**From CTG written to SiriusDisclosure website – March 25 2018**

Would Dr. Greer like to know, from someone knowledgeable in DNA research, what might be wrong with new GR paper by Garry Nolan and colleagues on the small Chilean mummy?

First of all, Dr. Nolan’s story has changed completely, since when we first discussed his early results on 50 Mb of sequencing several years ago. Then he was ecstatic that he had made a big history-making discovery, and we agreed to discuss and analyse those first 50 Mb once he had some free time. This never happened. Despite his strong interest on one day, after that we never heard from him again, and we never got a copy of the first set of sequencing results about which he was very excited, having done some kind of preliminary analysis.

Now onto the new paper 2018. He says he has done whole-genome sequencing on the entire sample, and that 89% of reads match uniquely to certain places in the human genome. I do not know exactly how a modern DNA sample might match, you would have to discuss that with bioinformatics people, but 89% seems a bit low, and suggestive of moderate DNA damage due to age or environmental exposure. His average DNA size is just 300 bp, which strongly suggests a lot of non-specific DNA damage (this is what we get for a modern sample after 10 minutes of intense sonication). He also reports a two-fold excess of C>T transitions near the ends of those 300 bp fragments, again consistent with “moderately damaged DNA”.

In summary, we know beyond any reasonable doubt that the DNA sample from that small Chilean mummy was “moderately damaged”, so as to decrease its mean size to just 300 bp, and to induce many C>T transitions near the ends of fragments. This would also mean, beyond any doubt, that “some” C>T oxidative damage mutations will be located within or near the centres of those fragments, at a somewhat lower level.

If they were my data, and I did the same analyses, my first conclusion after seeing so many mutations within coding regions, including lots of mutations never seen before in any medical database, would be to think that most or all of such mutations took place after the mummy died, due to 100-500 years of environmental exposure, which seems unavoidable. I would venture to say that the vast majority of molecular biologists would consider that as a primary hypothesis, unless the facts somehow pointed otherwise?

Now what Nolan and his colleagues did next was quite surprising, to say the least. They chose to interpret all of those many, extensive mutations within DNA coding regions as genetically significant to the mummy while it was still alive! If it were a fresh, modern undamaged sample, this might be reasonable. However for a sample which has been moderately damaged to the extent described, it is not a plausible hypothesis.

Interestingly enough, the spectrum of mutations from chemical exposure to sodium nitrate in model systems (there are no in vivo data) matches closely the spectrum of mutations due to age / environmental damage. Both take place by means of deamination of C or sometimes A bases. So there is no easy way of telling the two effects apart by DNA sequence analysis alone.

And there is not a single study of which I know, where exposure to sodium nitrate in vivo causes serious DNA mutations. Nolan cites only one paper of men with heart disease who take Monodur! Sodium nitrate is added to bacon and many other meats as a safe food additive. Thus the factual evidence that sodium nitrate might be “dangerous to pregnant women” is nil. And so a primary hypothesis of “environmental damage after death” seems strongly favoured. Which means that the whole paper is largely an artefact, unless the authors can present some kind of cogent arguments to the contrary, which they have not yet done?

It is hard to imagine that this paper passed peer review by experts, and it would be interesting to see what those reviews might have said? Please feel free to use this information freely without mentioning my name, because I do not wish to get into a public dispute over a subject with which I am not closely associated.

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