|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Taxonomic group** | **SIS.43** | **SIS.57+** | **SIS.57-** | **SIS.71+** | **SIS.71-** | **OI.43** | **OI.57+** | **OI.57-** | **OI.71+** | **OI.71-** | ***P* values\*** |
| **Proteobacteria** | 77.21 | 80.84 | 43.68 | 87.22 | 64.93 | 62.96 | 79.70 | 47.35 | 73.61 | 56.43 | 0.09470 |
| Rhodobacterales | 47.41bc | 8.79 a | 11.13 a | 3.96 a | 9.63 a | 12.94 a | 18.83 ac | 1.86 a | 4.43 a | 6.21 a | 0.00032 |
| Vibrionales | 27.93 | 71.60 | 31.95 | 82.70 | 54.44 | 47.76 | 59.04 | 45.01 | 63.86 | 48.19 | 0.07790 |
| Other Proteobacteria | 1.86 | 0.46 | 0.60 | 0.57 | 0.86 | 2.26 | 1.83 | 0.48 | 5.32 | 2.03 | ND # |
| **Bacteroidetes** | 4.80 ac | 11.99 ac | 45.98 b | 8.59 ac | 30.57 bc | 4.05 a | 5.24 ac | 1.14 ac | 1.47 ac | 4.49 ac | 0.00018 |
| **Verrucomicrobia** | 7.28 a | 3.66 a | 8.22 ac | 2.48 a | 2.53 a | 28.80 bc | 4.87 ac | 0.51 a | 1.01 a | 0.80 a | 0.00348 |
| **Firmicutes** | 0.47 a | 0.70 a | 0.42 a | 0.83 a | 0.48 a | 1.65 a | 7.56 ab | 50.13 b | 22.10 ab | 37.07 ab | 0.00159 |
| **Planctomycetes** | 2.97 b | 0.57 ab | 0.82 ab | 0.42 a | 0.80 ab | 2.09 ab | 0.51 a | 0.34 a | 0.87 ab | 0.50 a | 0.00435 |
| **Saccharibacteria** | 4.87 | 0.41 | 0.13 | 0.07 | 0.22 | 0.06 | 1.02 | 0.02 | 0.25 | 0.09 | 0.13700 |
| **Other Phyla** | 2.17 | 0.42 | 0.54 | 0.28 | 0.39 | 0.18 | 1.02 | 0.49 | 0.56 | 0.39 | ND # |

**Table 2.** Mean relative abundance (%) of main bacterial taxonomic groups in the intestinal tract of whiteleg shrimp from two genetic lines (SIS or OI), in the presence (+) or absence (-) of probiotic treatment, at three different sampling time points (d43, d57 and d71).

a, b, c. Values statistically different from each other based on Tukey adjustment are distinguished by different superscripts

\*determined by ANOVA

#ANOVA was not performed for these groups because they include multiple ranks of the same taxonomic level (i.e. orders or phyla).