

Molecular and morphological study of Leaping frogs (Anura, Ranixalidae) with description of two new species

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S3 Table. Uncorrected intraspecific pairwise distances between 16S mitochondrial gene sequences. The table gives mean and standard deviation values over all pairwise comparisons among individuals or populations of a species. N is the number of individuals for each species. The original p-distances are shown in percentage.

Species	N	Mean	SD	Min	Max
<i>Indirana beddomii</i>	22	1.2	0.9	0.0	3.5
<i>Indirana bhadrai</i>	1	–	–	–	–
<i>Indirana brachytarsus</i>	64	0.4	0.3	0.0	1.5
<i>Indirana chiravasi</i>	17	0.1	0.1	0.0	0.4
<i>Indirana duboisi</i>	19	0.5	0.3	0.0	1.3
<i>Indirana gundia</i>	21	0.2	0.2	0.0	0.7
<i>Indirana leithii</i>	20	0.7	0.7	0.0	1.7
<i>Indirana paramakri</i>	8	0.6	0.4	0.0	1.3
<i>Indirana salelkari</i>	6	1.2	0.9	0.0	2.2
<i>Indirana sarojamma</i>	5	0.2	0.2	0.0	0.4
<i>Indirana semipalmata</i>	38	1.1	0.7	0.0	2.4
<i>Indirana tysoni</i>	9	0.0	0.0	0.0	0.0
<i>Indirana yadera</i>	12	0.4	0.3	0.0	1.1
<i>Sallywalkerana diplosticta</i>	9	1.1	0.6	0.0	1.7
<i>Sallywalkerana leptodactyla</i>	16	0.3	0.3	0.0	1.4
<i>Sallywalkerana phrynoderma</i>	2	0.0	–	0.0	0.0