**The genetic status of the Hungarian brown trout populations; exploration of a blind spot on the European map of *Salmo trutta* studies**

**Ágnes Ősz1, Ákos Horváth1, György Hoitsy2, Dóra Kánainé Sipos1, Szilvia Keszte1, Anna Júlia Sáfrány1, Saša Marić3, Csaba Palkó4, Balázs Tóth5, Béla Urbányi1, Balázs Kovács1**

**Supplemental Table 1**

**Table S1** Estimates of evolutionary divergence between sequenced haplotypes. The number of base substitutions per site from between sequences are shown, analyses were conducted using the Tamura 3-parameter model. Da: Danubian haplotypes, At: Atlantic haplotypes

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | **Da1** | **Da2** | **Da3** | **Da4** | **Da5** | **Da6** | **At1** | **At2** |
| **Da2** | 0.001 | - |   |   |   |   |   |   |
| **Da3** | 0.001 | 0.001 | - |   |   |   |   |   |
| **Da4** | 0.003 | 0.003 | 0.001 | - |   |   |   |   |
| **Da5** | 0.003 | 0.001 | 0.003 | 0.004 | - |   |   |   |
| **Da6** | 0.003 | 0.003 | 0.001 | 0.003 | 0.001 | - |   |   |
| **At1** | 0.009 | 0.011 | 0.011 | 0.012 | 0.012 | 0.012 | - |   |
| **At2** | 0.008 | 0.009 | 0.009 | 0.011 | 0.011 | 0.011 | 0.001 | - |
| **At3** | 0.011 | 0.012 | 0.012 | 0.013 | 0.013 | 0.013 | 0.001 | 0.003 |