

IARC Meeting 14: May 11th 2018: minutes

The meeting commenced at 22:15 AEST. AC, MC, and CS were in attendance. MO excused himself from the meeting, so that a submission with which he is associated could be considered by IARC.

1. The minutes of Meeting 13 were accepted via email, prior to the commencement of the meeting.
2. The committee considered the TPA submission from Linnea Thörnqvist. The committee considered this to be an impressive submission, which should hopefully serve as a guide for future TPA and other submissions. The submission was sent to IARC on 16/4/2018 and has been designated submission IARC003 (Davide Bagnara's B12 and B16 datasets will be referred to as IARC001 and IARC002 respectively.)

The committee considered the sequence

>IGHV3-43D*01_S3103 (C195A)

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GAAGTGCAGCTGGTGGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCTC
CTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGTCAAGCTCCGGGG
AAGGGTCTGGAGTGGGTCTCTTATTAGTTGGGATGGTGGTAGCACATACTATGCAGACTCTG
TGAAGGGTTCGATTCACCATCTCCAGAGACAACAGCAAAAACCTCCCTGTATCTGCAAATGAACAGT
CTGAGAGCTGAGGACACCGCCTTGTATTACTGTGCAAAGAT
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NOTE: The submitted sequence is complete up to and including nucleotide 321, but highly similar sequences in the IMGT reference set include an additional nucleotide.

The sequence is present at low frequency (0.07%), in the IgDiscover analysis. It was inferred by IgDiscover. No information was provided by the submitter regarding analysis with partis or TIgGER. Haplotype analysis could not be performed. Analysis for chimerism did not provide evidence against the existence of the sequence. It was agreed that the sequence should be moved to Level 1, subject to the provision of additional information.

IARC will request that Linnea Thörnqvist provides information on PCR primers used (cell D18, Repertoire tab).

3. The committee considered the sequence

>IGHV3-7*02_A318G (A318G)

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GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTCCCTGAGACTCTC
CTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATGAGCTGGGTCCGCCAGGCTCCAGGG
AAAGGGCTGGAGTGGGTGGCCAACATAAAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTG
TGAAGGGCCGATTCACCATCTCCAGAGACAACGCCAAGAAGTCACTGTATCTGCAAATGAACAG
CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGGA
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NOTE: The submitted sequence is complete up to and including nucleotide 320.

The sequence is present at a moderate frequency (0.5%), in the IgDiscover analysis. No information was provided by the submitter regarding analysis with partis or TIGER. Haplotype analysis could not be performed. Analysis for chimerism did not provide evidence against the existence of the sequence.

Extensive analysis was submitted, including four additional IgDiscover analyses using modified germline gene reference datasets. Although IARC were strongly persuaded by the submitted data, it was agreed that the sequence should be moved to Level 0. Issues relating to the end nucleotides deserve wider discussion by the Working Group before IMGT is notified of such a potentially controversial decision. This will be raised by AC at the forthcoming WG meeting.

4. In the course of discussions CS highlighted the importance of including additional information in the Documentation sheets, noting whether this is the first consideration of a sequence, its review status, IARC decisions and reasons for those decisions. It was also agreed that IARC needs to determine the most informative frequencies to be included in the Documentation sheets relating to decision-making. Alternative could come from the IgDiscover 'Unmutated frequencies' or 'Unique CDR3s'.
5. The next meeting (Meeting 15) will be held on 18/5/2018 at 21:00 AEST. William Lees will be invited to join the meeting. Meeting 15 will be conducted via WebEx to facilitate shared viewing of files.

The meeting ended at 23:00 AEST.