

Table 1. PP and LP B-cell-derived IgMVH CDR3 nucleotide sequences that were identical to PEC B1-cell-derived CDR3 sequences.

| | | CDR3 ^{c)} | V | D | J | V-D | D- J | J |
|------------------------------|-----------|---|------|-----|---|-----|---------|---|
| Sort I ^{a)} | PP1 | TGTGCCAGACAAGCCTACTATGGTAACTACTGGTACTTTCGATGTC | Q52 | DSP | 1 | 0 | 0 | 0 |
| | PP2 | TGTGCAAGACACTACGGTAGTAGCTATGCTATGGACTAC | 7183 | FL | 4 | 0 | 0 | 2 |
| | PP3 | TGTGCCAAAAAATACGGTAGTAGCTACTACTATGCTATG GACTACTAC | Q52 | FL | 4 | 0 | 0 | 0 |
| | PP4 | TGTGCAAGACATAGGTACGACTGGTACTTTCGATGTC | 7183 | SP | 1 | 0 | 0 | 1 |
| Sort II ^{b)} (4) | PP1.1 (1) | TGTGCCAAAAATTACTACGGCTATTACTATGCTATGGACTAC | Q52 | FL | 4 | 0 | 0 | 0 |
| | PP1.2 | TAC | Q52 | FL | 4 | 0 | 0 | 0 |
| | PP1.3 (1) | TGTGCCAGAGATAGGTACTATGCTATGGACTAC | Q52 | SP | 4 | 0 | 0 | 0 |
| Sort III ^{c)} | LP 1 | TGTGCAAGACACTACGGTAGTAGCTATGCTATGGACTAC | 7183 | FL | 4 | N | 0 | 0 |
| | LP 2 | TGT GCA AGA TAT AGG TAC GAC TAT GCT ATG GAC TAC | 7183 | FL | 2 | 0 | 0 | 1 |
| Sort IV ^{d)} | B1b 1 | TGTGCAAGATCTTACTATGGTAACTACGGGTTTGCTTAC | 7183 | SP | 3 | P | N | 1 |
| | B1b 2 | TGTGCAAGAGGAACTGGGGAGTACTTTGACTAC | J558 | DQ | 2 | N | N | 0 |
| | B1b 3 | TGTGCCAAACTTATCTACTATGATTACGACGCTCCGCTTTGCTAC | Q52 | SP | 2 | N | N | 0 |

^{a)} IgMVH sequences derived from bulk sorted CD19^{hi/int}PNA⁺ B cells from PP of L2 mice that were identical to known PEC B1a-cell-derived IgMVH sequences from L2 mice.

^{b)} IgMVH sequences derived from sorted IgM⁺PNA⁻ SCs from PP of L2 mice that were identical to known PEC B1a-cell-derived IgMVH sequences from L2 mice. Numbers in the parentheses show the number of times a particular sequence was found from in a single set of experiment.

^{c)} IgMVH sequences derived from bulk sorted CD19⁺IgM⁺ cells from LP of L2 mice that were identical to known PEC B1a-cell-derived IgMVH sequences from L2 mice.

^{d)} IgMVH sequences derived from bulk sorted IgM⁺CD5⁻ cells from PEC of L2 mice that were identical to known IgMVH sequences derived from LP B cells of L2 mice.

^{e)} Nucleotide sequences belonging to the CDR3 region of displayed sequences. V = Variable region gene family; D = D region gene family; J = J region gene family, V-D = No. of N/P nucleotides found between V and D region; D-J = No. of N/P nucleotides found between D and J region; -J = J nibbling.

Table 2. N/P nucleotide additions at V-D and D-J junctions amongst LP B-cell-derived IgAVH sequences^{a)}

| Mouse | No D | Multiple D | N/P at V-D | N/P at D-J | On both ^{b)} | J nibbling |
|-------|--------|------------|------------|------------|-----------------------|------------|
| L2 | 30.30% | 21.21% | 100% | 96.97% | 96.97% | 72.72% |
| NTG | 26.19% | 14.28% | 90.48% | 97.62% | 90.48% | 59.52% |

^{a)} Data were derived from the analysis of 33 and 42 different IgAVH sequences derived from bulk-sorted LP CD3⁺B220⁻ population from L2 and NT mice respectively. ‘No D’ means no D sequence could be assigned to that particular VH sequence.

^{b)} Frequency of sequences containing N/P nucleotides on both (V-D and D-J) junctions.