans. The X chromosomes can recombine with each other, but since the Y chromosome does not have a homologous chromosome, therefore, The Y chromosome has not been recombining for a very, very long time, at least as long as our species has existed in the XY form. And therefore, over time the Y chromosome of human males has actually ended up acquiring a very large number of harmful mutations.

And people think that at some point, the number of mutations will be so high that this chromosome will essentially break down. So, this is a major example of Muller's ratchet happening in real life, and Muller's ratchet is named after Hermann Joseph Muller. So, Hermann Joseph Muller was associated with Thomas Hunt Morgan; you know, Morgan's famous fly lab. He is a Nobel laureate for discovering X-ray mutagenesis. And as we are going to see, ended up making a massive contribution to the field of genetics.

Now, understanding this particular problem of what happens if you do not have recombination. immediately tells us what the benefit of having recombination will be. So, recombination will end up recreating the genotypes every generation, and therefore, if you have, let us say, a genome, Let us say one genome has one harmful mutation, and another genome has another harmful mutation. Recombination can actually create a genome that will not have any harmful mutations. In other words, the least loaded genotype or the loading of the genotypes can actually go down because of recombination.

You can end up getting "clean" genotypes without any harmful mutations potentially every reproductive cycle. I mean, it does not happen every reproductive cycle; there are probabilities associated with them. But they can keep the process of throwing these kinds of clean genomes. Now, if that happens, if you have the clean genomes, so to speak, and if you have other genomes in which many harmful mutations have come together, then that actually allows selection to purge the mutations, right? And if that happens, then the number of harmful mutations in the population's gene pool actually goes down. In other words, selection becomes much more effective at eliminating harmful genetic mutations.

So I will give you a very nice empirical example for this, empirical validation of this. So this is the New Zealand mudsnail. I mean, the name is really a tongue twister: Potamopyrgus antipodarum. We just call it the mud snail. So, this particular species is very interesting because it exists in two forms.

It can exist both in the sexual form and in the asexual form, and sometimes in the same populations. We are talking about natural populations here. In the same natural population, it can have both sexually reproducing and asexually reproducing forms. So, what Neiman et al. did in 2010 was show that the asexual lineages are experiencing A substantially higher rate of accumulation of deleterious non-synonymous substitutions than that of the corresponding sexual lineages.

In other words, the accumulation of harmful mutations is greater for the sexuals than the sorry asexuals than the sexuals. Is this the only example that we have? Absolutely not. There are many more. So, I will give you one more. So, this is in the context of these stick insects, which are known as the Timema stick insects.

Henry et al. (2012) showed that there was a 3.6 to 13.4-fold higher rate. of mutation accumulation in asexual populations compared to sexual ones. So, this makes it a very nice strong mechanism for as a benefit of sex. So, another mechanism you know for the benefit of sex is related to another issue with asexual reproduction what is known as clonal interference. So, in this particular case, here is a diagram. We need to look at what this diagram is doing in detail. So, let us assume that we have a 1-locus, 2-allele scenario, where the population is starting with a genotype ab. We have time on the x-axis and frequency on the y-axis, so this is color-coded. So, the frequency of ab is white, the frequency of aB is red, the frequency of Ab is green, and the frequency of AB is yellow.

So, for any given color, the length of the line along the y-axis tells you the frequency of that particular type. So, for example, if you follow my cursor over here, the entire thing is white, which basically means that the entire population is ab. Over here, you know this much: the white is this much, and you have this much red; this much is green. So, this is telling you the relative frequency of aB, ab, and Ab in, let us say, this region and so on. So, what is happening here? So, let us assume that this is an asexually reproducing population and we are starting with the entire population being ab.

So, the only way in which a new mutation can come in here is through a new allele, which can come in through mutation. So, at some point, there is a new mutation over here, and let us say the b mutates to B. And after that, let us assume that going from a small letter to a large letter increases the fitness. So, aB has a larger fitness; therefore, the frequency of aB keeps increasing. That is what is meant when this thing, the thing, expands; the red color expands.

Similarly, at another point over here, the a allele in one individual in one lineage becomes A, and this is where Ab starts and begins to expand. Now what you have to realize is that in any asexual population, whenever you have a mutation occurring, that is when a new lineage starts. So, that is what I mean by saying that a beneficial mutation forms a new lineage. Why does it have to be beneficial? Because if it is not beneficial, then by selection it will go out right. So it will not be able to expand; only beneficial mutations in their lineages are going to expand greatly.

So now, if you have multiple beneficial mutations like the ones we have over here. Then there can be several distinct lineages that can be formed, and that is what is happening here. You have, let us say, in this range you have ab, but you also have Ab, and you also have aB. Now, when these mutations and lineages are expanding, These lineages are also competing with each other, right? Competing for survival, competing for reproduction. When they are competing with each other, if you look at the overall fitness of the population, The overall fitness of the population is actually getting reduced.

Why? Because let us assume for a moment, let us say that Ab is more fit than either ab or AB. So, if the entire population were composed of Ab like what it is over here, then the fitness of the population will be maximum. But because these guys, the Ab guys, are competing with aB and ab, all three of them are existing together over here. Therefore, this is going to take some time to reach to this you know this stage where you have only one genotype. So, that is what we mean by saying that the rate of increase of fitness is how fast Ab is able to get rid of the other two.

That rate of increase in fitness basically means the rate of adaptation; that rate of adaptation is what is going down because of the competition. And this also slows down the fixation of the beneficial mutation. Fixation is, remember, when frequency goes to 1, right? So, this is where the fixation happens, but because of this competition, the time taken to reach fixation is reduced. Now, here you have a stage, let us say, where AB has happened.

Now, remember, AB is the fittest phenotype. Now, the only way that you will go from Ab to AB is by waiting until the b mutates to B in one of the asexual lineages. And when that happens, in this case, let us say that it happens over here, after this point, again Ab is going to compete with AB. And therefore, going to this final AB is going to take quite a bit of time. In other words, you know that sometimes what happens in this process is, let us say, an allele that otherwise could have complemented. With another allele to give the fittest phenotype that might even get lost during this process when it competes with others.

And that is what I mean by saying that mutations that become fixed are from the most successful competing lineages, but that does not. necessarily mean that the final product you get is the combination that would have actually given you the highest fitness. In other words, this fact that you know you have competing lineages containing various mutations can end up not only slowing down. The rate of adaptation can also end up putting constraints on whether you are able to attain the genotype with maximum fitness or not. So, this particular stuff, this is what is known as clonal interference, and the definition is that The competition between lineages arises from different beneficial mutations in an asexually reproducing population.

So, clonal interference is simply the competitive part of it. The outcome of clonal interference is a slowing down of the rate of adaptation. Now, I have taken this definition from this particular paper, but that does not mean that these were the people who proposed it. Actually, this was proposed by Hermann Joseph Müller in 1932, the same Müller that we talked about a few minutes back. And it turns out that clonal interference actually plays an enormous role in the evolution of microbes and viruses.

It is also extremely important in the dynamics of cancer cells. So, if you remember the way people have been thinking about treating cancer, in fact, the way cancer is treated even now. is that you do chemotherapy or you you know zap them with lots of radiation and you end up killing everybody. And this kind of thing can often lead to relapse. So, one of the things that people figured out is that because cancer cells are reproducing clonally, There is a high chance of this kind of clonal interference and, therefore, competition among the cancer cells. And hence, people actually said, "Why do we not use this competition amongst the cells to keep the growth of the cancer in check?" And that is why one of the lines of therapy that I think is now in clinical trial is known as adaptive therapy where the whole idea is to not kill off all the cancer cells, particularly to not kill off the competitors, Identify where the competition is happening and do the treatment in such a way. That the competing cells, by competing with each other, actually end up keeping the overall cancer in check. This, as I said, is leading to new treatment possibilities, and people are actively trying to see if one can manage cancer in this way. Another massive example of this kind of competition, clonal interference, happening is in the context of what I am sure all of you are aware of how the COVID virus evolved during the pandemic.

So, if you remember all these terms—alpha, delta, omicron, etc.—these are different lineages of the COVID virus. So, if you remember, you know the first human infection happened somewhere around late 2019, the one in China, and then you know. These early strains kept evolving; they kept acquiring mutations. Remember, these are asexual lineages, right? So, they acquire mutations one after the other, and then at some point, there is a branching over here.

And at some point, we got to what is known as the alpha strain. So, this is where the alpha strains started increasing in number. So, if you look at this graph over here in the initial phase, you know the first early strains were evolving at some point. Alpha came in, and alpha was more competitive than the others. So, alpha increased in frequency greatly very soon. But while alpha was increasing in frequency, at some point from the early strains, we got the delta strain.

And then the delta strain came in somewhere over here, and delta was much, much more competitive than either alpha or the early strains. And therefore, delta, you know, moved very, very fast; delta frequency increased extremely fast. You can see that very soon these two are declining very, very quickly. This is where we have our second wave.

And then, while Delta was evolving, at some point you got Omicron from the other branch. Omicron turned out to be even more competitive than Alpha, and once Omicron came in, then Actually, it ended up, you know, just swamping the entire stuff all over the world, and very soon all we had was Omicron. Fortunately, omicron was a lot less virulent than delta, and therefore, although it caused a lot of deaths, it was relatively less. But the main thing that I want you to understand is that if COVID-19 were to reproduce sexually Then the rate at which you know delta and omicron evolved would have happened much, much faster. In other words, we would have gone into this high level of virulence and probably even higher levels. Much, much faster than what it actually ended up being, which was blindingly fast to begin with.

So what happens in a sexually reproducing population? So here I am showing the asexual graphs all over again; it is the same graph that we discussed a few slides back. But I am now discussing this in the context of the sexuals here. So the first part is the same; we start with "ab" in both cases. In both cases, the Ab and the aB appear roughly around the same time.

But what happens after that is the interesting part. Initially, they will expand on their own because you know. They are probably in very different parts of the population and are not coming close to each other. But once these genotypes come close to each other and mate, recombination happens. Then this formation of AB is going to happen much, much sooner. And once that happens, this is also going to spread much faster; therefore, You know, due to recombination, multiple mutations have arisen in different backgrounds.

They will be able to come into the same genome much faster, thereby reducing the competition. So, here the only way you will go from ab to AB is if the two mutations A and B arise one after the other in the same lineage. Otherwise, you cannot get here. But in this particular case, these mutations can happen; B mutation occurs in this lineage, and A mutation occurs in this lineage. And then recombination brings A and B into the same genome, which is what is happening over here. So, this ability of recombination to bring mutations that have occurred in different backgrounds into the same background, That is what is speeding up the overall rate of adaptation in these populations.

Now, this simply means that sexual populations can adapt much faster. Do we have, you know, okay, sorry, so this is, you know, the formal statement of it; this is what is known as the Fisher-Muller model. It simply says that the advantage of sex results from recombining competing beneficial mutations into one lineage. As you can see, it is named after Ronald Fisher and Hermann Müller, the same Hermann Müller that we talked about. So, you can see that he made serious contributions to the evolution of the field of sex.

And, interestingly, this is also known as the Vicar of Bray hypothesis. Now, what does that mean? What is a vicar and what is Bray? So, Vicar is a kind of priest in the Christian church, and Bray is a place in England. So, the Vicar of Bray is actually a fictional character who, essentially, you know, was basically adaptable. So, this particular person, so the story goes, changed his religious beliefs when the monarch of England changed. And when people actually questioned him about how he could be like that, he simply said, "Look," I have only one goal in mind, which is to remain the Vicar of Bray throughout my life, and in order to do that, I am adaptable along other axes. So, this is obviously a very, you know, tongue-in-cheek funny reference, but here the whole idea is that Sexual reproduction is able to bring together all kinds of benefits and create the most adaptable genotype possible.

The most beneficial genotype possible is simply achieved by putting together things that have mutations or that have happened in very different lineages. Now, do we have empirical reasons to believe that this works? It turns out that we do. So, I will give you one very famous study on this; it was by Tim Cooper in 2007, and here he actually ended up using E. coli. Now, this is very interesting; E. coli is a bacterium, right? So, normally you expect that this is going to reproduce asexually, which it does, but it turns out that in E. coli, There are these things known as F plasmids; right? You know, plasmids; these are circular pieces of DNA, extra chromosomal DNA. So, these F plasmids actually promote the exchange of genes across E. coli cells.

And in that sense, there is an exchange of DNA, and this is, you know, mimicking recombination essentially. It is not a regular recombination in the sense of exchanging homologous parts of homologous chromosomes. But it is actually at least exchanging genes. And he, of course, as a control, also had those E. coli that did not contain the F-plasmids; therefore, they were evolving asexually.

So, what he did was he took these two kinds of E. coli and he engineered this in a background where the mutation rate was high. How can you do that? So, it turns out that in E. coli, you have certain genes, such as mutase, mutil, etc., wherein if you introduce some mutations in those genes, Then the rate of mutation in the overall genome can go up quite a bit; you know, tenfold, hundredfold, and so on and so forth. So, he engineered one of those hypermutation things, thereby creating the background on which these F+, F- things are happening.

The background had a high mutation rate. Now, if that is the case, if the mutation rate is high, what is happening? You are getting lots and lots of mutations, right? Many of which are also going to be harmful. So, now the question is about the combination of beneficial mutations. If everything goes alright, then if the Weiker of Bray hypothesis is correct, you expect that the ones containing the F-plasmid. The ones that, you know, have a combination like phenomena, are the ones who will be able.

To access the beneficial mutation faster, they are the ones who will be able to increase their fitness better. And that is pretty much what he ended up finding. So, he showed that the bacteria which contain the F plasmid, those lines, The recombination actually ended up increasing the rate of adaptation about threefold, and this was due to a beneficial mutation. So, using sequencing he was able to identify precisely which mutation led to this increased adaptation. And this is the best part: he showed that in the F minus lines, in the absence of recombination, this mutation was taking much longer to fix and over the course of its substitution, it ended up conferring a much reduced competitive advantage. In other words, when you have an absence of recombination, then the competition among the various genotypes. was much greater compared to the situation in which you had the recombination. Interestingly, this entire thing works if and only if the mutation supply is high. If the mutation supply was low, which is what he did by having another set of lines where the mutation was, He did not have the mutase allele; therefore, the mutation supply is low.

In that particular case, there was no difference in adaptation. So, basically, what he ended up showing was that recombination increases the rate of adaptation, correct? But it does so only when there are competing beneficial mutations in the population. If you do not have competing beneficial mutations in the population, Then recombination is not going to play a role in increasing the rate of adaptation, which makes a lot of sense, right? Because that is the context in which the entire hypothesis has been put forth that this will work. If and only if you have competing beneficial mutations in the population. And this also tells you about the weaknesses of the hypothesis.

I mean the hypothesis is fine, but rather the specificity of the hypothesis, okay. This will only work under that particular scenario in which there are competing beneficial mutations. So, where are we? We today have a very good understanding of the benefits of sexual reproduction and all these benefits are theoretically proposed. They have been extensively empirically verified; they work. Now, remember, I gave you three hypotheses, but these are not all the hypotheses that we have there.

There are many others. So, for example, you have the so-called best man hypothesis and the tangled bank hypothesis. You have the mutational deterministic hypothesis, and so on and so forth. There are multiple options. Now, many of those hypotheses, almost all of them, have some empirical validation or the other. But all the hypotheses require specialized conditions, like what we discussed in the context of these three.

And because they require specialized conditions, there is no single hypothesis that has led to theoretical models. That can confidently account for the appearance of sex across a wide range of biological scenarios. This is the point. We have a bunch of hypotheses; all the hypotheses make sense, but all of them require specific scenarios. If those specific scenarios are present, they will work; however, there is no one thing that explains it across the board.

Nothing explains on its own why 99% of the animals are sexual. In other words, we do not have a general theory. Now, is this a problem? Because in biology, we hardly have any general theories. So, lots of people have argued that the lack of a general theory is not that big of an issue. But there are other people who suggest that even 99% is too big a number. There should be something that is more overarching.

And now, that is a you-know article of faith, that is a belief that there should be such a thing. It is like the, you know, theory of everything in physics; people are still searching for the theory of everything. That does not necessarily mean that all the specialized theories we have do not work; they do, and people are still searching. So, this is what we understand about sex at this moment, but one thing that we really understand about sex is its implication. In terms of explaining certain very, very strange patterns in the context of, you know, biology in the field known as sexual selection. What happens when one sex ends up choosing certain characteristics in the other sex? What does it lead to, and what kind of peculiar patterns does it explain? That is something we are going to discuss in our next meeting. See you then. Bye.