MINUTES

Gene/Disease Specific Database Advisory Council
Teleconference
Tuesday 8 November 2016
1200-1300hrs UTC/GMT

MEMBERS

Present
Peter E M Taschner (Chair)
Arleen Auerbach
Raymond Dalgleish
Mauno Vihinen
Martina Witsch-Baumgartner

ICO Staff
Timothy D. Smith

Apologies
Olubunmi K D Abel
Ammar Al-Chalabi
Stefan Aretz
Timothy Barret
David Baux
Jean-Pierre Bayley
Daniel Bichet
Nenad Blau
Nancy Braverman
Paola Carrera
Johan T den Dunnen
Rosemary Ekong
Pascal Escher
Almudena Fernández
Marc Ferre
Mary Fujiwara
Bruce Gottlieb
Daniel Hampshire
Tamas Hegedus
Raoul Hennekam
Alex Hewitt
Ammar Husami
Sarah E A Leigh
Derek Lim
Finlay Macrae
Eamonn Maher
Lluis Montoliu
Etienne Mornet
Magali Olivier
Sue M Povey
Yves Sabbagh
Judith Anne Savige
Sarah Sim
Carli Tops
Ronald Trent
Richard van Wijk
Katarzyna Wertheim-Tysarowska
Tom Winder
Bing Yu
Johannes Zschocke

AGENDA

1. **Welcome**
2. **Apologies**

   Apologies were noted as above.
3. **Confirmation of minutes of previous meeting**

   Minutes were confirmed unanimously.

   Raymond Dalgleish asked if any feedback had been received from the FDA as a result of the submission made by the Project. Timothy Smith reported that the submission had been acknowledged but no other response had been received. He directed the Council's attention to the website https://www.regulations.gov/docket?D=FDA-2016-D-1233 where the Project's submission, as well as others, could be viewed.
4. **Reports of actions since last meeting**

   a. **Letter to National Human Genetics Societies**

   Members of the Council reported on their progress on this initiative.

   - Raymond Dalgleish: letter sent. No formal response. Will chase.
   - Martina Witsch-Baumgartner: Is now on the board of the Austrian Society. Will propose a statement be made.
   - Arleen Auerbach: not aware of any statement from the ASHG. ACMG guidelines require diagnostic labs to use HGVS nomenclature.
   - Peter Taschner: Will check progress.

Peter Taschner raised another issue: cancer genetics. He suggested that the Project may need to get in touch with cancer societies. Mauno Vihinen asked what the COSMIC database is using as a nomenclature system. Peter responded that they use their own version of the HGVS nomenclature and have been asked to state on their website how they deviate from the HGVS guidelines but have not done so yet.

b. Genetics and Genomics Editors' Meeting at ASHG – Timothy Smith

Timothy Smith provided a summary of the outcomes of the meeting with journal editors that the Project hosted at the recent ASHG meeting. He mentioned that the editors present have requested from the Project a checklist that can be provided to authors, reviewers and editors as part of the submission process that, amongst other important things, such as checking the validity of variant names, specifically asks if variant level data has been submitted to a public database. Peter Taschner noted that this was an encouraging sign and flagged that the Council would need to provide feedback on the developed checklist. Raymond Dalgleish raised the point that non-specialty genetics journals are increasingly publishing variants and that they would need to be included in this effort. Timothy Smith raised the request from some editors for a webinar on how to use Mutalyzer. Peter Taschner undertook to progress this. Timothy Smith noted that the ICO would be able to help with technical production.

5. Standards Development Process

a. Joint Working Group: Minimum Content Requirements – Peter Taschner

Peter Tachner and Martina Witsch-Baumgartner undertook to progress this before the next meeting.

b. WG08: Ethics Checklist for LSDB Curators and Submitters – Rosemary Ekong

Rosemary Ekong provided a brief update via email: Comments have been received from 8 members. We are yet to finalise a document that incorporates these comments.

6. Future Meeting Dates

The ICO will work out a schedule for next meetings that works for the most people possible.

7. Reports from Members

Tamas Hegedus provided the following update via email:

1. We completed our database update and submitted a manuscript to Human Mutations. http://abcm2.hegelab.org/

It is not a simple update, we supplemented the database with predictions and gene level data, plus assessed the availability of data of ABC protein mutations in LSDBs.

- Unfortunately, in silico predictors of effects exhibit low performance on ABC proteins (as Mahuno evaluated earlier these tools).
- There are very low amount of data of ABC proteins mutations in databases. These include not only data on mutations, but also on regulation (e.g. transcription binding sites).

2. We should move our HAE database (http://hae.enzim.hu/) to a new platform. The MDs initiated this database 15 yrs ago, have data on a relatively large number of patients (also retrospective). They are not simply the center of HAE in Hungary, but the only place for diagnosis and treatment. I am trying to convince them to share some patient data at the international level, create a country node for HAE. However, I cannot, since they think that not primary data but guidelines are useful for MDs. So they perform clinical research (beside diagnosis and treatment) to generate/contribute to guidelines based on their primary data.

I just cannot give good reasons to generate a database including not "only" mutation but much more data which is more patient oriented.

Moreover, I start to be dubious/ambiguous regarding to country nodes and their objectives.

8. Other Business

Raymond Dalgleish directed the Council's attention to a potentially useful new tool: https://varsome.com/.