Minutes of IARC meeting 119, April 3rd, 2023

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

1. **Approval of minutes of meeting 118**
   Approved

2. **Next meeting**
   April 24th, 2023 at 10.00 UTC

3. **IUIS nomenclature process**
   Process to begin with the human Ig nomenclature. WL and AC will discuss the allele label approach.

4. **Germline reference set manuscript**
   Discussion. Discussion of examples of problems associated with erroneous/truncated entries in data sets. Discussion of how/when to implement light chain alleles are to be included in this process. CW will produce a phylogenetic tree. AC/AP and AC/MO will deal with 3'-end and 5'-end matters of alleles.

5. **Assessment of inference TRBV7-7*01_C315T in P4_I9_S1 (S00036)**
   TRBV7-7*01_C315T has been inferred in seventeen genotypes in the VDJbase P4 data set, including in VDJbase P4_I9_S1, a haplotypable data set (based on heterozygocity in TRBJ1-6). The genotype is also implied to carry TRBV7-7*01. No other gene apart from IGHV7-6 (alleles of which also carry C315) in the IMGT database is highly similar to these alleles of TRBV7-7. The novel allele is the most expressed allele in the repertoire (58% allelic frequency; 0.16% of the total error-free population). It is represented by 37 error-free sequences and 33 unique CDR3s in the error-free set. Haplotyping based on allelic diversity in TRBJ1-6 demonstrates association of TRBV7-7*01_C315T with only one of the haplotypes (only few recorded cases; TRBV7-7*01 was not associated with any allele of TRBJ1-6).

The allele has also been identified as TRBV7-7*01_S0326 and Sanger validated (GenBank MZ339373) (Corcoran et al. (2023) Immunity 56, 635-652.E6 (DOI: 10.1016/j.immuni.2023.01.026)).

>MZ339373
TTGAGAGAGGAAGTGATGTCACTGTGGGAACTGCCCTGTGGAGACAAGGACATC
CCTCATCCTCCGCTCCTGCTCACAGTGACACTGATCTGGTAAAGCCCCCATCCT
GGTCTGACACTGTC**ATGGGTACCAGTCTCCTATGCTGGGTGGTCCTGGGTTTCC**
TAGGGACAGGTGAGTCCTCAAAACACAAAGTAGTTTCATATTTTTTCTGTATGT
AGGTGTGTGTGTGTATGCATGTGTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGT
GTGTGAGATGACTACAAATGTTTTCCTTATTCTGTTGCCAGATTCTGTTTCCAC
AG**ATCACACAGGTGCTGGAGTCTCCCAGTCTCCCAGGTACAAAGTCACAAAGAG**
GGGACAGGATGTAACTCTCAGGTGTGATCCAATTTCGAGTCATGCAACCCTTTA
TTGGTATCAACAGGCCCTGGGGCAGGGCCCAGAGTTTCTGACTTACTTCAATTA
TGAAGCTCAACCAGACAAATCAGGGCTGCCCAGTGATCGGTTCTCTGCAGAGAG
GCCTGAGGGATCCATCTCCACTCTGACGATTCAGCGCACAGAGCAGCGGGACTC
AGCCATGTATCGCTGTGCTAGCAGCTTAGCCACAGCATGGCACAGTCGCCTCCT
TCCTGTTCACAAACCTCATCCTTCT
heptamer 23-mer nonamer

It has also been identified in a BAC clone with accession number AC229888

Discussion of the process of submission and management of novel alleles based on inference only, both inference and genomic data, or genomic data alone, of which this inference is a good example of the second type. MC will have a look at the data supporting the genomic sequencing confirmation made as support of the inference published in the Immunity paper (DOI: 10.1016/j.immuni.2023.01.026).