

Table S3. Intraspecific and interspecific genetic divergence (K2P model) for 31 species of Hynobiidae

Species	No. of specimens	Intraspecific (Mean/ SE)		Intrageneric (Mean/ SE)	
		COI	16S	COI	16S
<i>Batrachuperus karlschmidti</i>	2	0/0	0/0		
<i>Batrachuperus londongensis</i>	4	0.003/0.002	0.001/0.001		
<i>Batrachuperus pinchonii</i>	10	0.02/0.003	0.004/0.001		
<i>Batrachuperus taibaiensis</i>	2	0/0	0/0	<i>Batrachuperus</i> 0.084/0.007	<i>Batrachuperus</i> 0.011/0.003
<i>Batrachuperus tibetanus</i>	9	0.028/0.005	0.005/0.002		
<i>Batrachuperus</i> sp1	3	0/0	0/0		
<i>Batrachuperus yenyuanensis</i>	1	n/c	n/c		
<i>Hynobius amjiensis</i>	1	n/c	n/c		
<i>Hynobius chinensis</i>	4	0.003/0.002	0/0		
<i>Hynobius arisanensis</i>	1	n/c	n/c		
<i>Hynobius formosanus</i>	1	n/c	n/c		
<i>Hynobius guabangshanensis</i>	1	n/c	n/c	<i>Hynobius</i> 0.094/0.009	<i>Hynobius</i> 0.023/0.004
<i>Hynobius leechii</i>	20	0.004/0.001	0/0		
<i>Hynobius maoershanensis</i>	2	0/0	0/0		
<i>Hynobius quelpartensis</i>	1	n/c	n/c		
<i>Hynobius yangi</i>	1	n/c	n/c		
<i>Hynobius yiwuensis</i>	10	0.029/0.005	0.007/0.002		
<i>Liua tsinpaensis</i>	4	0.018/0.004	0.003/0.002	<i>Liua</i> 0.039/0.005	<i>Liua</i> 0.011/0.003
<i>Liua shihi</i>	18/20*	0.01/0.002	0.002/0.001		
<i>Onychodactylus fischeri</i>	5	0.061/0.008	0.013/0.004	n/c	n/c
<i>Pachyhynobius shangchengensis</i>	7	0.006/0.002	0.001/0.001	n/c	n/c
<i>Paradactylodon gorganensis</i>	1	n/c	n/c	<i>Paradactylodon</i> 0.134/0.016	<i>Paradactylodon</i> 0.026/0.007
<i>Paradactylodon mustersi</i>	1	n/c	n/c		
<i>Pseudohynobius puxiongensis</i>	3	0.006/0.002	0.002/0.001		
<i>Pseudohynobius flavomaculatus</i>	5	0.024/0.005	0/0		
<i>Pseudohynobius kuankuoshuiensis</i>	2	0/0	0/0	<i>Pseudohynobius</i> 0.110/0.009	<i>Pseudohynobius</i> 0.031/0.005
<i>Pseudohynobius shuichengensis</i>	3	0.001/0.001	0.002/0.001		
<i>Pseudohynobius guizhouensis</i>	1	n/c	n/c		
<i>Pseudohynobius jinbo</i>	3	0.006/0.003	0.005/0.003		
<i>Ranodon sibiricus</i>	1	n/c	n/c	n/c	n/c
<i>Salamandrella keyserlingii</i>	11	0.058/0.007	0.019/0.005	n/c	n/c

n/c: evolutionary distances not computed

*: 18 specimens for COI sequence and 20 specimens for 16S rRNA sequence