Minutes of IARC meeting 133, February 26, 2024

In attendance: Ayelet Peres, Andrew Collins, Martin Corcoran, William Lees, Corey Watson, Mats Ohlin, Tahel Ronel

1. Approval of minutes of meeting 132

Approved

2. Next meeting

Wednesday March 20th, at 10 UTC.

3. TR-IG process

Discussion. Discussion with TR-IG is pending but will likely take place in the near future.

4. AIRR-C-meeting in Porto 2024

Discussion. Need to have two IARC co-chairs was addressed.

5. Roadmap for building Ig germline sets on genomic data; evidence, assessment, and naming

Data and read support is being built to allow for assessment, and processes that are also being built into TR-IG policy documents. IARC would ideally be part of the evaluation and affirmation process based on underlying data provided by the submitter. Discussion of challenges associated with certain loci and genes. It is expected that example data will be available to IARC for discussion ahead of the AIRR-C meeting in Porto.

6. Inference of IGKV3-15*01 G107A

https://ogrdb.airr-community.org/submission/S00044

The inference was originally reported in Mikocziova et al. iScience 2021, 24, 103192 (https://doi.org/10.1016/j.isci.2021.103192).

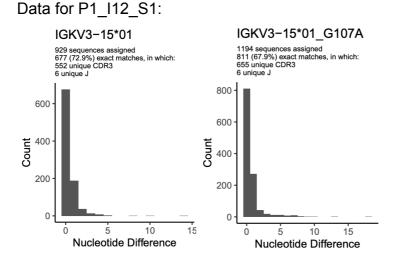
IGKV3-15*01_G107A was inferred in VDJbase sample P1_I12_S1. This sample's genotype that also carry IGKV3-15*01 and a substantially lower number of sequences of IGKV3D-15*01 (about 9-fold). The relatively high expression of IGKV3-15*01_G107A suggests that the allele was found in the proximal and to the typically less expressed distal IGKV locus. It was supported by 811 unmutated sequences and 655 unique CDR3s in the unmutated sequence set. The allelic ratio for IGKV3-15*01_G107A / IGKV3-15*01 was 56/44. Haplotyping associated IGKV3-15*01_G107A to IGKJ2*01 while IGKV3-15*01 associated to IGKJ2*04. IGKV3D-15*01 associated to both haplotypes as defined by alleles of IGKJ2.

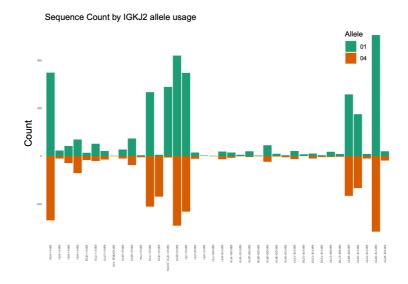
The sequence is also inferred in VDJbase P1_I43_S1 and P1_I91_S1 but no haplotyping data are available for those samples.

There is no entry in GenBank or among genomic entries in VDJbase that is identical to the full sequence of IGKV3-15*01 G107A.

>IGKV3-15*01_G107A

GAAATAGTGATGACGCAGTCTCCAGCCACCCTGTCTGTGTCTCCAGGGG
AAAGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAACAGCAACTT
AGCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTAT
GGTGCATCCACCAGGGCCACTGGTATCCCAGCCAGGTTCAGTGGCAGTG
GGTCTGGGACAGAGTTCACTCTCACCATCAGCAGCCTGCAGTCTGAAGA
TTTTGCAGTTTATTACTGTCAGCAGTATAATAACTGGCCTCC





We are, prior to a final decision, awaiting full assessment of the 3'-end nucleotides of, and potential finding of genomic evidence for this and the other novel allele of IGKV3-15 (IGKV3-15*01_A117G) initially inferred from transcriptomic data.