IARC Meeting 31: February 8th 2019: minutes

The meeting commenced at 22:00 AEDT. AC, CS, MC, and MO were in attendance. William Lees joined the meeting.

1. The minutes for Meeting 30 were accepted.
2. AC reported that he contacted IMGT regarding the 5 Level 1 sequences, but has not yet received a response.
3. The committee discussed inconsistencies with italicising of gene names in the IARC manuscript. The policies of HUGO and IMGT were noted to be different. The manuscript will be submitted without italicising antibody gene names, but the issue will be raised with the Frontiers editor. AC will also write to Menno van Zelm in his capacity as Chair of the IUIS Nomenclature Committee, as this may be an issue that could be resolved by his committee.
4. WL will further develop OGRDB to facilitate access to the genotyping data that supports sequence submissions.
5. An email from Chaim Schramm, responding to questions regarding the assignment of germline genes by partis, was circulated. The committee hopes to receive additional advice from the partis team.
6. The committee continued its review of the submission S0007 from Chaim Schramm. The committee discussed the lack of second alleles for some genes for which inferences were made. This implies either homozygosity for the inferred allele or the presence of a deletion polymorphism on the alternate chromosome. It was pointed out that the submitted genotype had similarities to some African genotypes, highlighting to the committee that care should be taken not to assume that submitted genotypes will always have familiar features.
7. The committee noted that the submitted IGHV1-8 variant is now recognized by IMGT as IGHV1-8*03. The submitted IGHV2-70 variant is now recognized by IMGT as IGHV2-70*15.
8.. The committee then considered the submitted IGHV4-59 variant. This analysis was used by the committee to support the evaluation of the submitted data. The submitted sequence is as follows:

   >IGHV4-59*01+T260C
   CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCC
   CTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGGC
   AGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAA
   CTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAG
   TTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGA
   GAGA

   This sequence represents IGHV4-59*01 T288C in terms of the IMGT numbering system. The committee noted a rearrangement frequency of about 1.7%, with 1515 alignments including 341 perfect matches to the inferred allele. IGHV4-59*01 is also present in the

genotype and is represented by larger number of reads than IGHV4-59*01 T288C (ratio: 17:83). The S0007 submission noted that haplotyping was not possible, but MC indicated that it was possible to haplotype this individual using the IGHJ4 locus. He suggested that a previously unreported J4 allele was present in this individual, and agreed to send his analysis to members of the committee. Diverse reads representing the IGHV4-59*01 T288C inference have been submitted to SRA/ENA under accession numbers SRR8298738 and SRR8298744. All members of the committee agreed that the sequence should be accepted as a Level 1 sequence. Only 116/339 (34%) of bases at position 320 among sequences submitted to SRA were an A (95 were G). In line with previous policy, the submitted sequence will be recognized up to and including nucleotide 319 as follows:

>IGHV4-59*i01
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCGGAGACCCTGTCC
CTCACCTGCACTGTCTCTGGTGGCTCCATCAGTAGTTACTACTGGAGCTGGATCCGGC
AGCCCCCAGGGAAGGGACTGGAGTGGATTGGGTATATCTATTACAGTGGGAGCACCAA
CTACAACCCCTCCCTCAAGAGTCGAGTCACCATATCAGTAGACACGTCCAAGAACCAG
TTCTCCCTGAAGCTGAGCTCTGTGACCGCCGCGGACACGGCCGTGTATTACTGTGCGA
GAG

This decision will be recorded in OGRDB.

The next meeting (Meeting 32) will be on Friday March 1st at 22:00 AEDT.

The meeting ended at 23:10 AEDT.