**NRSP-8 Discussion and Business Meeting 1/12/2020**

Starting time: 4:45 pm PST

Introduction: Alison Van Eenennaam

* What is the future of NRSP-8? This program will end in three years, where do we want to take the program for the community moving forward?
* Historically, genome coordinators get individual funding to handle start-up projects or “general good” projects such as chips for the community.
* Tomorrow, there is a meeting to discuss the future vision of animal genomics at the Handlery Hotel. They will be discussing the genome to phenome blueprint, and how to change the structure of NRSP-8. For example, go from individual species to more unified interests but conduct studies in each individual species. The community needs to work out how to move forward with this program.
* Do we set up working groups to craft a white paper?

Discussion

Jim Reecy:

* As part of the re-envisioning team, one of the discussion points was what do we do with the bioinformatics portion of NRSP-8.
* The group has written a white paper laying out options, which could become an NRSP project.
* One possible option for hosting some of the databases is seeking new funding to flow through/to USDA ARS and could they take over some of those activities, or the National Ag Library.
* If this is something we do, this could open up entirely new options, which are not possible to run though the NRSP program.

Fiona McCarthy

* Bioinformatics is a tool driven by the biological questions.

Alison Van Eenennaam

* Bioinformatics is a shared skill that is needed, and we need core infrastructure, and it something that needs to be maintained and kept current.

Jim Reecy

* There are not many new resources, but we need something new to fund, which makes it hard to run through a competitive program.
* Could we find the funding of the day-to-day activities and programs needed for the community, but then use competitive grants for new tools.

Noelle Cockett

* What is that you are seeking funds to maintain or expand? There are many databases, but what would be fitting for this particular domain?

Jim Reecy

* QTL database, correlation database would be options.
* The survey from QTLdb and CorrDB asked if universities would pay subscriptions, and 1/3 thought the universities would, 1/3 thought no, and 1/3 didn’t know.
* Funding could help with the curation and computation for databases in the community that are already used. However, new databases are desired. Is there a way we could take genotypes with phenotypes and put it into a database for the community to access and perform research?
* Could all ag experiment stations put all phenotypes together, as well as genotypes, and then incorporate others such as nutritionists and physiologists to characterize new phenotypes and collaborate? This may foster collaborations for geneticists across universities that may not have the animal numbers individually. From an ARS standpoint, they are interested in making sure producers have useful data, but also facilitate research that we are doing today.

Question about grants and data ownership – if a grant is received and data is generated, who owns the data and who is legally responsible for the data?

Jim Reecy

* If the government mandates that you share all of the data generated as part of a federally funded project in whole or in part.
* You can make it publicly available or if someone wants to use your data you can sign a material transfer agreement.
* This will reside with your university, which would have to provide the cite to share the data. If you submit on the open science framework, this will not need to happen.

Noelle Cockett

* Proposed discussion of species-specific projects versus functional groups.

Alison Van Eenennaam

* Asked if it made sense to keep species separate or do something more functional across the entire group, though there might be groups working across species on different projects such as pangenomes, precision phenotyping, etc.

Ernie Bailey

* Is this about growth in general? We still need to have some species-specific projects, especially looking at physiological traits

Bob Schnabel

* The vertebrate presentation demonstrated value of looking across species

Alison Van Eenennaam

* There is potential to use cell lines for research questions, and using the same concept for cell culture and phenotypes in different species

Ernie Bailey

* There are many specific targets for each species, such as PRRSV in pigs. The species emphasis will still be important moving forward.

Benjamin Reading

* Do we want to look at species/organisms, or do we look at overall techniques or traits?

Joan Lunney

* Microbiome is an example of a topic that is covering broader topics including disease

Lakshmi Matukumalli

* FAANG is another example of this broad coverage

Annette McCoy

* We need horizontal and vertical integration component but don’t cut out species specificity but work together for common ways to answer questions.

Archie

* There are great ideas in the blueprint. There could be real value in building concise case studies around targets – starting with health space (diseases in each species), embryonic loss, etc.
* Target outcomes for each species and then discuss technologies needed for deliverables on these targets, including sequencing, bioinformatics, workforce.

Dr. Angle

* There is no doubt about quality and the great value of NRSP-8, the question is this was a project started to develop tools to reduce cost of researchers across the entire community for access.
* Off the top money from experiment directors (500K per year) but there are only 8 or 10 of these, and the goal is to not fund these permanently.
* If you are going to make this work (species, technique, etc.) there has to be things that add value to all conversations in the country. I would love to know the value to all of the research that puts data into the databases – likely more than was funded through experiment stations.

Noelle Cockett

* We are the resource. Everyone is beginning to use genomics, but we know how to do it. We are still learning things about the genome, but we need to know more.
* What if our research was supported internally with researchers within our universities and experiment stations?

Chris Tuggle

* We should move from mapping the genome to using the genome.
* Push towards predictive science, have bioinformatics decision support tools.
* Create tools that people can then use the genomics – producer, reproductive biologist, etc. so that people go to a website and get back data/information to help them use the genome.
* Create the underlying knowledge about function and which genes are important.
* Train experiment stations on how to use data science to do their own work.

Benjamin Reading

* Methods such as machine learning allow for predictive phenomics with genomics. Also, if you have a phenotype in a specific environment you may be able to predict phenotype.

Alison Van Eenennaam

* We will table this discussion to tomorrow at 10:30 in Balboa room in Handlery hotel from 10:30-12:00.
* At this time, I would like to introduce Dr. Scott Angle, director of NIFA.

Dr. Angle

* We visit with those on Capitol Hill, and people understand more human information (i.e. curing cancer).
* And he would like to challenge us to find the long term support for an impactful plan for funding – we have to understand politicians and what is going to make a difference for them.
* Think about what would be desirable for a congress person to consider funding – make sure it is big, bold, audacious.
* Data management will cost quite a bit of money. These will be multi-year endeavors what will be expensive, the National Ag Library can do this but who will pay for it? Subscriptions, or write into grants data management fees?
* There are many open positions since the move from DC to Kansas City.
* There will be some delay with processing grants and funding.
* NIFA’s budget is 1.7 billion dollars this year. We are looking at starting a new investigator’s program with a higher success rate to encourage new people and retain individuals.
* Total funding for NIFA will increase and has been increasing for the last 10 years. The most important program is AFRI, it will likely grow.
* Wheat project is developing new germplasm project and have been doing a great job of selling themselves to congress, trained graduate students, numbers to display success rate, etc. – take a look at this program.

Hasan Khatib

* Where is NIFA heading and where is the vision?

Dr. Angle

* Plant side – NSF co supports the NIFA funding. Animal side – more difficult to get NIH/NSF funding.
* We have to do both basic and applied science.
* We need something that will have political support with immediate as well as long term deliverables.

James Koltes

* Question about trainings and if that would help gain support, are there ways within NIFA to meet industry needs for workforce?

Dr. Angle

* Challenge grants, training/support for students in 1890 and tribal colleges (most underrepresented in the sciences and bringing in students from diverse backgrounds). Otherwise, look at the wheat project that is working very well. Bioinformatics is one clear area.

**NRSP-8 Business Meeting 1/12/2020**

Alison Van Eenennaam

* Eric Young will be retiring. Archie Clutter will be replacing as administrative advisor.
* Jack Dekkers will be incoming NRSP-8 chair in 2022. Brenda Murdoch will be running NRSP-8 in 2021.
* Station reports need to be given to your species coordinator, and species coordinator needs to be into Alison Van Eenennaam to write within 90 days of this meeting.
* None of the coordinators had additional information to add: aquaculture, cattle, swine, poultry, sheep, bioinformatics

Jim Reecy

* If the coordinators want to support the request please let him know (to help with funding with bioinformatics resources for QTLdb and CorrDB)

Alison Van Eenennaam

* Seeing no further action, this meeting is adjourned. 6:06pm.