Vertucci, Charles

From:	Scott Blankenship <scott.blankenship@fishsciences.net></scott.blankenship@fishsciences.net>
Sent:	Friday, May 31, 2019 2:05 PM
То:	Onanian, Benjamin
Cc:	Poxon, Brian; Vertucci, Charles
Subject:	RE: Bear River eDNA Questions

I just forwarded two emails (threads) to you Ben. One was the results spreadsheet and .kml, while the other was the only reference I had to design. Design email did not mention anything about sample volume though, so we must have spoken about that on the phone.

As flows were super high, far in excess for original sampling purpose re: 2000 cfs flow migration trigger, I recall having a discussion about turbidity and sampling volume. On the order of aggregating proximate samples during interpretation. I also recall that the number of filters collected increased from 2 to 5 per site to accommodate conditions at time of sampling.

While the exact probability of detection (per filter) was not estimated prior to sampling (as that task was not requested and well beyond project scope), sampling should have been fine for Camp Far West application, given the replication of both sites and filters. Volumes should be sufficient for DNA detection. We had positive DNA detections from species other than sturgeon during eDNA field survey, so it is unlikely that volume, varying (by filter) across survey, had a material effect on design. It is more likely that sturgeon were not present during surveys. With all that said, we have a sampling (statistical error) model showing effect sizes on DNA detection given relevant covariates (filter volume, distance from source, etc). We could simulate an eDNA survey given assumed covariates.

Scott

From: Onanian, Benjamin <Benjamin.Onanian@hdrinc.com>
Sent: Thursday, April 25, 2019 2:22 PM
To: Scott Blankenship <scott.blankenship@fishsciences.net>
Cc: Poxon, Brian <Brian.Poxon@hdrinc.com>; Vertucci, Charles <Charles.Vertucci@hdrinc.com>
Subject: Bear River eDNA Questions

Hey Scott,

Hope everything is well, just had a few questions regarding the lower Bear River eDNA analysis Genidaqs did for us in 2017.

The first is regarding a personal communication from February 2017, the purpose of the communication was to discuss the volume of water we were able to filter during sampling. Originally, it was stated that 2 L of water would be filtered, however, due to high turbidity the actual sampling volume ended up being closer to 1 L per sampling location. The personal communication in question would have likely been with Joel Passovoy to discuss any potential ramifications of reducing the volume of water filtered at each location. Is it possible that you still have an email record of that conversation?

The second question I have is whether or not a pdf report, like the one prepared for the Piru Creek sampling, was ever generated for the lower Bear analysis? I was going through our files and located a excel spreadsheet with the detection results but could not find an official report with a coversheet, methods, etc.

Thanks for your time Scott, let me know if you need any further clarification or information.

Ben Onanian

Aquatic Scientist I

HDR

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