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ME **Me XXX** to Robert Waterston **XXX**

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2 attachments: 2017 Robert Waterston, e-mail communication to authors, 17 Feb 2017.pdf (255 KB) and 2017 Robert Waterston, e-mail communication to authors 4 & 9 Jan 2017.pdf (618 KB)

Dear Bob,

Happy New Year. We have completed our manuscript on the Bermuda Principles [...]

Our correspondence early last year was invaluable to filling major gaps in the narrative. I have taken the liberty of condensing this correspondence into two PDF files, one from January and the other from February of 2017. These emails [...] provide a bulk of the documentation where we discuss the crucial period from 1994 through 1996. Rather than repeatedly citing our e-mail correspondence without any links, I wonder if you might give us permission to put these PDFs, attached to this email, into our digital archive [...]. Our readers will then be able to refer to the quotations you provided, with one stable URL per PDF. [...] I think that having a stable link to these sources cited frequently will make the references not only cleaner, but also more reliable, if you're willing.

Please let us know at your convenience.

Warmest wishes, and with enormous gratitude,

Kathryn (and Bob and Rachel)

--

Kathryn Maxson Jones
Ph.D. Candidate
Program in History of Science
Princeton University

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2017 Robert Waterston, e-mail communication to authors, 17 Feb 2017.pdf

255 KB | [preview](#) | [open](#) | [save](#)



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RW **Robert Waterston** **XXX** to Me **XXX**

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Waiting on others | x

Kathryn,

[...] Glad to hear of the progress and that our input was helpful. You certainly have my permission to put the aggregated emails into your digital archive. I read the document over quickly and didn't see any problems.

Best,

Bob

Bermuda

Note: Some details have been redacted for privacy.

RW **Robert Waterston**

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from: ★ Robert Waterston
to: ★ Kathryn Maxson
cc: ★ Robert Cook-Deegan
★ Rachel Ankeny
folder: [Gmail]/Important
date: Wed, 4 Jan 2017 15:28:55 -0800
user-agent: ~~reply-to:~~
subject: Re: Bermuda

Kathryn,

The short and reflex answer is, yes, of course. But since I don't trust my memory of specific events so long ago, I've pulled out our initial application for the human pilot award, submitted 8/2/95 to get a clearer picture of what we were doing before Bermuda.

First, we were well along in the Merck EST project (begun in late 1994, I believe), where we were submitting human ESTs to GenBank within 48 hours after the sequences came off the machines -- this rapid release was very important to Merck, since they did not want to be seen in any way as having special early access to the ESTs. [...] By 8/95 we had submitted 163k sequences from 96k clones (both ends were sequenced).

Second, we had been doing some human genome sequencing as part of our 1993 worm grant renewal (the study section in 1993 was divided about this part of our grant, advising us to keep focused on the worm, but not forbidding us to use funds to explore human sequencing). By 8/95 we had completed about 250 kb of human sequence (5 cosmid clones and a 70 BAC clone), with another 150-200kb underway. This amount was small, but not insignificant, compared to the Sanger, which had completed about 1Mb at the time.

I don't find an explicit statement of how we handled the release of those sequences, but the proposal does describe unambiguously what we will do with sequence obtained with the grant, and I have no reason to suspect we were doing anything different with the prior sequence. The proposal states:

"To provide early access to partially finished and partially contiguous data, contigs longer than 1 Kb will be posted immediately upon receipt from Project 2 [project 2 was sequence production, project 3 the analysis and submission of the data] after vector checking, but independently of whether the data has been reviewed further for content.

This is a policy that was instituted for the C. elegans project and has been well received. After manual finishing, new sequences will be analyzed for the last time, annotated with manual review and submitted to public repositories promptly within 2 weeks."

I should point out that at the time GenBank/EMBL did not accept unfinished genome sequence so we could only post it on our web site. Only after Bermuda did the public databases agree to host our initial assemblies.

[...]

Thanks,

Bob

On 1/4/17 2:30 PM, Kathryn Maxson wrote:

- show quoted text -

RD **Robert Cook-Deegan**

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from: ★ Robert Cook-Deegan

to: ★ Kathryn Maxson

cc: ★ Robert Waterston

★ Rachel Ankeny

folder: [Gmail]/Important date: Wed, 4 Jan 2017

19:23:54 -0500

subject: Re: Bermuda

Bob,

This is extremely helpful.

Is this grant proposal the origin of the "1kb contiguous sequence" trigger for release? Or was that already a norm for C. elegans sequences when you applied? And as you and John were thinking about what to propose at Bermuda, it looks like you could have chosen 2 weeks ("kind of finished") or daily release (sequenced but not reviewed at all). Any insight into how you arrived at daily release?

I'm guessing you're quoting from the proposal for Grant P01 HG000956 "Large Scale Genome Sequencing." If we cite, we should make sure we have the specific grant right. Looks like you first got that grant in 1993, and 1995 was a \$2.5M budget boost. That the right grant?

BCD

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RW **Robert Waterston**

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from: ★ Robert Waterston
to: ★ Robert Cook-Deegan
★ Kathryn Maxson
cc: ★ Rachel Ankeny

folder: [Gmail]/Important
date: Wed, 4 Jan 2017 17:31:54 -0800
user-agent: ~~reply-to:~~
subject: Re: Bermuda

Bob and Kathryn,

The quote is from our pilot human sequencing grant, which had no number at the time of submission since it was a completely new grant. The title is "The Human Genome Sequence -- A Pilot Project". In a later grant I refer to it as P50 HG01458. The grant you refer to was the one that supported the worm sequencing and gave us the okay to do some human. The initial grant ran to '93 (1/4 of those funds went to the UK) and the renewal ran to '98. I don't remember a 2.5M boost.

While I was into archeology, I pulled out the 10/30/92 renewal submission to see what we said about data release at that time. In searching through that, for the worm we were simply submitting the finished sequence to GenBank. We do mention that we also are posting the sequence in the ACEDB database, which was available by anonymous ftp. I don't think we had confidence in the initial shotgun assemblies at the time so weren't posting those. Indeed it wasn't until 18 months into the grant that we decided to do deep enough shotgun to produce good initial assemblies. Once we started doing deeper shotguns and using Phil Green's PHRAP, the assemblies were much more reliable, but we hadn't made the transition by 10/92 apparently. On both the human and yeast projects in the grant we have a rather vanilla statement:

"Our purpose is to make yeast (human) sequence data available to the scientific community as quickly as possible. Therefore, data will be released to the public databases immediately upon completion. We will define completion as an annotated contiguous double stranded sequence."

We do go on to make clear that for sequences that are extremely difficult, we will not delay submission, but will annotate them as problematic. But in case the intent is clear that we will submit the sequence as soon as it is ready, not waiting for publication or imposing any other delay. In the next couple years this obviously evolved into

ME **Me**

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from: ★ Kathryn Maxson
to: ★ Rachel Ankeny
cc: ★ Robert Waterston
★ Robert Cook-Deegan
folder: [Gmail]/Sent
date: Mon, 9 Jan 2017 16:29:20 -0500
subject: Re: Bermuda

Dear Bob,

[...]

A few brief follow-ups:

[...]

2. It seems like the “vanilla” statement, to which you refer below, was from an application, so would not appear in NIH Reporter. But it’s very helpful, and with your permission I’d like to cite it. Might I cite your email communication, noting as well that the grant application is in your personal files? Relatedly, when referring to human and yeast, (a) is the human grant you’re referencing the 01458? (b) and might you share the yeast #? There are a few options on Reporter.

Much obliged,
Kathryn

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<http://www.princeton.edu/histgrads/profiles/kmaxson/>
<https://dukecpq.wordpress.com/former-research-assistants/>

RW **Robert Waterston**

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from: ★ Robert Waterston

to: ★ Kathryn Maxson
folder: [Gmail]/Important
date: Mon, 9 Jan 2017 13:44:49 -0800
user-agent: reply-to:
subject: Re: Bermuda

Hi -

[...]

2) You can certainly cite that as you propose. The texts for both human and yeast were from the renewal of our worm sequencing grant, not separate grants. The original grant number was R01 HG00136. In the renewal application, we proposed 1) to complete the rest of the worm sequence; 2) to contribute 3 Mb to complete the yeast sequence; and 3) to initiate human sequencing on the PKD region and on gene rich regions of chromosome 7 in order to test our methods on human genomic DNA. To add confusion, the project was apparently given a new number when the renewal was awarded -- P01 HG00956. Perhaps this change was because we had gone from an R01 to P01, but who knows!

Thanks,

Bob

... 2/10/17

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