**Table S6.** Pairwise genetic distances (%) estimated between *Pangasius mekongensis*, *Pangasianodon hypophthalmus*, *Pangasius krempfi*, and the published or GenBank-deposited representative Pangasiidae species based on mitogenome coding nucleotide sequences

|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Species/Sequencea  and accession no | Length of coding mtDNA used (nt) | No. of base substitutions/No. of sites in sequencesb | | | | | | | | | |
|  | 1 | 2 | 3 | 4 | 5 | 6c | 7 | 8 | 9 | 10 |
| 1 | *Pangasius mekongensis*  Pmek-PNST-VN (MZ272451) | 15,571 |  |  |  |  |  |  |  |  |  |  |
| 2 | *Pangasius krempfi*  Pkre-VNAG-VN (MZ272453) | 15,576 | 6.57 |  |  |  |  |  |  |  |  |  |
| 3 | *Pangasius pangasius*  Ppan-(Odisha)-IN (KX950698) | 15,575 | 4.24 | 6.36 |  |  |  |  |  |  |  |  |
| 4 | *Pangasius pangasius*  Ppan-(Lucknow)-IN (KC572135) | 15,571 | 4.31 | 6.51 | 0.29 |  |  |  |  |  |  |  |
| 5 | *Pangasius larnaudii*  Plar-(byMiya-JP) (AP012018) | 15,574 | 7.06 | 7.27 | 6.86 | 6.93 |  |  |  |  |  |  |
| 6 | *Pangasius sanitwongsei*  Psan-(Lancang)-CN (MN809630)c | 15,576 | 7.59 | 7.68 | 7.32 | 7.44 | 7.52 |  |  |  |  |  |
| 7 | *Pangasius bocourti (?)*  Psp.-(bySun-CN) (MN842723) | 15,568 | 8.90 | 9.19 | 8.86 | 9.03 | 9.25 | 6.32 |  |  |  |  |
| 8 | *Pangasianodon hypophthalmus*  Phyp-CTIBT-VN (MZ272452) | 15,568 | 8.97 | 9.30 | 8.98 | 9.15 | 9.30 | 6.45 | 0.21 |  |  |  |
| 9 | *Pangasianodon hypophthalmus*  Phyp-(byZhao-CN) (KC846907) | 15,569 | 9.00 | 9.30 | 8.92 | 9.10 | 9.31 | 6.39 | 0.18 | 0.34 |  |  |
| 10 | *Pangasianodon hypophthalmus*  Phyp-(RIA2)-VN (CM010854) | 15,568 | 8.95 | 9.28 | 8.96 | 9.14 | 9.30 | 6.44 | 0.21 | 0.07 | 0.34 |  |
| 11 | *Pangasianodon gigas*  Pgig-(MEKO)-TH (AY762971)c | 15,566 | 8.90 | 9.34 | 8.78 | 8.88 | 9.25 | 8.68 | 7.57 | 7.66 | 7.62 | 7.65 |

a Sequence and species abbreviation is listed in **Table S2**; b Genetic distances were inferred by the analysis of 15,566–15,576 coding nucleotide sequences of the mitochondrial genomes; c Pairwise genetic distance between *Pangasius sanitwongsei* and *Pangasius* spp. (1−5); and between *Pangasius sanitwongsei/Pangasianodon gigas* and *Pn. hypophthalmus* (7−10) are shaded.