

From: Steve Trim [<mailto:s.trim@venomtech.co.uk>]

Sent: November 24, 2017 1:02 PM

To: secretariat

Cc: United Kingdom of Great Britain and Northern Ireland - Mr. Thomas Murphy

Subject: peer review of digital sequence information document

It is clear that digital sequence data presents a major challenge for ABS and the fact finding and scoping document goes along way to identifying the challenges of use of genetic material in this way. However the solutions will take much more work and there may need to be some pilot trials to test how potential ABS processes may work in practice. I think the concerns about restrictions driving commercial users to look for other sources of sequence from non restricted sources are very pertinent as are concerns over proving provenance when BLAST searches could reveal identical sequences from multiple sources. Unique identifiers to track access would help but still leave gaps as to which sequences were used out of the list of conserved sequences accessed and transfer of such sequences through private transactions which then may lead to a commercial use.

I also have some direct comments from specific parts of the text, see below.

Page 14, line 34 Laboratoriews needs correcting.

I also agree with the removal of the word "digital" and consider genetic sequence as the CBD focuses on genetic resources. The use of the word "sequence" doesn't appear to involve metabolites but the metabolome of an organism is determined to some extent by its genome and the resulting proteome, Thus I agree with the continued use of this word.

p

age 30, line 25

ENSEMBL

, a genome browser for vertebrate genomes. Although

ENSEMBL

describes itself as a vertebrate genome database it does include non vertebrates such as Drosophila, C.elegans, Saccharomyces and some parasites.

Page 31 - line 27 Roslin link doesn't work and line 36 NCBI link doesn't open

page 32 - first NCBI stats link works however the second doesn't, line 24 - Petabyte - Terrabyte conversion looks wrong.

Page 62, line 33-36 pertain to academic research leading to sequences being deposited that then become used commercially, and this is reported back. however this is reactive rather than proactive and it is unclear whether this sort of notification could lead to an ABS agreement or

punishment for commercial use without prior benefit sharing being agreed. This would need to be defined clearer in a digital sequence use policy.

Kindest regards

Steve

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