Supplementary Materials:

Table S1. Numbers of unmatched nucleotides (upper right) and sequence identities (lower left) between the SSU rDNA of five species of the genus *Sterkiella* (ten populations). * indicates the strain sequenced in our study.

	Sp1	Sp2*	Sp3	Sp4	Sp5	Sp6	Sp7	Sp8	Sp9	Sp10
Sp1 *S.histriomuscorum* (HQ615720)	0	1	19	19	18	17	12	22	13	21
Sp2 * *S. histriomuscorum* (KX355209)	0.999	0	20	20	19	18	13	23	14	22
Sp3 *S. histriomuscorum* (AF508770)	0.987	0.985	0	0	1	1	7	21	17	30
Sp4 *S. histriomuscorum* (FJ545743)	0.987	0.985	1.000	0	1	1	7	21	17	30
Sp5 *S. histriomuscorum* (KC193240)	0.988	0.986	0.999	0.999	0	2	6	22	18	31
Sp6 *S. histriomuscorum* (GU942566)	0.988	0.986	0.998	0.998	0.998	0	6	22	16	36
Sp7 *S. cavicola* (GU942565)	0.991	0.989	0.996	0.996	0.996	0.995	0	22	16	31
Sp8 *S. subtropica* (KM924307)	0.985	0.983	0.987	0.987	0.986	0.985	0.986	0	21	31
Sp9 *S. tetracirrata* (KF668619)	0.991	0.989	0.989	0.989	0.989	0.989	0.99	0.987	0	22
Sp10 *S. nova* (AF508771)	0.986	0.984	0.981	0.981	0.981	0.976	0.981	0.981	0.986	0

Table S2. Morphometric characteristics of populations of *Sterkiella histriomuscorum* reported in this and other studies.

Source	BL (μm)	BW (μm)	AZM, length (μm)	AZM no.	FC no.	VC no.	TC no.	LMR no.	RMR no.	CC no.	DK no.	MA Length (μm)	MA Width (μm)
[1]	57-75	28-42	25-32	27-32			4-5	12-18	17-21				
[2]	85-129	41-62	39-53	34-44			4-6	18-25	24-32				
[3]	100-114	47-59	41-47	27-31			4	15-20	20-23				
[4]	66-102	35-57	31-45	26-31	8	5	5	15-21	18-22	3	5-6	14-29	8-15
[5]	85-160	42-85	35-52	29-38	8	5	3-5	17-23	20-24	3	6	15-20	10-15
Current study	93-138	35-60	34-52	28-38	7-8	5	4-5	18-25	22-27	3	5-7	25-42	18-22

BL: Body length; BW: Body width; AZM: Adoral zone, length; FC: Frontal cirri; VC: Ventral cirri; TC: Transverse cirri; LMR: Cirri in left marginal row; RMR: Cirri in right marginal row; CC: Caudal cirri; DK: Dorsal kineties; MA: Macronuclear nodule.

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