

IARC Meeting 30: February 1st 2019: minutes

The meeting commenced at 21:30 AEDT. AC, CS, MC, and MO were in attendance. William Lees joined the meeting at 22:00 AEDT.

1. The minutes for Meetings 28 and 29 were accepted.
2. In considering the minutes of previous meetings, it was noted that some action items from these meetings have not been concluded. AC undertook to contact IMG T regarding the 5 Level 1 sequences, and will raise the possibility with IMG T that they receive automated notifications of decisions regarding sequences at Levels 1, 2 and 3. AC will also ask IMG T whether they intend to include these sequences in their own directories, and will ask that IARC and IMG T work together to complete the development of such a system prior to the Genoa meeting of the AIRR community.
3. The committee agreed to discuss the future make-up of the committee, so that recommendations can be taken to the Genoa meeting of the AIRR community.
4. The committee discussed the make-up of the panel for the Germline Database Panel Discussion at the Genoa meeting. It was agreed that Gur Yaari and Gunilla Karlsson Hedestam should be invited to join the panel, as representatives of leaders of groups involved in the generation of population-based genotype data. William Lees should be invited as the developer of OGRDB. Two or three representatives from industry should also be invited.
5. There was discussion of the IARC manuscript, and reviewers comments that were recently received. MO will be providing a revised version of Figure 3B as requested. AC will write to Patrick Wilson to ask whether we should submit a revised manuscript or wait for additional comments from a second reviewer.
6. The committee continued its review of the submission from Chaim Schramm. It was noted that sequences that have been submitted by CS to IgPdb, based on the data that is now before the IARC, are not included in the submission to IARC. It was also noted that the partis genotype output that is before the committee includes inferences called with almost no alignments, and inferences with thousands of alignments but almost no exact matching alignments. These inferences are not proposed for consideration by IARC, but if we are to properly understand partis, we need to understand why these sequences are being called. AC will write to CS seeking an explanation.
7. The committee discussed variation in the percentage of alignments, within the CS genotypes, which are exact matches to germline genes. The committee discussed the variation that might be expected, and technical issues that can give rise to such variation. The committee will explore other datasets to arrive at expectations of percentages of exact alignments that should be seen in IgM libraries.

The next meeting (Meeting 31) will be on Friday February 8th at 22:00 AEDT.

The meeting ended at 22:40 AEDT.