

Bison Sampling Correspondence (ordered from most recent)

Peter Dratch/FTCOLLINS/NPS
07/25/2010 04:43 PM
To Robert Schnabel <schnabelr@missouri.edu>
cc
Subj Re: Workshop Report⁽¹⁾
ect

Bob,

Thanks for your comments. I did change that recommendation to reflect that bison from hybrid herds should not be transferred to herds with no evidence cattle ancestry.

Have a good week. When you have the data done to your satisfaction, I hope we can arrange a conference call for next steps.

Peter

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
Work phone: 970 / 225-3596
Cell phone: 303 / 514-7792

Robert Schnabel
<schnabelr@missouri.edu>
07/20/2010 08:46 AM
To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
cc
Subj Re: Workshop Report
ect

The wording of Table 1 is fine. I didn't have time to read the whole thing, just skimmed it but I did notice something though...

1) No molecular evidence of cattle ancestry: Herds with no molecular evidence of potential cattle ancestry constitute a genetic resource that must be protected from inadvertent introgression. **There should be no exchange of bison between these herds and those that do show molecular evidence of cattle ancestry** or for which the genetic status is unknown.

I'm not quite sure what your intention is here. If you have a herd that you believe has no evidence of cattle ancestry why would you not want to move animals OUT of that herd and INTO a herd that does have evidence of cattle?

Decker et al *in review*

Here is the citation:

Decker JE, Pires JC, Conant GC, McKay SD, Heaton MP, Vilkki J, Seabury CM, Caetano AR, Johnson GS, Brenneman RA, Hanotte O, Eggert LS, Wiener P, Kim J-J, Kim K-S, Sonstegard TS, Van Tassell CP, Neibergs HL, Chen K, Cooper A, McEwan JC, Brauning R, Coutinho LL, Babar ME, Wilson GA, McClure MC, Rolf MM, Kim J-W, Schnabel RD, Taylor JF. 2009. High-Throughput Phylogenomics: From Ancient DNA to Signatures of Human Animal Husbandry. Proc Natl Acad Sci USA 106:18644-18649.

http://animalsciences.missouri.edu/animalgenomics/publications/Decker_PNAS_2009.pdf

Robert Schnabel
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Animal Sciences Unit, Rm.162
920 East Campus Drive
Columbia, MO 65211-5300
Phone: 573-884-4106
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<http://animalgenomics.missouri.edu>

Peter Dratch/FTCOLLINS/NPS To Robert Schnabel <schnabelr@missouri.edu>
07/19/2010 04:54 PM cc
Subj Re: Workshop Report⁽¹⁾
ect

Bob,

I have gotten back the first review of the Genetic Workshop Report and I am incorporating comments. The formal review required that we not ask anyone who did bison analysis for the Department of Interior or is anticipated will do analysis in the near future.

Still, I want you to look it over and make sure that you agree with the way we characterized the herds (Table 1, page 8). Particularly the herds where hybridization is Suggested and the reason footnoted. Let me know if that is OK or you would prefer it were worded differently. We know that most of these herds have cattle ancestry because of the source herd, but your SNP work confirms it.

Any comments on other aspects of the report would be also welcome.
Thanks.

Peter

(See attached file: Bison Genetics Report _Edited Draft.doc)

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
Work phone: 970 / 225-3596
Cell phone: 303 / 514-7792

Rick Wallen/YELL/NPS

07/08/2010 07:30 PM

To Elaine Leslie/FTCOLLINS/NPS@NPS, Peter
Dratch/FTCOLLINS/NPS@NPS

cc

Subj Fw: Elaine Leslie
ect

Elaine, can you respond to Dr. Schnabel? Rw

Robert Schnabel

<schnabelr@missouri.edu
>

07/08/2010 04:07 PM

To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>,
"Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>

cc

Subj Elaine Leslie
ect

It has come to my attention that Elaine Leslie presented data from my bison project at a recent conference and showed a direct quote by me. First, I would like to know how she obtained this data? The only people that I distributed this data to were those directly involved in this project and there was an explicit understanding that this was preliminary data and was not to be distributed to other people nor made public. The fact that she publicly presented unpublished data that was not hers to present is highly unprofessional. Additionally, quoting someone regarding unpublished data without permission is also unprofessional. Can either of you please clarify how this occurred?

Whoever sent her this data needs to inform her that the data is not hers, is not public and she is not to present it, distribute it or discuss it with anyone that I have not explicitly approved to view the data.

Bob

Robert Schnabel
<schnabelr@missouri.edu>
>

06/21/2010 09:12 PM

To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>
cc "Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>, "stephen.amish@umontana.edu" <stephen.amish@umontana.edu>, "Taylor, Jerry F." <taylorjerr@missouri.edu>, "Roffe, Tom" <troffe@montana.edu>, 'Bryce Christensen' <Bryce@americanprairie.org>, Sean Gerrity <sean@americanprairie.org>, Kyran Kunkel <kyran@montana.net>, "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>, "Wilson,Greg [Edm]" <Greg.Wilson@EC.gc.ca>
Subj Almost final results
ect

This email discusses preliminary results and is omitted.

Robert Schnabel
<schnabelr@missouri.edu>
>

06/03/2010 07:57 AM

To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
cc
Subj Re: Bison Genetics Analysis
ect

I got the ok from Tom and the APF guys so when I send out a report I'll include you as well. I see Kyran has already sent you his proposal for Wind Cave.

Bob

Peter Dratch/FTCOLLINS/NPS

06/02/2010 09:22 AM

To Robert Schnabel <schnabelr@missouri.edu>
cc
Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Thanks, Bob. I have talked with Tom Roffe about integrating FWS and NPS results, and it was Tom who suggested that I contact him. By all means, contact him, and if we could arrange an initial call that would be great.

And I look forward to your discussion of Yellowstone animals, and how those samples compare with the APF samples of Wind Cave progenitors.

We also need to think about putting together a cooperative agreement if we are going to pursue this.

Peter

Peter A. Dratch, PhD
National Park Service

Endangered Species Program Manager
Work phone: 970 / 225-3596
Cell phone: 303 / 514-7792

Robert Schnabel
<schnabelr@missouri.edu>
>
06/01/2010 03:35 PM
To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
cc
Subj Re: Bison Genetics Analysis
ect

I got the genotypes back from the Yellowstone samples. I haven't had a chance to do the analysis "for real" but I had a quick look at one of the metrics and it looks like they are all clean. Now that I have all of the data for this project I'm going back to square one and rerunning all of the analyses. That's why I haven't got it done yet. My hope is to have this done next week and then I'll be able to give you a detailed description of the results.

As to the \$50k, it would help me to better advise you if I had an idea of what populations you were interested in testing and how you would use the information for management decisions. If you would agree to us sharing the data and being able to use it for a publication we could do the DNA extractions here and see if Geneseek will still give us our \$150/sample price. That would allow you to genotype ~330 samples. Without knowing how you intend to use the results for management or what populations you have available my gut feeling would be to genotype a lot more Yellowstone samples and just survey 10-30 animals from your other populations. Any population that Derr has already identified as a hybrid population I guarantee you will find more hybrids with the snp chip.

Have you talked much with Tom Roffe, Kyran Kunkel or anyone at the American Prairie Foundation? If not then let me approach them to see if they would mind you joining the discussions we've been having based on their samples. Below is a table that has the number of animals from each population that I'm working with. As you can see, the paper is going to be written using 479 animals which is quite a few. If you are thinking about genotyping another ~300 samples I assume you would like to know the results of the animals/populations that we've already run. Let me run it by Tom and the APF guys.

Bob

Peter Dratch/FTCOLLINS/NPS
06/01/2010 01:16 PM
To Robert Schnabel <schnabelr@missouri.edu>
cc
Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Bob,

You asked in your last dispatch to find out how much money we have to devote to genetic testing. Since then I have been looking for that funding.

We have at least \$50,000 to spend this year. That is to allocate by September. I would welcome your proposal about how we should spend it.

And of course we (myself and several biologists in parks) are looking forward to learning your results from the Yellowstone samples.

Thanks, Bob, for helping me with a genetics proposal on short notice.

Peter

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National Park Service
Endangered Species Program Manager
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Cell phone: 303 / 514-7792

**Peter
Dratch/FTCOLLINS/NPS**

05/25/2010 09:46 AM

To Rick Wallen/YELL/NPS@NPS

cc

Subj Re: Any news from Univ. of Missouri?⁽¹⁾
ect

Not yet Rick, in a few weeks I hope. Did learn that 5 of 20 samples from progeny of WICA bison now in MT have evidence of cattle ancestry. As soon as I hear of results, I will organize a conference call with Bob. Hope all is going well there. Peter

Rick Wallen/YELL/NPS

05/24/2010 01:21 PM

To Peter Dratch/FTCOLLINS/NPS

cc

Subj Any news from Univ. of Missouri?
ect

Any feedback from your colleague Bob Schnabel at U of Missouri about our DNA samples and the likelihood of cattle gene introgression based on high volume SNP data?

Robert Schnabel

<schnabelr@missouri.edu> To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
>

cc

05/05/2010 12:29 PM

Subj Re: Bison Genetics Analysis
ect

We got 20 samples from YNP. Geneseek is doing the genotyping of these samples for us at \$150/sample so it's \$3,000 worth of genotyping. This is a "friends and family" discount for us with Geneseek because we help each other out at various times. The list price of the chip is \$200 per sample for an order of up to 1152 samples. There is a price break above 1152 samples but you would need to round up \$230k in order to even get the discount.

Once we get this paper published I imagine it will cause quite a stir in the bison and conservation communities. When that occurs I think it may be wise for the interested parties to start talking about how to move forward. There are options of developing lower density assays that will yield similar results but at a cost point to where a lot of animals could be tested. As it stands right now, at >\$200 per sample you are really limited to sampling populations. If we could get the assay cost down to maybe \$40-\$50 per sample then you would be able to genotype every animal in a population.

My recommendation to you, and everyone who is contemplating this, would be to start looking into how much money you could find, or are willing to devote, to genetic testing. Think in terms of dollars rather than samples. Once you have an idea of the total dollars available then you ask what is the best way to spend those dollars. The technology is available to go in several different directions but it always come back to how much money do you have to spend on the project? That will determine the course of action, if any, that you decide to pursue.

Just so we're clear, I don't stand to make any money off of any of this, either directly or indirectly, because none of this would likely be run through our lab. So when I talk about money it's always looking out for your best interest. :-)

Bob

Peter

Dratch/FTCOLLINS/NPS To Robert Schnabel <schnabelr@missouri.edu>

05/05/2010 11:49 AM

cc

Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Bob,

Thanks for the update. How many samples did you get from Gordon, and what would be the cost per sample if you had done this first set gratis?

I want to let people here know not only of your generosity, but a ballpark figure of what we are talking about for cost if SNP analysis becomes the routine. Thanks.

Peter

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
Work phone: 970 / 225-3596
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Robert Schnabel
<schnabelr@missouri.edu>
>
04/27/2010 04:52 PM
To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
cc
Subj Re: Bison Genetics Analysis
ect

Hopefully I'll have the Yellowstone samples done within the next 4-6 weeks so I should have data before ISAG. However, nothing is going to be made publicly available until the paper is accepted. This is actually turning into a very cool project. I think the results are going to have a big impact on the management of public bison populations and there is going to be some really cool biology come out of it.

I went to ISAG in Brazil and Amsterdam. I'm not going this year and probably won't be going again. There are other conferences that are closer to my area of interest so we've decided to skip ISAG. Keep in mind that we generally take our entire lab to at least one conference a year and it gets expensive with 12 people. :-(

One comment on the abstract, you mention a 150k chip. Are you talking about the bovine chip or are you developing your own custom chip? If you're talking about the bovine chip the correct name is the Bovine SNP50 and it has 54,001 snps on it. There are going to be two new high density (HD) bovine chips coming out shortly. Both will have on the order of 600-750k snps. Other than that it looks good.

Bob

**Peter
Dratch/FTCOLLINS/NPS**

04/27/2010 11:25 AM

To Robert Schnabel <schnabelr@missouri.edu>

cc

Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Bob,

That is great that you got the samples. I look forward to finding out what the SNPs tell about ancestry. As I mentioned to you, I am planning to go to the ISAG meeting this summer. You've been before so you know how that meeting works, everyone puts in poster submissions. Attached is mine on the bison for you to review. If you think you will have preliminary results on historic hybridization from Wind Cave and Yellowstone and want to share them, I would be happy to have you as a co-author. Let me know.

Thanks.

Peter

Conservation Genetics of U.S. Federal Bison Herds

Peter A. Dratch¹ and Peter J. Gogan²

¹National Park Service, Biological Resource Management Division, 1201 Oakridge Drive, Fort Collins, CO, U.S.A. ²Peter J. Gogan, USGS - Northern Rocky Mountain Science Center, 2327 University Way, Suite 2, Bozeman, MT, U.S.A.

Corresponding author: peter_dratch@nps.gov

American bison (*Bison bison*) were reduced from tens of millions at the time of European colonization to a few hundred by the mid-1880s. There were remnant herds of both North American subspecies, plains bison and wood bison; crosses between the bison subspecies and between plains bison and domestic cattle were widespread. The 12 plains bison herds that occur in U.S. national parks and wildlife refuges are an important resource for the long-term conservation of American bison, and have been analysed at mtDNA and microsatellite loci. While most of the herds show low levels of introgression (<1% cattle alleles) dating from the time when they were saved from extirpation, no historical hybridization has been detected in bison from Yellowstone or Wind Cave National Parks. Despite the fact that most of the U.S. federal herds had few founders and have been maintained for many generations at relatively low population sizes, they do not show effects of inbreeding. They have retained significant amounts of genetic variation when measured by average heterozygosity and allelic diversity. There are presently few conservation herds that are large enough to maintain genetic variation over centuries. It is recommended that the federal herds be expanded or established as metapopulations. Analysis using single nucleotide polymorphism (150K SNP chip) is currently underway in the federal herds to further evaluate the variation in individual bison.

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
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Cell phone: 303 / 514-7792

**Peter
Dratch/FTCOLLINS/NPS**

04/27/2010 09:12 PM

To Robert Schnabel <schnabelr@missouri.edu>

cc

Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Bob,

Thanks for getting back to me so quickly, and your answer was what I expected. I will modify the abstract accordingly. I also don't generally go to ISAG anymore either as my work has moved to conservation genetics, the last one I attended was in France. But Edinburgh is where I went to grad school so I am anxious to get back.

Do let me know when you get back the Yellowstone results. Like you I think they could have major conservation implications and I would like to be part of those discussions. Thanks again for running those samples. When I was at the wildlife forensics lab, some of the most interesting work was the "end of the gel" experiments.

Thanks again, and I look forward to hearing from you in six weeks or so.

Peter

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
Work phone: 970 / 225-3596
Cell phone: 303 / 514-7792

**Peter
Dratch/FTCOLLINS/NPS**

04/22/2010 02:46 PM

To Rick Wallen/YELL/NPS@NPS

cc

Subj Re: Yellowstone Bison Genetics Analysis @ UM⁽¹⁾
ect

Rick,

My first goal was to get it done. I will contact Bob about how we should proceed with the analysis. Great you prevailed on Gordon. Peter

Rick Wallen/YELL/NPS

04/22/2010 12:09 PM

To Peter Dratch/FTCOLLINS/NPS

cc

Subj Yellowstone Bison Genetics Analysis @ UM
ect

Peter, are you doing the analyses with the genotype data or is Bob going to do that part and complete a report to the National Park Service? RW

Robert Schnabel

<schnabelr@missouri.edu
>

04/21/2010 04:16 PM

To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>

cc "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>,
"Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>,
"stephen.amish@umontana.edu"
<stephen.amish@umontana.edu>, "Taylor, Jerry F."
<taylorjerr@missouri.edu>

Subj Re: Bison Genetics Analysis
ect

All the samples look good. We'll get them on the next plate going out to be genotyped.

Bob

Luikart, Gordon wrote:

Bob,

Thanks for the good news.

Sorry for the delay; we were trying to help Yellowstone Park by sending you DNA from bison of known breeding area, so that the same data could be used to address questions about substructure in the Park. We will try to analyze more samples in the near future to address the substructure question.

We look forward to the results.

Best,

Gordon

Robert Schnabel
<schnabelr@missouri.edu>
>

04/20/2010 11:37 AM

To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>
cc "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>,
"Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>,
"stephen.amish@umontana.edu"
<stephen.amish@umontana.edu>, "Taylor, Jerry F."
<taylorjerr@missouri.edu>
Subj Re: Bison Genetics Analysis
ect

Just got the DNA samples. We will put them on the next plate going out to Geneseek.

Bob

Luikart, Gordon wrote:

Bob,

Can you please email to us your mailing address to ship the DNAs?

Rick Wallen/YELL/NPS

05/24/2010 01:21 PM

To Peter Dratch/FTCOLLINS/NPS
cc
Subj Any news from Univ. of Missouri?
ect

Any feedback from your colleague Bob Schnabel at U of Missouri about our DNA samples and the likelihood of cattle gene introgression based on high volume SNP data?

RW

Rick Wallen/YELL/NPS

04/22/2010 12:09 PM

To Peter Dratch/FTCOLLINS/NPS
cc
Subj Yellowstone Bison Genetics Analysis @ UM
ect

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Robert Schnabel
<schnabelr@missouri.edu>
>
04/21/2010 04:16 PM

To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>
cc "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>,
"Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>,
"stephen.amish@umontana.edu"
<stephen.amish@umontana.edu>, "Taylor, Jerry F."
<taylorjerr@missouri.edu>
Subj Re: Bison Genetics Analysis
ect

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Bob

Luikart, Gordon wrote:

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We look forward to the results.

Best,

Gordon

Robert Schnabel
<schnabelr@missouri.edu>
>
04/20/2010 11:37 AM

To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>
cc "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>,
"Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>,
"stephen.amish@umontana.edu"
<stephen.amish@umontana.edu>, "Taylor, Jerry F."
<taylorjerr@missouri.edu>
Subj Re: Bison Genetics Analysis
ect

Just got the DNA samples. We will put them on the next plate going out to Geneseek.

**Peter
Dratch/FTCOLLINS/NPS**

04/16/2010 03:55 PM

To Rick Wallen/YELL/NPS

cc Elaine_Leslie@nps.gov

Subj RE: Bison Genetics Analysis⁽¹⁾
ect

Thanks very much Rick. We will see if this moves him. If not I will call Fred next week.

Peter

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
Work phone: 970 / 225-3596
Cell phone: 303 / 514-7792

Rick Wallen/YELL/NPS

04/16/2010 03:43 PM

To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>

cc "Gruber, Matthew" <Matthew.Gruber@mso.umt.edu>, "Amish,
Stephen" <Stephen.Amish@mso.umt.edu>, Peter
Dratch/FTCOLLINS/NPS

Subj RE: Bison Genetics Analysis⁽²⁾
ect

Gordon, the known breeding range is irrelevant for this work with Peter and Bob. This is an opportunity that will address the hybridization questions that exist following Natalie's previous work with Yellowstone bison. And you already know that Bob has offered to run the genotypes at no cost. So, DNA from any of the purple top tubes that John provided to you guys should work. Like I mentioned on my phone message, If funding is an issue here for you, let's talk. Peter has some funding parked with Mike Schwartz and can reallocate some of that to do the DNA extractions. All you need to do is get the purple top tubes to Mike to do the extraction work. Apparently Bob has already received the Wind Cave National Park DNA and run them on his equipment to get genotypes. We are behind the curve on this now since we agreed to send the DNA about a month ago. Call me this evening, I need to know how we will resolve this and get the extracted DNA to Missouri as soon as possible.

RW

"Luikart, Gordon"
<gordon.luikart@mso.umt.edu>

04/16/2010 02:14 PM

To <Rick_Wallen@nps.gov>

cc "Amish, Stephen" <Stephen.Amish@mso.umt.edu>, "Gruber,
Matthew" <Matthew.Gruber@mso.umt.edu>

Subj RE: Bison Genetics Analysis
ect

We were hoping to get purple top bloods from you with known breeding range... But now will try to extract FTA cards (sorry to be brief... I am in meetings all PM)

Rick Wallen/YELL/NPS

04/16/2010 01:46 PM

To Gordon Luikart <gordon.luikart@mso.umt.edu>
cc "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>, Robert Schnabel <schnabelr@missouri.edu>
Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Gordon? RW

Robert Schnabel
<schnabelr@missouri.edu>
>

04/16/2010 01:31 PM

To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
cc Gordon Luikart <gordon.luikart@mso.umt.edu>, "Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>
Subj Re: Bison Genetics Analysis
ect

No problem. I now have genotypes on 23 Wind Cave animals so it will be interesting to see what those look like. I haven't touched them yet so I can't say one way or another. Do you all talk with Tom Roffe? I'm also doing samples he provided. I'll leave it to him to describe his own results.

Bob

Peter Dratch/FTCOLLINS/NPS

04/16/2010 01:26 PM

To Robert Schnabel <schnabelr@missouri.edu>
cc "Gordon Luikart" <gordon.luikart@mso.umt.edu>, Rick Wallen/YELL/NPS@NPS
Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Bob,

I thought you would have had them by now. In copying Gordon and Rick I hope to track them down. Thanks for your patience.

Peter

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
Work phone: 970 / 225-3596
Cell phone: 303 / 514-7792

Robert Schnabel
<schnabelr@missouri.edu>
>
04/16/2010 12:00 PM
To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
cc
Subj Re: Bison Genetics Analysis
ect

I just checked with Sarah and we have not received anything. If you can get us 10-20 Yellowstone samples ASAP we will get them on the next plate we send out.

Bob

Peter Dratch/FTCOLLINS/NPS
04/16/2010 11:20 AM
To Robert Schnabel <schnabelr@missouri.edu>
cc
Subj Re: Bison Genetics Analysis⁽¹⁾
ect

Bob,

Did you get the Yellowstone bison samples from Gordon, and have you had the chance to run them?

Peter

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
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Cell phone: 303 / 514-7792

Robert Schnabel
<schnabelr@missouri.edu>
>
04/16/2010 09:36 AM
To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>
cc "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>,
"Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>,
"stephen.amish@umontana.edu"
<stephen.amish@umontana.edu>, "Taylor, Jerry F."
<taylorjerr@missouri.edu>
Subj Re: Bison Genetics Analysis
ect

Just realized I never replied to this one either, my apologies. The snps you discovered in candidate genes won't help with the development of the high density chips because the snp lists

have already been submitted and they are already in manufacturing. However, sometime in the future it would be interesting to compare your list to the ~15 million we found during the snp discovery process to develop the chips.

Bob

Luikart, Gordon wrote:

Hi Bob,

Sorry for delayed response. I was traveling.

Thanks for the information and offering to genotype bison on the cattle SNP chip. It would be interesting to talk & collaborate as we just discovered >1,000 SNPs in bison candidate genes using exon capture and next gen sequencing. They might help you develop your SNP chips etc. I somehow thought you had offered to run 20 individual bison on the cow chip; No worries, I realize it is expensive. We will start working on getting you some bison DNAs now and will look into getting more individuals (40 total) run eventually on the cow chip, which would greatly help YNP wildlife managers and bison conservation in general. It would be quite helpful if you could indeed provide the data eventually from the 300 bison and cattle; it could help interpret and publish together collaboratively the data from Yellowstone Bison. In the mean time, I'll try to raise funding for SNP chips for 30-40 more bison.

Gordon

Robert Schnabel

<schnabelr@missouri.edu

>

03/18/2010 04:38 PM

To "Luikart, Gordon" <gordon.luikart@mso.umt.edu>

cc "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>,
"Rick_Wallen@nps.gov" <Rick_Wallen@nps.gov>,
"stephen.amish@umontana.edu"
<stephen.amish@umontana.edu>, "Taylor, Jerry F."
<taylorjerr@missouri.edu>

Subj Re: Bison Genetics Analysis
ect

Let me back up a bit and clarify some things. One of the things our group is interested in is the evolution of cattle and closely related species. We "pay the bills" by developing diagnostics for economically important traits in cattle. In the process of doing QTL work in cattle we have developed tools, such as the snp chip, that have application in other species. We are not interested in hybridization between bison and cattle per se or the management implications. What we are interested in is the question of whether or not the genome is differentially permeable to introgression from another species? If so, what are the genes in the regions capable of retaining foreign species DNA and what are the genes in the regions intolerant to foreign DNA? This has application to domestic cattle when you cross *Bos indicus* with *Bos taurus* cattle. The bison/cattle hybridization is really just a side project that was brought about because of my historical interest (I did my Ph.D. in Derr's lab and helped Todd Ward develop all the

microsatellite markers currently used at A&M), the fact that I used to raise bison and the fact that we built this snp chip and we wanted to see how it would work in bison. Turns out it works really well for identifying cattle introgression in bison. We are still working on the questions of whether or not the regions with introgression are biologically meaningful or if they are just random.

So, I offered to run 10 animals from YNP because they are an important population and would fill out our list of populations for our study. We have run probably around 1,000 samples (\$100 each) for people from all over the world out of our own pocket because they fit into projects we are working on. However, we have exhausted our supply of chips and in fact we are having to send our own samples to a genotyping company to get them to genotype them for us. Therefore, we really are not in a position to genotype the number of samples you are wanting to do. If you have the money, it's fairly easy to get someone to genotype the samples for you. If that's your intention we would be more than happy to collaborate with you on the analysis and interpretation. We can provide data from the >300 bison that we have already genotyped as well as genotypes from over 15,000 cattle samples.

We could potentially also compare your SNP data to microsatellite data as well

Quite honestly, once you see the snp data you'll pretty much just ignore the microsatellite data. In terms of evaluating introgression it's not even a fair comparison. In terms of using the snp data for population analyses you need to filter out the loci in the introgressed regions first. I just ran a quick query of my own herd (Arrowhead Buffalo Ranch, N=160). After filtering out loci in hybrid regions and requiring >90% call rate and >5% heterozygosity there were 2486 informative snps. So now consider what your F_{st} would look like using >2000 markers versus 20 or 30 microsatellites. These snp chips really have revolutionized what we are able to do! Now consider the fact that we are currently building two new chips with two different companies and each chip will have approximately 650-800k snps! The high density chips are probably not economically feasible for population genetic analysis like you want to do but the tool will be available. For your project it would be feasible to use the BovineSNP50 if you could find about \$175/sample (ballpark). You would generate enough data on those animals that you would never have to test them again and you could probably answer all the questions you can think of.

I won't even go into sequencing except to say that we are at a point now where we are resequencing the entire genome of individual animals. ;-)

Bob

Luikart, Gordon wrote:

Hi Bob,

We are wondering how many individual samples you might run. We also have a proposition for a possible collaboration and additional use of your data, if you might agree. I

understand you are interested in hybridization between cattle and bison, and diagnostic markers perhaps. Rick and YNP are interested in estimating gene flow between the two breeding ranges (Hayden Valley and Lamar Valley) and perhaps detection of selection (molecular adaptation) between them. If you were to run 20-30 individuals per breeding area it would provide a data set extremely helpful to YNP and an important publication co-authored by all involved & lead by someone in your lab, for example. Possible management implications include the potential recognition of each breeding group as a separate resource for management and restoration (e.g. maximizing diversity when founding/supplementing new herds). We could potentially also compare your SNP data to microsatellite data as well (interestingly, mtDNA Fst is near 0.4 but msat is near 0.01). It is likely we can quickly get high quality DNA from (FTA cards or frozen blood) from 20-30 per breeding area. We certainly can quantify it and send at least 0.5 ug.

Best,

Gordon

PS. Nice recent paper on bison vs. cattle SNP variation.

Robert Schnabel

<schnabelr@missouri.edu
>

03/17/2010 05:03 PM

To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>

cc "Luikart, Gordon" <gordon.luikart@mso.umn.edu>

Subj Re: Bison Genetics Analysis
ect

Absolute minimum is 300 ng or relatively high quality (not fragmented to hell) and high purity (260/280 > 1.8). The purity is the key part. There's a lot of chemistry that goes into producing genotypes and high purity DNA makes all the difference in the world. Pretty much anything that has gone through a PCI extraction with ETOH precipitation is generally good.

We prefer to get 1.5 ug of DNA that way we can quantify it and make sure it works the first time. At \$100-\$175 per sample it doesn't take too many screwups before it starts to hurt. :-) We've processed close to 15,000 samples through our lab and have only had maybe <50 fail.

Bob

**Peter
Dratch/FTCOLLINS/NPS**

03/17/2010 04:55 PM

To Robert Schnabel <schnabelr@missouri.edu>

cc "Luikart, Gordon" <gordon.luikart@mso.umd.edu>

Subj Bison Genetics Analysis⁽¹⁾
ect

Bob,

I spoke to Rick Wallen at Yellowstone, Gordon Luikart at the University of Montana, and both will help to provide the samples you need to do the screen with the 50K chip. Gordon asked about the amount and quality of the DNA you require. I have copied him here for your response.

I really appreciate everyone's cooperation in getting this analysis done on the Yellowstone bison herd, which of course belongs to the American people.

Peter

Peter A. Dratch, PhD
National Park Service
Endangered Species Program Manager
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**Peter
Dratch/FTCOLLINS/NPS**

03/11/2010 04:59 PM

To Robert Schnabel <schnabelr@missouri.edu>

cc

Subj Re: Bison Genetics⁽¹⁾
ect

Bob,

It was really great to talk with you today. I feel I understand so much more about SNPs and what they offer to bison conservation.

I have the PNAS paper for reading this evening. Attached in the paper by Phil Hedrick who attended the bison genetics workshop.

Again, many thanks for your time. I will be in touch soon about DNA from Yellowstone bison.

Peter



hedrick.bison 2009.pdf

Peter A. Dratch, PhD
National Park Service
Superintendent (Acting)
Missouri National Recreational River

Work phone: 605 / 665-0209 ext 22
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Peter Dratch/FTCOLLINS/NPS To Robert Schnabel <schnabelr@missouri.edu>
03/10/2010 03:19 PM cc
Subj Re: Bison Genetics Workshop⁽¹⁾
ect

I fully understand about the details. I look forward to talking with you at 3.

Peter A. Dratch, PhD
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Robert Schnabel To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>
<schnabelr@missouri.edu> cc
03/10/2010 03:01 PM Subj Re: Bison Genetics Workshop
ect

3:00 works for me. You can call me at 573-884-4106. I can answer all those questions but I'm afraid I may have to be a bit vague in terms of some of the details. I'm still working on the analysis and am trying my best to not divulge too much about the methods until I get a paper accepted.

Bob

Robert Schnabel
Research Assistant Professor
University of Missouri-Columbia
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920 East Campus Drive
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<http://animalgenomics.missouri.edu>

**Peter
Dratch/FTCOLLINS/NPS**

03/10/2010 02:52 PM

To Robert Schnabel <schnabelr@missouri.edu>

cc

Subj Re: Bison Genetics Workshop⁽¹⁾
ect

Bob,

How about if we talk tomorrow at 3pm.

My questions are largely about the identification of single nucleotide polymorphisms in bison and their application to the detection of cattle introgression and variation.

- 1) How far along is the development of SNP technology in bison?
- 2) How much greater is the resolution of this methods than current screening protocols (mtDNA and microsatellites)?
- 3) Is SNP variation assumed to be selectively neutral?
- 4) How many SNPs would you need to develop to get a good scan of the bison genome?
- 5) Is the technique the right one on which to choose individual breeders to preserve bison variation?
- 6) Have any herds (Interior Dept or otherwise) been screened with SNPs?
- 7) Have do any herds where no cattle ancestry been previously detected show historic introgression using SNPs?
- 8) Are there other markers/methods out there that show promise in screening bison conservation herds?
- 9) Are there some papers that I should read and cite in discussion of the next generation of bison markers?

Thanks. Let me know if tomorrow at 3 works for you.

Peter

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Robert Schnabel
<schnabelr@missouri.edu>
>

03/10/2010 12:07 PM

To "Peter_Dratch@nps.gov" <Peter_Dratch@nps.gov>

cc

Subj Re: Bison Genetics Workshop
ect

I'm pretty busy today so sometime Thursday or Friday would be better for me. I am available the following times (Central):

Thursday 12:00-5:00
Friday 10:30-5:00

Next week is open except Tuesday from 1:00 - 3:00.

Also, it would help me a bit if you could send me a list of some of the questions/topics you need info on that way I'm prepared. Let me know when would be a good time for you and we can set up a time for you to call me.

Bob

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<http://animalgenomics.missouri.edu>

Peter_Dratch@nps.gov wrote:

Bob,

I am going over the recommendations of a bison genetics workshop held in 2008, and they include the application of SNPs. So several people suggested that I call you and get an update on the application of those molecular tools to bison. Could you give me a call or an email and let me know when we might take a few minutes to discuss this.
Thanks.

Peter

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