



Science Magazine Podcast Transcript, 24 April 2009 show

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Music

Host – Robert Frederick

Hello and welcome to the *Science* Magazine Podcast for April 24th, 2009. I'm Robert Frederick. This week,

[farm animal sounds]

a barnyard special podcast: first, the effects of genomic technologies on livestock, particularly in light of our second story – the complete sequence of the cow genome; third, using retrovirus integrations as genetic markers to understand the domestication of sheep; and finally, the money question – we'll hear an argument for why the U.S. federal government needs to spend more money on basic farm animal research.

Promo

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Host – Robert Frederick

The first agricultural systems, which included rearing domesticated livestock, developed around 11,000 years ago in Southwest Asia.^{1,2} For thousands of years, breeding for agriculturally desirable traits occurred slowly, as farmers recognized that a desirable trait of a parent could be found in its offspring. Genetics, as a field, grew rapidly after the rediscovery of Mendel's work in the early 20th Century, and further sped up the process of breeding animals for genetically desirable traits. Recent advances in genomic technology, including the ability to resolve single nucleotide polymorphisms, or SNPs, between members of a species, will likely speed up the process even more. In a Perspective in this week's *Science*, Harris Lewin provides an overall view of the effects of genomic technologies on livestock—including breeding—but also of the advances in understanding in evolutionary biology, as well as in using livestock animals for models of human diseases. I spoke with Lewin from Big Sur, California. Lewin is a immunogeneticist at the University of Illinois at Urbana-Champaign.

Interviewee – Harris Lewin

¹ M. A. Zeder, *Proc. Natl. Acad. Sci. U.S.A.* **105**, 11597 (2008).

² S. Colledge, J. Conolly, S. Shennan, *Eur. J. Archaeol.* **8**, 137 (2005).

Genomic technologies are having an enormous effect in livestock genomics and animal agriculture in general – that the ability to obtain genomic information from the sequence to the SNPs is really permitting an analysis of the livestock species from the genome all the way up to the phenotype. And this is really something, I think, that is unique and heralds a new era for us in livestock genomics. It also allows us to dig very deeply into the original events, the domestication events, which, I think, has really not been possible before except from an archaeozoological perspective. Now we can use SNPs to do genome archeology and to do historical analysis on the timing and locations of domestication events of livestock species. So, I think, in all, putting it all together, you know, we're in a fantastic position to understand the biology, for the first time, of the livestock animals from sheep and horses to cattle and others, and it's a very exciting time to be in the field.

Interviewer – Robert Frederick

In your view, what's the most important insight worth the most study, the most financial resources, to be gained by comparing the genomes of livestock to other genome sequences?

Interviewee – Harris Lewin

Well, I'll try and avoid the financial gains part, because there are really no results yet that are immediately applicable to livestock breeding, so I'll try to leave that to the end. I will say that the most exciting result scientifically that we have is the discovery of the really species-specific genomic features – that is, those features of the genome that tell us more what makes a cow a cow, what makes a horse a horse, what makes a sheep a sheep, what makes a human a human. And that could only come from the comparison of one genome to another and doing it multiple times. So, comparing a horse to a cow, or a cow to a mouse, a mouse to a human, a human to a cow – from all those multispecies comparison now comes the genetic evidence of what makes one species different from another.

Now, as far as the technology that will be most applicable toward really improving livestock breeds for breeding and for sustainable agricultural practices, I think, this map, this resource of single nucleotide polymorphisms – more than 50,000 individual single nucleotide polymorphisms that was developed for scanning the genome of multiple breeds – will really permit for the first time the ability to select animals on the basis of their genotype rather than their phenotype only. So, animal breeding has traditionally been accomplished by selecting on the phenotype. An example of selection on phenotype is selection, for example, from milk production. And what this large panel of single nucleotide polymorphisms will permit and is already being done in practice, although not reported in this particular paper, is the ability to associate all of those different important, economically important, traits, such as milk production, protein content, for example, in milk – these would be the dairy traits – in beef traits it could be tenderness and carcass quality and growth rate. Now, for the first time, you can pinpoint the location in the genome of those variations in the genome, those single nucleotide polymorphisms, that are most highly associated with those individual traits, and use those pinpoint markers for breeding. So, you can begin to either add on the genetic information in a very global way to the breeding and selection strategies to the phenotypic information. And the hope is to

eventually completely replace the phenotypic breeding with genotypic breeding, which will save the breeding industry millions and millions of dollars every year. Now, an animal can be born and by its genotype you can predict, what the performance of its offspring are going to be.

Interviewer – Robert Frederick

Are there any concerns that this genomic understanding of livestock will speed up the homogeneity, as you said, for these economically important traits as we get animals with better milk, meat, or hide production?

Interviewee – Harris Lewin

Yeah, one of the most extraordinary findings of the HapMap consortium paper is the absolutely amazing and deep genetic diversity that remains in the current breeds that we have today even after generations and generations of selection. So, cattle still have at least two times the genetic diversity that humans have, and when selection is being applied on a genomic scale you're selecting for multiple traits simultaneously. So, there is some concern that you would restrict the genetic diversity in very, very small regions of the genome, probably less than 1% of the genome, as you select for, you know, homogeneity, if you will, or homozygosity for individual traits. But, there's so much genetic diversity in the, for example, in the bovine genome, that it's going to be a very, very long time, if not, you know, I don't think it's ever going to happen that we're going to reach the point where we're going to select cattle and reduce genetic diversity to a point where it would be actually dangerous for the survival of the breed.

Interviewer – Robert Frederick

Other than what makes a cow a cow or a cow different than a human, will this genomic understanding help in understanding our genome better and our diseases better?

Interviewee – Harris Lewin

Yeah, the comparison of the Bovine genome to the human genome will certainly allow geneticists to really zero in on the differences that are responsible for some very specific human disease traits. For example, cattle rarely develop spontaneous cancers. They seem to have, and they almost never develop – I don't know a single example of an autoimmune disease in cattle. And, of course, this is a very important classification of diseases in humans. And it appears that cattle have a very powerful immunosuppressive system – that they're able to suppress responses against self-antigens. So, their immune systems are tuned in a different way than the human immune system is tuned, and through the study of the cattle immune system I think we're going to be able to reveal some of these suppressive mechanisms that are going to be able to help us to understand how to treat diseases, such as autoimmune diseases, and also, how to manipulate the immune system of a human, so as to reduce or augment the responses against newly arising cancer cells in individuals.

Interviewer – Robert Frederick

So, rather than a laboratory rat or mouse we'd have a laboratory cow.

Interviewee – Harris Lewin

Yeah. We already have laboratory cows – we will laboratory cows, and we're going to have more laboratory cows, because in many cases a cow is a better predictor of a human phenotype, or a human physiological condition, than a mouse. It's also impossible to do certain things with mice or rats that you can do with a ruminant. For example, if you're going to do an organ transplant you can't really use a mouse kidney to do a model for organ transplantations in humans – the mouse kidney is simply too small. You need to have an organ that's of a similar size to the human, and that can be provided, for example, by pigs, cattle, or sheep. And so, there are many cases where mouse or rodent models simply don't apply. There are other cases where the physiology, the way a particular drug is metabolized in the human body, is very different from the way it's metabolized in the mouse or a rat. And so, that's the reason why many drugs fail in their drug trials later on, is because the human metabolizes the drugs differently than does a rat or a mouse. And what you really need to do, when you look for a good animal model, is to find individual animal models – and it could be a cow, or it could be a sheep, or it could be a pig – that has a metabolism that is more similar to a human than a mouse or a rat. And therefore, you would select your animal model based on your knowledge, preexisting knowledge, of that metabolism, which can come from the genomic information. So, you're able to use the genomic information to help select the models, and, I think, in many cases, a cow or a pig or a sheep will be a better model for a human disease or for a human drug trial than will be a rat or a mouse, simply because of its genetic and genomic features.

Interviewer – Robert Frederick

Harris Lewin, thank you very much.

Interviewee – Harris Lewin

Thank you, Rob. I appreciate the opportunity. Have a nice day.

Host – Robert Frederick

Okay, you too. Harris Lewin of the University of Illinois at Urbana-Champaign writes a Perspective on the scientific advances from research on domesticated livestock.

Music

Host – Robert Frederick

The evolution of cows, like the evolution of any living thing, is written in its DNA.³ But having the cow's genome will do much more than provide insights into mammalian evolution, particularly because of the cow's place in the global agricultural economy and its use in biomedical research. Now, in two papers in this week's *Science*, Kim Worley and colleagues of The Bovine Genome Sequencing and Analysis Consortium and the Bovine HapMap Consortium report their completion of the genome sequence of the taurine cattle as well as report on the genetic structure of cattle breeds. I spoke with

³ S. B. Carroll, *The Making of the Fittest* (Norton, 2006)

Worley from her office at Baylor College of Medicine in Houston, Texas, and asked her for a glimpse of what's been learned thus far.

Interviewee – Kim Worley

We sequenced the genome of the Hereford cow and analyzed it for genomic features, and we compared it to a number of other breeds to understand the differences between breeds and the history of cattle over time.

Interviewer – Robert Frederick

How much coverage did you get of the cow's genome?

Interviewee – Kim Worley

We sequenced to 7-fold coverage of the genome. So, the 6 additional breeds – we had sample sequencing less than 1x coverage of those breeds – so the 6 breeds that we compared to the Hereford to identify single nucleotide polymorphisms, those are also called SNPs, individual sequence variants that can be used to identify particular individuals. And then we used those SNPs to analyze a number of different breeds to study the history of cattle – both domestication and history of the breeds. And there two times of selection in the history of the cattle species – there's the bottleneck that happened at the domestication events, there appeared to be two major domestication events – one in the Taurine cattle and the other in the Indicine cattle, the Indicine or the humped cattle from South Asia and East Africa, that includes the Brahman, and the Taurine are the European, African and Asian breeds. So, we can see the history from the two different domestication events, and we can also see more recent history when the breeds were defined in the last several hundred years, so we can see individual breeds or groups of breeds that have a common, more recent history.

Interviewer – Robert Frederick

And the effects of further domestication or further choice.

Interviewee – Kim Worley

Right. So, the Taurine Indicine seems to be pre-domestication, and then there's the domestication history within those populations. And relative to the outgroups that we used, so the Anoa and the *Bubalus* breeds instead of the *Bos* species – those are the outgroups.

Interviewer – Robert Frederick

From your study, how has the diversity among the two main groups of cows – Taurine and Indicine – changed over time?

Interviewee – Kim Worley

So, there was a large amount of diversity in the population that was domesticated initially. And there was greater diversity in the population that was domesticated in the Indicine population than in the Taurine population, okay? And the effective population size, which is a measure of the diversity of the populations, has been decreasing over time, even though the population of domesticated animals is increasing, but that decrease

in effective population size, or diversity, is not as great as the decrease in effective population size or diversity in the dog, for instance. So, companion animals and livestock animals are different in this respect – or cattle and dogs, anyway. And, at the same time, the human effective population size has been increasing – so, the diversity.

Interviewer – Robert Frederick

Are there unique features to the cow's genome compared to other species that you don't see in its morphology – so, something other than, you know, it's got four stomachs and that it ruminates – something that's unique and that you see only in the genome. I guess, what makes a cow really a cow in its genome?

Interviewee – Kim Worley

So, they're genomic features that differ with any genome, and for the cow some of those features are the large number of bovine-specific transposable elements, or repeats, that are found, and the distribution of those with respect to chromosomal breakpoints that are ruminant-specific or cattle-specific, so that those more recent ruminant and cattle-specific repeats tend to cluster at those cattle and ruminant-specific chromosomal breakpoints.

Interviewer – Robert Frederick

Suggesting more genetic difference?

Interviewee – Kim Worley

Right. So, that would be a concentration of cattle-specific differences in those regions, compared to other mammals. And, then there's some history that we can see in the genome. So, for instance, the chromosome organization is more conserved from cattle with respect to human than rodents with respect to human – and that's even though rodents and primates share a more close lineage, but more rodents are more quickly evolving, so they have diverged from human more than in the chromosome rearrangements and also in the orthologs.

Interviewer – Robert Frederick

And what are those?

Interviewee – Kim Worley

Orthologs are protein relatives between species. So, if you have a one-to-one ortholog that would be a gene, the protein product of that gene, that has a common ancestor between the two species that you're talking about, okay? So, a cow ortholog to a human ortholog sequence means that there was a common ancestor between cow and human that shared that gene. So, we looked at the number of orthologs and looked at how many were shared among different species. So, we grouped the rodents (mouse and rat), the group that includes cattle and dogs, and then we have a group that includes nonplacental mammals, so that's the platypus and the opossum. And many of the proteins are found in all of the species, but there are proteins that are found that are, say, only common between humans and cows, or between humans and rodents – and there're about twice as many proteins orthologs that are found between humans and cows and dogs as between humans and the rodents, so 313 versus 172, for instance. And then, there are other

categories that are, say, only found in cows and dogs, 147, versus only found in rodents where there are 1,112. So, it's just more information about the rodents being quickly evolving and the cow proteins being similar to humans compared to the rodent proteins being similar to human, even though humans and rodents have a more recent common ancestor than humans and cows and dogs.

Interviewer – Robert Frederick

So, there's an argument to be made, then, that cows might serve as better laboratory animals in looking at human diseases than rodents would.

Interviewee – Kim Worley

In some cases, yes, definitely. And there are cow-specific biology features that show up in the genome that make cows better for studying certain types of things like lactation, the milk production, and embryological development. So, certainly a lot of the techniques for in vitro fertilization were developed first in cattle, so those kinds of things have a history – techniques that are used in humans.

Interviewer – Robert Frederick

Is there any concern that this genomic understanding will “speed up” the cows' homogeneity, or lack of diversity, as breeders have more tools to select for these economically important traits?

Interviewee – Kim Worley

Certainly that's a concern, but I think breeders are aware of the problem of having too homogenous a population, so that the breed could not respond to new challenges. And so, these tools that we've developed from this study can help to maintain diversity in the population while you're selecting for features of interest. So, I think it's a win instead of a lose in terms of being able to better manage the populations, and the tools can be used for even following populations that are threatened and maintaining diversity and populations which have low numbers of individuals.

Interviewer – Robert Frederick

Kim Worley, thank you very much.

Interviewee – Kim Worley

You're welcome. Thank you.

Host – Robert Frederick

Kim Worley of Baylor College of Medicine is a named author of the paper by the Bovine Genome Sequencing and Analysis Consortium and is the genome assembly leader of the Bovine HapMap Consortium. The consortia have two papers in this week's *Science*: one on the genome sequence of the Taurine cattle, and the other on the genetic structure of cattle breeds.

Music

Host – Robert Frederick

Scientists widely consider sheep to be one of the first domesticated animals⁴, but understanding how the domesticated sheep spread from Southwest Asia across Eurasia and Africa has been limited by a lack of archaeological evidence, particularly regarding when and where sheep were selected for their wool. Now, not all the mysteries are solved, but in a paper in this week's *Science*, Massimo Palmarini and colleagues report how they used retrovirus integrations as genetic markers to trace the history of sheep domestication. The research shows two main waves of sheep domestication, and confirms past morphological studies that separate so-called "primitive" breeds from more modern breeds. I spoke with Palmarini from his office at the University of Glasgow.

Interviewee – Massimo Palmarini

We have used the viruses that are integrated in the genome of sheep to study their history of domestication. And by using viruses that are integrated stably in their genome we've been able to track how sheep migrated. And we've been able to differentiate a primitive sheep from more modern breeds of sheep, and we've been able to show that basically we had two major waves of migrations. A first migration that has been then followed up by breeds that have all the characteristics of more modern breeds, and our study seemed to suggest that this selection occurred first in southwest Asia, and then these improved breeds – especially for wool – have been then moved across Europe and other parts of the world.

Interviewer – Robert Frederick

How do these viruses work? Is it as a genetic marker in differentiating genetically primitive sheep from more modern breeds?

Interviewee – Massimo Palmarini

Well, basically, what we use are the retroviruses, but more specifically endogenous retroviruses. So, retroviruses are like other viruses – during their replication they have to integrate their genome in the host cell genome. So, what it means that once they're integrated they'll stay there. And this is for any retroviruses that we are, for example, human immunodeficiency virus, or HIV, is a virus that is a retrovirus. However, during evolution every animal species, the genome of every animal species, has been colonized by endogenous retroviruses, because what happens the germ cells have been infected by retroviruses.

Interviewer – Robert Frederick

The germ cells – the egg and sperm cells?

Interviewee – Massimo Palmarini

That's correct. And once a germ cell is infected then the subsequent generation of somatic cells are going to carry these endogenous viruses. So, what you'll have is, you'll have basically the mother – that the germ cells of the mother – are infected, and then the

⁴ M. L. Ryder, *Sheep & Man* (Duckworth, London, 1983).

offspring will carry in their genome endogenous viruses, and then they just transmit it through their subsequent generations. So, if you have two individuals that have the same endogenous retrovirus in the same chromosomal location are de facto phylogenetically related, because each is a single event, or regionally you have an infection of a single animal – of a single germ cell – then it's transmitted through the subsequent generations. And what you have to think of is that these endogenous retroviruses have colonized—infected—the host at different time points. And by using some endogenous retroviruses that are differentially distributed in the sheep population we have been able to use them as genetic markers. And they are wonderful genetic markers, because as I said before – if they are shared among different individuals, there is no way out – they have to be phylogenetically related at one point or another. And this is in contrast to, for example, microsatellites or SNPs, where there are particular regions of the genome that have a different compositional basis, and they have to have a large number of markers to make sure that the similarities between different individuals is really given by phylogenetic relatedness.

Interviewer – Robert Frederick

Now, is this use of endogenous retroviruses as genetic markers well established? Has it been used with other genomic analyses?

Interviewee – Massimo Palmarini

Well, it depends. I think this is probably the first time they have been used to study recent events like, for example, the domestication. When I say a recent it's from the evolutionary point of view, because domestication began approximately 10, 11 thousand years ago in Southwest Asia. Sheep have these endogenous viruses that we call the enJSRVs that are rather young from the evolutionary point of view. So, the particular viruses that we studied have integrated in the sheep in the last few thousand years. And so, they are useful markers to study this process. Now, most endogenous retroviruses that we know are more ancient, so they've integrated before speciation. So, for example, if you want to study the phylogenetic history of different species, and if you have endogenous viruses that integrated before speciation, so before the species diverged, then you can use those ancient endogenous retrovirus as well, as an aid to study the phylogenetic tree of that particular group of animal species that you're looking at. In this case, we have these viruses that are much younger, and so they are useful to study a much more recent event. We have other endogenous viruses of sheep that are a bit older and that integrated before, for example, wild sheep and wild goats diverged. So, this happened billions of years ago. So, these endogenous viruses are present at the same chromosomal location in every single sheep in the planet and every single goat in the planet. So, these endogenous viruses will not be discriminatory on any event to study, for example, domestication has with it. In order to study a recent event you would have to have a recent endogenous virus.

Interviewer – Robert Frederick

I don't suppose there's some sort of confounding factor that the single virus might have gotten into several sheep at the same time?

Interviewee – Massimo Palmarini

Well, the fact is that we study a virus at a specific chromosomal location, so it doesn't matter. The same virus can go somewhere else, can go in different sheep, but the test is to detect the virus at that specific chromosomal location and nowhere else.

Interviewer – Robert Frederick

Okay.

Interviewee – Massimo Palmarini

So, even if the same virus enters in different sheep that doesn't make any difference to our test.

Interviewer – Robert Frederick

So, how many recognized breeds of sheep are there, and how many breeds and numbers of breeds did you and your team study?

Interviewee – Massimo Palmarini

How many there are – oh, I guess this is a tough question that I can't give you an answer without having nightmares that I'm being wrong. I think it's safe to say that there are a few hundred. We studied about 130 breeds. And also, I think an important point is that we studied local breeds, so they had not been crossed and improved extensively, so that you have a good feel for being representative of that particular geographical area. When we studied most modern sheep that we know that have been derived by crosses or a variety of breeds would be a bit less informative in this sense. So, again we studied about 130 breeds from all over the Old World. We group the breeds in 65 geographical areas, and we studied a total about 1,300 – between 1,300 and 1,400 – samples, and each group advised by treating 10 to 30 samples per group.

Interviewer – Robert Frederick

Were there any surprises in the genomic analyses as to which were the primitive breeds and which were the more modern breeds? Or, was this more a genetic confirmation of other, perhaps morphological, work?

Interviewee – Massimo Palmarini

Yeah, I think that the rewarding aspect of this study was that all the breeds that came out as being primitive from our retrotype analysis, you know, well, indeed, quite looked primitive and were in geographical areas that would make sense to have primitive breeds. So, we have, I guess, for the first time, a genetic confirmation of something that, from the morphology of the breeds, one would assume to be more primitive and less improved.

Interviewer – Robert Frederick

Are there still any mysteries to tease out – genetic evidence of breeds that are isolated or don't fit into this endogenous retrovirus tree, if you will, relating one type of sheep to another?

Interviewee – Massimo Palmarini

I guess probably the next thing to work out carefully is the timing. So, our study cannot provide, cannot estimate when this process occurred – in the how many thousands of years ago [it] occurred, so we go with the archeological evidence. And I think that the next generation of just the classical markers, like SNPs or mitochondrial, and then on the larger scale in different breeds, using similar breeds that we have, we'll be able to integrate our studies and date them and date the main events. That, I think, will be very, very interesting from historical perspective.

Interviewer – Robert Frederick

Well, Massimo Palmarini, thank you very much.

Interviewee – Massimo Palmarini

Thank you so much.

Host – Robert Frederick

Massimo Palmarini of the University of Glasgow is senior author of a paper on the history of sheep domestication using retrovirus integrations.

Music

Host – Robert Frederick

Also in this week's *Science*: the color of the first horses. Arne Ludwig and colleagues analyzed the DNA sequence polymorphisms responsible for coat color in horse fossils and typed eight mutations in six genes responsible for coat color variation in the ancient samples. Their results show a rapid and substantial increase in the number of coat colorations in both Siberian and Eastern European horses beginning about 5000 years ago. That timing coincides with other research showing that people were domesticating horses in Kazakhstan as early as 5500 years ago, and so suggests that the increase in coat colorations were due to selective breeding by people. The original horse colors were bay or bay-dun, meaning they were shades of brown and the manes, tails, and lower legs were black.

Music

Host – Robert Frederick

The U.S. Department of Agriculture spent about 0.04% of its 2007 budget on competitive grants for research involving agriculturally important domesticated animals such as cows, sheep, pigs, and chicken. That's around \$32 million. That's not enough, argue Jim Ireland and colleagues in a Policy Forum in this week's *Science*, because it threatens research needed for food supply and safety as well as research for human health. I spoke with Ireland from his office at Michigan State University.

Interviewee – Jim Ireland

We believe farm animal research is in crisis primarily because the competitive grants program at USDA is miniscule compared with that that is at NIH for extramural research. We also think that it's problematic because the primary comparative animal model that's

used at NIH is the mouse, and farm animal species are very rarely used for biomedical research. So, both of these things combined make it very difficult for animal and veterinary scientists, because of the lack of federal support for basic research using farm animals, to carry out their research projects.

Interviewer – Robert Frederick

Now, every scientist would like more money for his or her work – why particularly is farm animal research in crisis?

Interviewee – Jim Ireland

Well, we believe it's in crisis because farm animals are necessary and provide the meat, milk, and eggs for the human diet, and basic research is necessary to ensure that the production efficiency, that health of the animals, their well-being, you know, is optimized. Because global competition, you know, makes it imperative that the farmer and the producer in the United States have the optimal ways to enhance production efficiency and ensure the health and the well-being of the animals is maintained at the same time. This ensures that the general public—or the consumer—has a high quality nutritious supply of meat, milk, and eggs in their diet.

Interviewer – Robert Frederick

Is the U.S. not producing enough food from farm animals, or do some diseases threaten our food production that...

Interviewee – Jim Ireland

Well, there's continually emerging diseases that must be counteracted. For example, Merrick's disease in chickens – there must be a vaccine to control that, or there would be no poultry industry in the United States or elsewhere. So, there's continuously diseases of that nature that must be controlled in animals. Infertility is a problem that it costs farmers more to produce and raise these animals because of infertility. So, finding ways to eliminate infertility is very important to maintaining economically producing food in the animals. So, yes, it's critical that while we do have plenty of food to provide from U.S. agriculture, it's necessary that we have a basic research program to continually ensure that we're optimizing the economics of animal production, if you will. Otherwise, global competition in other countries will be able to flood the U.S. market with much cheaper foods. And then, of course, when that happens we may be losing some control over the quality of the food, as well as food safety. So, it's important that basic research is strong, viable in in the U.S. so we can maintain a safe and nutritious food supply. But, food production is only half the story. Biomedical sciences and the role that farm animals play is the other side of the coin that we're interested in.

Interviewer – Robert Frederick

So, biomedical sciences presumably to help with human diseases.

Interviewee – Jim Ireland

Well, we're arguing that most of the comparative animal research that's done at the NIH uses a couple of different species of mice. And mice are important, because they're

obviously small, they're easier to maintain. The genome has been sequenced in the mouse, and the genes can be knocked out or eliminated in mouse – so they've been used routinely as a model for biomedical research because of those advantages. But, farm animals also have a lot of advantages – not only their size and physiology more mimics that of the human, but their genome much more closely matches that of the human than does the rodent – but nevertheless, there's very, very few studies at NIH where farm animal species are used. But I should point out, on the other hand, that NIH still funds a lot more research using farm animals than does the USDA. So, it's not as if they don't use farm animals. But there needs to be a concerted effort, we believe, to enhance the use of farm animals in biomedical research because of some of its advantages, compared with the rodent.

Interviewer – Robert Frederick

What's preventing the NIH from simply migrating more funding from mouse and rodent studies to farm animals?

Interviewee – Jim Ireland

Well, that's a very good question. I don't think the blame for that is totally at NIH – part of that is because the biomedical programs in animal and veterinary science departments may not be strong. And biomedicine may not be a major part of those traditional departments, so if the faculty that are in those departments are not trained to conduct biomedical research, then the number of grants that NIH might receive using farm animals as models for biomedical research might be relatively low. And they are indeed probably low compared with those using the mouse as a model. So, that's a problem that the land grant institutions and traditional animal science departments have to resolve themselves. So, that's one of the problems. The other potential problem is at NIH most of the scientists that set on the study sections may be primarily trained in mouse biology and are not nearly as familiar with the advantages of farm animals. So, the panel and panel members need to be more educated on some of the advantages of farm animals for biomedical research. And there has been some effort for USDA and NIH to get together to try to have interagency cooperation to fund and develop programs to look at alternative animal models for biomedical research.

Interviewer – Robert Frederick

Government funding aside, isn't there a lot of additional funding that's provided by the private sector for animal research?

Interviewee – Jim Ireland

Well, yes, the private sector would provide funds for research that's primarily related to commercialization of products, such as vaccines and new diet formulations and things of that nature. But, the research we're talking about is more basic discovery-level research, and that's not primarily funded by industry – that's usually funded by strong federal competitive grants programs.

Interviewer – Robert Frederick

How about money from the states – and potentially from earmarks – specific funds set aside by legislators?

Interviewee – Jim Ireland

There are clearly influential scientists and individuals that obtain earmarks for research, and it's hard to get a handle on how much of that actually would go into animal research. Most of our experience suggests that it would go more into plant research than into research on farm animals. But, even if you enhance the competitive grants program 10 to 20 fold at the USDA and added in all the earmarks and funding that's done in the private industry, it's still probably inadequate to create a vibrant basic research program using farm animals.

Interviewer – Robert Frederick

Jim Ireland, thank you very much.

Interviewee – Jim Ireland

Well, thank you very much. I appreciate the opportunity.

Host – Robert Frederick

Jim Ireland from Michigan State University is corresponding author of a Policy Forum arguing for more funding for farm animal research.

Music

Host – Robert Frederick

If you missed our regular *ScienceNOW* segment, it will be back next week. In the meantime, you can check out the latest science and policy news at sciencenow.sciencemag.org. For now, that wraps up the April 24th, 2009, special barnyard *Science Magazine* Podcast. If you have any comments or suggestions for the show, please write us at sciencepodcast@aaas.org. The show is a production of *Science Magazine* with the support of AAAS, the Science Society. Jeffrey Cook composed the music and I'm Robert Frederick. On behalf of *Science Magazine* and its publisher, the American Association for the Advancement of Science, thanks for joining us.

Music ends