

Table S1. Genetic distance matrix for mitochondrial cytochrome C oxidase I sequences. Pairwise genetic distance (p-distance) is in the lower left corner of the matrix, and standard error is in the top right corner denoted by blue text.

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	
<i>S. festinus</i> Southeast U.S.	1	MN88849	-	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		0		2	2	2	2	3	3	2	2	2	2	2	2	6	6	6	6	6	6	8	6	9	7	7	8	7	
	2	MN88849	0.00	-	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		1		2	0	0	0	3	2	2	2	2	2	2	2	6	6	6	6	6	6	7	6	8	7	8	7	7	
	3	MN88850	0.00	0.00	-	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		1		2	0	0	0	3	2	2	2	2	2	2	2	6	6	6	6	6	6	7	6	8	7	8	7	7	
	4	MN88849	0.00	0.00	0.00	-	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		3		2	0	0	0	3	2	2	2	2	2	2	2	6	6	6	6	6	6	7	6	8	7	8	7	6	
	5	MN88849	0.00	0.00	0.00	0.00	-	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		4		2	0	0	0	3	2	2	2	2	2	2	2	6	6	6	6	6	6	7	6	8	7	8	7	6	
<i>S. festinus</i> California	6	KF919668	0.10	0.10	0.10	0.10	0.10	-	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
			6	4	4	4	4		3	2	2	2	2	2	4	3	7	7	7	7	7	7	7	7	8	9	9	7	6
	7	MN88849	0.10	0.10	0.10	0.10	0.10	0.00	-	0.00	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		5		6	3	3	3	3	4		2	2	2	3	3	4	3	6	7	6	6	6	6	6	7	8	8	6	6
	8	MN88849	0.10	0.10	0.10	0.10	0.10	0.00	0.00	-	0.00	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		0		4	1	1	1	1	2	2		0	0	2	2	3	2	7	7	6	6	6	6	6	7	8	8	7	6
	9	MN88849	0.10	0.10	0.10	0.10	0.10	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		1		4	1	1	1	1	2	2	0		0	2	2	3	2	7	7	6	6	6	6	6	7	8	8	7	7
	1	MN88849	0.10	0.10	0.10	0.10	0.10	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		8		4	3	3	3	3	2	2	0	0		2	2	3	2	7	7	7	6	6	6	6	7	8	8	7	7
	1	MN88849	0.10	0.10	0.10	0.10	0.10	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		9		6	3	3	3	3	2	3	2	2	2		0	4	3	7	7	6	6	6	6	6	7	8	8	7	6
	1	MN88849	0.10	0.10	0.10	0.10	0.10	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		2		6	3	3	3	3	2	3	2	2	2	0		4	3	7	7	6	6	6	6	6	7	8	8	7	6
	1	MN88850	0.10	0.10	0.10	0.10	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		3		8	5	5	5	5	9	8	7	7	7	8	8		2	7	7	6	6	6	6	5	7	8	8	7	7
	1	MN88850	0.10	0.10	0.10	0.10	0.10	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	-	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
		4		4	1	1	1	1	5	5	3	3	3	5	3		7	7	6	6	6	6	6	5	7	8	8	7	6
Other	1	KR576466	0.18	0.18	0.18	0.18	0.18	0.17	0.17	0.17	0.17	0.18	0.18	0.18	0.18	-	0.00	0.00	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	
			5		5	2	2	2	2	5	7	9	9	9	9	1	1	6	2		2	5	6	6	7	6	8	7	8

Table S2. Genetic distance matrix for internal transcribed spacer 2 sequences. Pairwise genetic distance (p-distance) is in the lower left corner of the matrix, and standard error is in the top right corner denoted by blue text.

		1	2	3	4	5	6	7	8	9	10	11	12	13
<i>S. festinus</i> California	1 MN887241	-	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00367	0.00367	0.00367	0.00367	0.00367
	2 MN887235	0.00000	-	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00367	0.00367	0.00367	0.00367	0.00367
	3 MN887236	0.00000	0.00000	-	0.00000	0.00000	0.00000	0.00000	0.00000	0.00367	0.00367	0.00367	0.00367	0.00367
	4 MN887237	0.00000	0.00000	0.00000	-	0.00000	0.00000	0.00000	0.00000	0.00367	0.00367	0.00367	0.00367	0.00367
	5 MN887242	0.00000	0.00000	0.00000	0.00000	-	0.00000	0.00000	0.00000	0.00367	0.00367	0.00367	0.00367	0.00367
	6 MN887239	0.00000	0.00000	0.00000	0.00000	0.00000	-	0.00000	0.00000	0.00367	0.00367	0.00367	0.00367	0.00367
	7 MN887238	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-	0.00000	0.00367	0.00367	0.00367	0.00367	0.00367
	8 MN887240	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	0.00000	-	0.00367	0.00367	0.00367	0.00367	0.00367
<i>S. festinus</i> Connecticut	9 MN887247	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	-	0.00000	0.00000	0.00000	0.00000
	10 MN887243	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00000	-	0.00000	0.00000	0.00000
	11 MN887245	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00000	0.00000	-	0.00000	0.00000
	12 MN887244	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00000	0.00000	0.00000	-	0.00000
	13 MN887246	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00674	0.00000	0.00000	0.00000	0.00000	-