**S2 Table. Genetic similarity (%) between the presumed transcribed region of 5S rDNA from several anurans and the more conserved region of the PcP190 sequences of *Physalaemus*, *Leptodactylus*, *Crossodactylus* and *Pseudis*.** Numbers in parentheses indicate the standard error. Only complete monomers sequences from PcP190 were used in this analysis. Because no complete monomer of PcP-6 was achieved, this kind of sequence was not included.

| PcP190 sequences / 5S rDNA sequences | *Physalaemus* spp.[a] | *Leptodactylus latrans*[b] | *Crossodactylus gaudichaudii*[c] | PcP-1 | PcP-2 | PcP-3 | PcP-4 | PcP-5 | PcP-7a | PcP-7b |
|---|---|---|---|---|---|---|---|---|---|---|
| *Lithobates pippiens*[d] | 70.08 (±3.81) | 68.16 (±4.15) | 67.80 (±3.99) | 68.91 (±4.20) | 61.45 (±4.00) | 68.33 (±4.14) | 68.26 (±4.03) | 69.75 (±4.11) | 65.74 (±4.20) | 67.07 (±3.95) |
| *Lithobates catesbeianus*[e] | 70.13 (±3.84) | 68.16 (±4.18) | 67.80 (±4.05) | 68.91 (±4.22) | 61.66 (±4.03) | 68.33 (±4.17) | 67.95 (±4.14) | 69.75 (±4.17) | 65.91 (±4.25) | 67.07 (±3.98) |
| *Pelophylax lessonae*[f] | 68.42 (±3.94) | 65.45 (±4.33) | 67.52 (±4.04) | 66.67 (±4.36) | 59,87 (±4.17) | 69.49 (±4.07) | 66.13 (±4.17) | 66.67 (±4.30) | 62.26 (±4.30) | 64.86 (±3.99) |
| *Pelophylax ridibundus*[g] | 68.42 (±3.94) | 65.45 (±4.33) | 67.52 (±4.04) | 66.67 (±4.36) | 59,87 (±4.17) | 69.49 (±4.07) | 66.13 (±4.17) | 66.67 (±4.30) | 62.26 (±4.33) | 64.86 (±3.99) |
| *Anaxyrus americanus*[h] | 70.03 (±3.84) | 67.43 (±4.21) | 67.80 (±4.02) | 68.91 (±4.23) | 62.29 (±4.01) | 69.17 (±4.12) | 68.28 (±4.08) | 68.91 (±4.18) | 65.74 (±4.33) | 66.73 (±3.91) |
| *Gastrotheca riobambae*[i] | 70.27 (±3.81) | 67.43 (±4.21) | 67.80 (±4.00) | 70.59 (±4.16) | 64.04 (±3.96) | 70.83 (±4.03) | 68.28 (±4.02) | 68.91 (±4.14) | 67.48 (±4.31) | 68.36 (±3.85) |
| *Pseudis tocantins* 5S-I[j] | 61.10 (±5.28) | 56.29 (±5.75) | 58.67 (±5.30) | 59.87 (±5.52) | 56.56 (±5.53) | 58.55 (±5.52) | 59.65 (±5.47) | 62.50 (±5.55) | 62.76 (±4.27) | 60.13 (±4.07) |
| *Pseudis tocantins* 5S-II[k] | 68.03 (±4.81) | 64.76 (±5.14) | 65.67 (±4.83) | 64.47 (±5.34) | 64.39 (±4.97) | 72.37 (±4.94) | 66.97 (±4.92) | 67.11 (±5.10) | 66.55 (±4.25) | 65.91 (±3.93) |
| *Engystomops petersi* 5S-I[l] | 67.29 (±3.86) | 64.89 (±4.21) | 65.25 (±4.04) | 68.07 (±4.26) | 62.98 (±4.01) | 67.50 (±4.17) | 65.57 (±4.08) | 66.39 (±4.19) | 65.97 (±4.19) | 66.54 (±3.92) |
| *Engystomops freibergi* 5S-I[m] | 67.72 (±3.84) | 65.85 (±4.15) | 65.73 (±4.04) | 67.98 (±4.24) | 63.48 (±3.97) | 67.41 (±4.14) | 65.76 (±4.05) | 66.29 (±4.16) | 66.46 (±4.20) | 66.57 (±3.96) |
| *Physalaemus cuvieri* 5S-I[n] | 68.52 (±4.83) | 65.19 (±5.20) | 65.33 (±4.88) | 70.07 (±5.21) | 63.92 (±5.05) | 71.38 (±4.99) | 65.73 (±4.94) | 70.07 (±5.13) | 67.30 (±4.17) | 66.41 (±4.00) |
| *Engystomops petersi* 5S-II[o] | 65.24 (±3.93) | 64.33 (±4.23) | 63.78 (±4.10) | 62.82 (±4.31) | 61.66 (±4.08) | 64.25 (±4.33) | 64.82 (±4.17) | 62.82 (±4.28) | 63.41 (±4.14) | 63.74 (±4.05) |
| *Engystomops freibergi* 5S-II[p] | 66.59 (±3.90) | 65.89 (±4.20) | 65.07 (±4.07) | 64.29 (±4.31) | 61.76 (±4.09) | 65.42 (±4.29) | 65.46 (±4.16) | 64.29 (±4.26) | 63.57 (±4.20) | 64.42 (±3.98) |
| *Physalaemus cuvieri* 5S-II[q] | 69.06 (±4.62) | 66.00 (±5.13) | 66.00 (±4.88) | 66.45 (±5.26) | 58.99 (±5.05) | 70.39 (±4.84) | 66.00 (±4.89) | 69.08 (±4.94) | 62.57 (±4.28) | 65.03 (±3.89) |
| *Xenopus laevis som*[r] | 70.15 (±3.84) | 68.16 (±4.21) | 68.64 (±4.00) | 68.91 (±4.21) | 62.50 (±4.01) | 68.33 (±4.17) | 68.28(±4.09) | 69.75(±4.13) | 66.61 (±4.32) | 67.31 (±3.93) |
| *Xenopus laevis ooc*[s] | 69.58 (±3.77) | 68.19 (±4.09) | 68.67 (±3.92) | 68.58 (±4.08) | 62.40 (±3.91) | 67.17 (±4.05) | 68.31 (±4.00) | 69.56 (±4.01) | 66.18 (±4.23) | 66.71 (±3.87) |
| *Xenopus tropicalis som*[t] | 69.40 (±3.86) | 68.04 (±4.17) | 67.37 (±4.05) | 69.75 (±4.23) | 63.17 (±4.03) | 69.17 (±4.16) | 67.68 (±4.07) | 68.91 (±4.17) | 67.48 (±4.27) | 68.00 (±4.02) |
| *Xenopus tropicalis ooc*[u] | 69.40 (±3.81) | 66.59 (±4.23) | 66.95 (±4.01) | 69.75 (±4.15) | 61.90 (±4.02) | 69.17 (±4.08) | 67.37 (±4.06) | 68.91 (±4.13) | 65.74 (±4.15) | 67.77 (±3.94) |
| *Xenopus borealis ooc*[v] | 69.28 (±3.71) | 68.16 (±4.06) | 67.80 (±3.90) | 68.07 (±4.09) | 61.21 (±3.96) | 67.50 (±4.03) | 67.37 (±4.01) | 68.91 (±4.01) | 64.00 (±4.21) | 65.38 (±4.03) |

[a] *Physalaemus* spp. PcP190 sequences: JF281121.1, JF281117.1, JF281124.1, JF281119.1, KM361675.1 - KM361706.1; [b] *Leptodactylus latrans* PcP190 sequences: KM361718.1 - KM361724.1; [c] *Crossodactylus gaudichaudii* PcP190 sequences: KM361725.1 and KM361726.1; [d] *Lithobates pippiens* 5S rRNA gene: X58368.1; [e] *Lithobates catesbeianus* 5S rRNA gene: X58367.1; [f] *Pelophylax lessonae* 5S rRNA gene: FJ572051.1; [g] *Pelophylax ridibundus*

5S rRNA gene: FJ572052.1; [h]*Anaxytus americanus* 5S rRNA gene: X58365.1 (as *Bufo americanus*); [i]*Gastrotheca riobambae* 5S rRNA gene: M74438.1; [j]*Pseudis tocantins* type I 5S rRNA gene: present work; [k]*Pseudis tocantins* type II 5S rRNA gene: present work; [l]*Engystomops petersi* type I 5S rRNA gene: JF325859.1, JF325866.1 and JF325867.1; [m]*Engystomops freibergi* type I 5S rRNA gene: JF325868.1 - JF325870.1; [n]*Physalaemus cuvieri* type I 5S rRNA gene: JF281127.2, JF281128.2, JF281130.2 and JF281131.2; [o]*Engystomops petersi* type II 5S rRNA gene: JF325847.1, JF325848.1 and JF325858.1; [p]*Engystomops freibergi* type II 5S rRNA gene: JF325844.1 and JF325845.1; [q]*Physalaemus cuvieri* type II 5S rRNA gene: JF281132.2 and JF281134.2; [r]*Xenopus laevis* somatic 5S rRNA gene: M35055.1; [s]*Xenopus laevis* oocyte-specific 5S rRNA gene: J01012.1, J01898.1, K02695.1, M10027.1, M10676.1 and M63899.1; [t]*Xenopus tropicalis* somatic 5S rRNA gene: NR 033271.1; [u]*Xenopus tropicalis* oocyte-specific 5S rRNA gene: X12624.1; [v]*Xenopus borealis* 5S rRNA gene: V01425.1 and K01537.1.