

BARBARA TAYLOR

HR: Thank you, Paul, for that illustrative talk on how some recent genetic technologies particularly in the use of historical specimens can really help in aiding conservation priority-setting.

We're going to change gears here a little bit. And our next speaker, Dr. Barbara Taylor, is a conservation biologist with The National Marine Fisheries Service. Her diverse background ranges from developing analytical tools in light of uncertainty for conservation decision-making, to bridging the interface between science and the implementation of policy at the domestic and international levels.

She coordinates the IUCN Red List for cetaceans and is a delegate to the International Whaling Commission where she annually brings her perspective and expertise to bear on the problems of defining units particularly management units in the context of international policy and political agendas.

My short description of this process does not do Barb's work any justice here, for her efforts to protect endangered species, based on sound results. You really have to see her in action at the IWC.

Her talk today, *Maintaining Populations as Functioning Elements of Their Ecosystem: The Role of Management Units*, will focus on how understanding population structure using genetic data aids in management. I'm happy to welcome Dr. Barbara Taylor.

(Applause)

MAINTAINING POPULATIONS AS FUNCTIONING ELEMENTS
OF THEIR ECOSYSTEM: THE ROLE OF MANAGEMENT UNITS

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BT: I am going to shift gears a little bit today, and I'm going to be talking about what I hope is a broadening of the idea of the use of conservation genetics to actually help in managing species to remain at healthy levels. And not just focus entirely on sort of the trench work of helping out endangered species. Although, of course, I think that's very important, as well. So I'm going to be talking about the importance of defining management units as part of the effort that I think needs to be undertaken in order to preserve ecosystem function.

And I'm going to go back to the management paradigms that I was raised under, and how they've shifted through time. And sort of help put in perspective the idea of using conservation genetics to sort of reformulate our ideas of how we manage wild populations.

I was raised under quite a different paradigm than most people are today. I was raised under traditional game management. And the idea in traditional game management was to maintain fish populations, and game populations, so that they could be harvested in perpetuity. Basically, so that your children and your grandchildren had the same hunting and fishing opportunities that you did. And those populations were managed on very small units, and they are today and those are traditionally called management units.

Unfortunately, traditional game management neglected many, many species, and resulted in a lot of problems that we've been discussing today including habitat fragmentation and the endangerment of many species. And, as a result, conservation biology the paradigm of conservation biology as

a management scheme really has, in large part, replaced traditional game management. And the focus of conservation biology has been to manage species to preserve biodiversity. And, as we've been just talking about, this has largely replaced management units with evolutionarily significant units. And these units tend to be much larger than the traditional management units.

Today I'm going to assert that, for resource management, perhaps we should go back to the traditional game management as being a healthier paradigm when it comes to maintaining ecosystem function. And the primary reason I'm going to assert that is that healthy ecosystems require healthy populations. And they require healthy populations of not only rare species, naturally rare species but, perhaps more importantly, they require good healthy populations of the abundant and continuously distributed populations.

Also, if we set maintaining ESUs as our goal, it does two things. First of all, many species are not being treated until they get to the emergency room. In other words, there's no proactive management scheme that's put in place to keep populations from getting to the point where we're wondering about whether we can preserve their evolutionary function. And the other problem is, is that you're telling resource users that you have very low standards for them. That if you just barely maintain populations, that, basically, you've succeeded in managing those species. And I think that's a dangerous priority.

I'm going to illustrate this with a couple of examples. One that I have had a lot to do with lately is the management of North Pacific minke whales, which are being considered for commercial harvest within the next few years. And I'm going to use that to illustrate why I think management units and, in particular, the use of conservation genetics to define those units is important. And then I'm going to come back to discussing those two management paradigms through an example with Steller's sea lions, and a recent major change in ecosystem function within the Aleutian Islands.

First, let me introduce myself as a marine biologist. A very famous New Yorker, George Costanza, said: Marine biologist? I didn't even know that was a job. (Laughter) And it turns out that marine biologists have quite a different perspective. Because, actually, the state of exploitation by humans in the marine environment is very different than the state in the terrestrial environment. So let me make a few points on that.

First of all, of course, because humans live in a terrestrial environment, our ability to modify or eliminate the habitat is much greater. And the era of major exploitation of wild populations for animals, at least is in the past. Of course, the great exception to that is the exploitation of the world's forests. Also, terrestrial organisms have some unfortunate properties for them. There are many species that have limited distributions, and a lot of species that have what I would call low resilience that is, low population growth rate.

It's quite a different story in the marine realm. Humans have a more difficult time modifying or eliminating the habitat, although the technology to do that is fast upon us. We are in a state now of the highest level of exploitation of wild living resources in the oceans in history. So we're really at quite a different stage perhaps the stage that terrestrial biologists would have been if they had arrived on the continents here, when there were still buffalo that were roaming the plains.

Also, marine organisms have some properties that are good for them, in terms of endangerment, and that is they tend to have large distributions, and they also tend to have high resilience. There are some exceptions, and those are the animals that I spend most of my time working with marine mammals. And, of course, the exploitation overexploitation of the large whales is one of the flagship examples of overexploitation of wild species.

And, as a result, we have some quite restrictive legislation in place. Domestically, we have the Marine Mammal Protection Act, and on the international front we have the International Whaling Commission at least when it comes to regulating whaling.

We also learned some lessons from this overexploitation, and I think these are interesting and important lessons. Because we're now watching the recovery of most of the species of whales, great whales, on the planet. Unfortunately, this recovery is very patchy. There are places that used to be some of the highest exploitation for whaling in the world, that are still whale deserts. And, even more interesting, right next door to them, frequently, will be populations that have recovered to near historical levels. So we can see, by the pattern of recovery, that, in fact, despite our inability to see barriers to dispersal in the ocean, there actually is a lot of structure that's present.

Well, because of the failure of managing whaling, The International Whaling Commission called a halt, or a moratorium, to whaling in 1984, and they commanded their scientists to go out and come up with a better whaling scheme. I'm not going to go into the details of that, except as it pertains to population structure.

They knew that population structure was a problem. And, so, in their whaling scheme they set out to initially manage whales, set up whaling quotas, by what they called small areas. Now, ideally, what a small area is, is you get all the experts together in a room, the biologists, and you have them define a small area, draw a line on a map. And you think: Inside that, there's no possibility that there's population structure. You can only, then, go to larger areas. Unfortunately, they didn't set up any rules for how to go to larger areas to go from a small area, to a medium, to a large area. And, yet, the quotas for the whalers get higher and higher as you go from small areas to large areas. So, guess what? That's a very strong reason for the resource users to want to have larger and larger units.

And that's exactly the case with this species. This is a North Pacific minke whale. It's the smallest of the baleen whales. It's only about 10 meters long. It's a fish-eater, so it eats at the top of the marine trophic levels. And it's a very important marine predator, because it's quite abundant, and it's continuously distributed in all of the world's oceans.

Since 1994 the Japanese have been harvesting North Pacific minke whales in the North Pacific, expressly to prove that there's no population structure. And I'm going to talk about what's been done in the scientific whaling. Because it was the smallest species, it was the last species that was exploited because it wasn't as commercially valuable as blue whales. And it was taken only in coastal whaling right along the coast of Japan.

So when it came to setting up these small areas some of which you see denoted here there actually were no data at all. Those lines were drawn on the map in a completely arbitrary fashion. And the Japanese then set out to gather samples across this area again, with the idea of proving that there was no population structure.

Well, why do they want to do that? Well, the reason why is because, for one thing, all of the whaling came out of this area. If you only thought that the population was here, The International Whaling Commission wouldn't allow whaling, because that area would be considered to be depleted.

Here's the other reason. The other reason is that that there are 26,000 whales in this whole area there's only 5,000 whales in this coastal area. Of course, they'd like the quota for the whales that they want to take out of this area to be based on 26,000, not 5,000. So they want to show that there isn't population structure in the area.

They use traditional hypothesis testing for looking at population structure. And this is what you would see in most molecular journals, where the null hypothesis is that the populations are panmictic. In other words, every whale in that large, many-thousands-of-square-mile area has an equal chance of mating with every other whale in that area. And the alternate hypothesis is what, in statistics, is called a nonspecific hypothesis. That is, that there is population structure.

Now, the problem with that is that we're not able to address questions like this. If there was 1% per year of dispersing between, say, two different populations in that area, what's the probability that we would correctly reject the null hypothesis of panmixia? And manage it as a population that had structure.

Let me review a few terms in statistical hypothesis-testing. There's two mistakes that you can make. You can either have the case where panmixia is true, but you say that there's population structure. That's a type-one error, and it occurs with the probability of alpha. That's generally set at a 5% chance.

The other error that you can make is that there was population structure, but you failed to reject that the panmictic hypothesis was the correct case. That type of error is a type-two error it occurs with probability beta. The converse of that that there is population structure; you went out, and you did your genetic study, and you detected it is the statistical power of the test.

Here's why that is relevant. Here's those three sections that you saw the two that are closest to Japan. When they took 89 whales out of those areas, they got a P value of .7. But if you compare the coastal area to the far-off shore area, you get a P value of .07. Now, if you use that criterion of .05, which most people use, you would conclude that there's no population structure. And, in fact, surprise that's what the Japanese did. They concluded that there's no population structure in the North Pacific.

So let's make this a little bit simpler problem, and ask a more specific question, and estimate what our statistical power is. What we did was, we looked at: What if there are two stocks? O stock, for offshore Japan, and W stock, for Western stock. And we simply asked: What's the probability that, if there was population structure there, I would have detected it?

What we do to estimate statistical power is, we simulate the populations. We put it into a model. We put the same spatial structure in, we put the same abundance in, and we take the same sample size out. It's a little bit trickier than that, though. Because it turns out that even if there's constant dispersal between two populations, the level of genetic differentiation that you're looking for actually fluctuates through time, just by the random chance of inheritance. So sometimes populations are randomly more closely related, and sometimes they're more distantly related.

And that's what you're seeing in this line bouncing up and down. Here's time in the simulation 150,000 years to 175,000 years. Here's this measure of genetic differentiation which is zero if it's panmictic, and 1 if they were perfectly fixed. You can see that these are tiny levels. For those of you can't read it, that's .0005. But it's bouncing around here, and that makes it, actually, a little bit difficult to estimate statistical power.

But we've come up with a way to do that, by simply sampling through time. So we incorporate the uncertainty about the state of the population by sampling the simulation through time. And so we stop the simulation. We sample it, just the way the Japanese did, except we don't kill any whales. And we save our genetic statistic, and we save this P value that tells us how different the populations are.

And so we end up with this big long list, and then we can say: What's the probability that we would have correctly been able to tell those two populations

apart for the dispersal rate that we decided to look at?

So we looked at several different dispersal rates. This is an annual dispersal rate. So this one, for example, is two tenths of a percent per year going from O stock to W stock, and vice versa. And you can see the observed value, right here. Again, it's this little teeny-tiny number. It's likely, for all of those; it's most likely for this one. So there's some gene flow, but it's pretty small.

So what does that mean in terms of managing minke whales? Well, first of all, we can go back, and we can estimate what our statistical power was. This is the alpha equals .05, that most scientists use. But I want to make the point that that is not an unvalue-laden judgment. Because, in this case, an alpha .05 for the most likely dispersal rate gives you a beta that type-two error of .19.

The type-two error, remember, is: There is population structure, but you incorrectly concluded that there wasn't. So I would call that an underprotection error, and this one an overprotection error. And we can look at the ratio of those. And we can see that, roughly, if you decided to use an alpha .05, you'd be four times more willing to commit an underprotection error than an overprotection error.

Another way that you can look at it is to say: Well, I don't like that. I'd at least like to have an equal chance of making either one of those mistakes. So we can equalize those two. And when we do that, we end up with alpha equals beta, equals .1. What does that mean? Well, it means that if you've got a P value of .07, that you would conclude that there was population structure there. So you can see that this choice of what you want to use for alpha makes a big difference when it comes to actually saying how you're going to manage those animals.

But we can actually go one step further and say: Well, what if we took the Japanese recommendation, and we said, There's no population structure there? Go ahead. Take all of your whales out of this area, and that's okay with us. We think that the data's plenty good enough. But what if it wasn't? What if the dispersal rate really was at two tenths of a percent per year between these two areas?

So we can go back, and we can ask: What if we harvested the population like that, but there really was population structure? What we have along the X axis is the annual dispersal rate, and this is the proportion of that O stock the coastal population that would remain. Running from zero on up to .6 in this case.

Just look at this one harvest rate. This is a 1% per year harvest rate very conservative harvest rate. And you can see that unless there's at least a half a percent per year, that population is going to go extinct. And, in fact, our most likely value at .02 is going to be one of those cases where the population would go extinct. So very tiny genetic differences, but it's enough limited demographic exchange between those populations that it would result in exactly what we're talking about wanting to avoid fragmentation or contraction of the range.

Okay. So let me go on to my next example and try to connect that up. So what if we lose those minke whales? From a biodiversity standpoint, I have to tell you it's probably not going to make much difference. There's tens of thousands of minke whales. Basically, you're looking at teeny-tiny genetic differences between the animals that are right next to Japan and the animals that are a little bit further out in the ocean. So, from a genetics perspective, or an evolutionary perspective, you're probably not going to lose much.

So let me ask the question of: Who needs top predators, anyway? And what does it mean to, sort of generally, how we perceive resource management? Well, let me go to an example where, actually, that experiment has sort of been done with Steller's sea lions. Steller's sea lions are a very similar species when

it comes to what role they play in the marine environment.

They're a top predator; they have a very wide distribution. In fact, they have the same distribution in the North Pacific that North Pacific minke whales do. They're very abundant. In fact, originally they numbered in the hundreds of thousands. They have many remote breeding and feeding sites. They're not feeding specialists. They're exactly the sort of species that you wouldn't worry about from the biodiversity perspective. They're a very abundant species.

Here you can see the range. The highest number of animals were found right here in the Central Aleutians. They breed along these islands they feed up in the Bering Sea. This distribution that you see is also a distribution for the largest fishery in the world for pollack. And, about 30 years ago, Steller's sea lions started to decline. And in the Central Aleutians, many of the breeding sites have lost 95% of their population.

Now, the Central Aleutians have actually been a very well-studied marine ecosystem. Because Jim Estes and others started looking at it in the 1960s, to look at the recovery of sea otters, and how sea otters interacted with their environment. And in the 1960s there were two very distinct types of habitats out there. There were the habitats with otters, and the habitats where otters hadn't recolonized yet, after the exploitation for their fur overexploitation.

The ones without otters were two trophic-level systems. There were very small levels of kelp and very high levels of sea urchins the main grazer on kelp. Where there were sea otters, there were large forests of kelp, a few urchins, and lots of otters. In the last 10 to 15 years, the otters in that same area have declined by 90%, as well so this is sort of a delay, a lag, after the Steller's sea lion decline. And now, in those areas, there's, evidently, a four-trophic-level system. The kelp forests, again, are decimated; the urchins are high; the otters are 5 to 10% of their former abundance; and now killer whales have entered into the system.

Well, the cause of the shift is very speculative, but I think it's very intriguing, and tells us a lot about resource management. Killer whales, Jim Estes thinks, have shifted their diet because of the loss of Steller's sea lions, and shifted it over to eating sea otters. And this predation has been observed, and there's been several interesting articles about this in *Science*. And the sea lions, in turn what caused their decline? Well, again, that's speculative. There has been a major oceanographic shift in the area. But there's also quite good evidence that the competition with the pollack fishery is driving a good deal of the loss of Steller's sea lions.

So we have this dramatic shift a complete ecological shift in an area that's very remote from where this pollack fishery is occurring. Well, what does this tell us about both of our management schemes?

Well, the pollack are basically being managed under traditional game management, which is focused on a single-species view of the world. And, clearly, that still isn't working, the way it didn't work before. On the other hand, the biodiversity-management paradigm didn't work, either. The Steller's sea lion is now listed, and the sea otter is a candidate for listing, but it's far too little, too late.

So what can we do that's better than that? Well, I think one of the main lessons that we've learned is, we really have to think about managing these abundant populations if we want to maintain healthy ecosystems. And one of the things that we can do to manage populations better is to understand how connected all those populations are. And with marine species, where we still have a chance at managing healthy ecosystems, one of the ways to do that is through using genetics to tell us what the population structure is just like we used it with the minke whales.

And we can also learn from this whole lesson that we have to be cognizant of our own ignorance about population structure, and feature all of that uncertainty into how we manage populations and how we make decisions.

Thank you.

(Applause)