|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **OTUs** | **SIS.43** | **SIS.57+** | **SIS.57-** | **SIS.71+** | **SIS.71-** | **OI.43** | **OI.57+** | **OI.57-** | **OI.71+** | **OI.71-** | ***P* values\*** |
| **Proteobacteria** |  |  |  |  |  |  |  |  |  |  |  |
| SD\_Shr-00002 | 6.89 bc | 2.24 a | 3.07 ac | 0.83 a | 1.91 a | 1.73 a | 2.48 a | 0.56 a | 0.59 a | 0.68 a | 0.00011 |
| SD\_Shr-00004 | 2.38 a | 7.45 ac | 7.22 ac | 24.58 bc | 33.16 b | 2.09 a | 3.88 a | 3.03 a | 6.03 a | 5.63 a | 6.22E-06 |
| SD\_Shr-00006 | 21.91 b | 2.78 a | 3.02 a | 1.00 a | 0.90 a | 6.82 a | 4.54 a | 0.39 a | 1.08 a | 2.92 a | 0.000824 |
| SD\_Shr-00010 | 22.02 | 58.69 | 21.32 | 50.01 | 14.78 | 40.06 | 49.16 | 38.13 | 48.11 | 34.66 | 0.114 |
| **Firmicutes** |  |  |  |  |  |  |  |  |  |  |  |
| SD\_Shr-00003 | 0.39 a | 0.52 a | 0.33 a | 0.64 a | 0.38 a | 1.56 a | 2.81 a | 49.00 b | 21.44 ab | 36.14 ab | 0.00161 |
| **Bacteroidetes** |  |  |  |  |  |  |  |  |  |  |  |
| SD\_Shr-00097 | 1.95 a | 8.13 a | 40.11 bc | 2.11 a | 25.68 ac | 3.13 a | 2.46 a | 0.68 a | 0.60 a | 2.30 a | 0.000345 |
| **Verrucomicrobia** |  |  |  |  |  |  |  |  |  |  |  |
| SD\_Shr-00098 | 2.50 a | 1.26 a | 6.43 ab | 0.42 a | 0.83 a | 25.27 b | 4.18 ab | 0.41 a | 0.72 a | 0.51 a | 0.00626 |

**Table 3.** Mean relative abundance (%) of main bacterial Operational Taxonomic Units 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).