

Supplement to: D. V. Goryunov, M. D. Logacheva, M. S. Ignatov, I. A. Milyutina, A. V. Fedorova, and A. V. Troitsky, The Mitochondrial Genome of the Moss *Brachythecium rivulare* (Hypnales, Brachytheciaceae) (ISSN 0006-2979, Biochemistry (Moscow), 2017, Vol. 82, No. 11, pp. 1373-1379)

Table S1. The comparison of selected features of five bryophyte mitochondrial genomes

Species name		<i>B. rivulare</i>	<i>A. rugelii</i>	<i>A. attenuatus</i>	<i>P. patens</i>	<i>T. pellucida</i>
Number of bases		104,460	104,239	104,252	105,340	107,730
Number of features in annotations		224	227	210	140	137
Genes (CDS features without a /pseudo or /pseudogene qualifier):						
spliced:	count:	16	16	16	16	15
	bases:	16,791	16,791	16,788	16,737	15,606
	introns:	27	27	27	26	25
non-spliced	count:	30	30	24	26	26
	bases:	20,937	20,937		18,966	19,140
all	count:	46	46	15570	42	41
	partials:	0	0	0	0	0
	bases (excluding introns):	37,728	37,728	32,358	35,703	34,746
	bases (including introns):	69,800	70,239	64,833	65,559	65,722
	exons:	73	73	67	68	66
	average exon length:	516.8	516.8	482.9	525.0	526.4
	average intron length:	1187.8	1204.1	1202.7	1148.3	1239.0
	average number of exons per gene:	1.58	1.58	1.67	1.61	1.6
	density: genes per kb	0.44	0.441	0.383	0.398	0.38
	density: bases per gene	2270	2266	2606	2508	2627
	average length:	820	820	808	850	847
	average length (including introns):	1517	1526	1620	1560	1602
	coding percentage:	36.1	36.1	31.0	33.8	32.2
	coding percentage (including introns):	66.8	67.3	62.1	62.2	61.0
gene sequence composition	A content:	10,894 (28.87%)	10,877 (28.83%)	9322 (28.8%)	10,455 (29.28%)	9960 (28.66%)

	C content:	6833 (18.11%)	6849 (18.15%)	5624 (17.38%)	6222 (17.42%)	6369 (18.33%)
	G content:	7391 (19.59%)	7400 (19.61%)	6147 (18.99%)	6790 (19.01%)	6831 (19.65%)
	T content:	12,610 (33.42%)	12,602 (33.4%)	11,265 (34.81%)	12,234 (34.26%)	11,586 (33.34%)
	GC percentage:	37.7	37.77	36.38	36.45	37.99
rRNA:	bases (excluding introns):	5231	5230	5246	4655	4822
	bases (including introns):	5231	5230	5246	4655	6287
rRNA sequence composition	A content:	1546 (29.55%)	1543 (29.5%)	1545 (29.45%)	1345 (28.89%)	1387 (28.76%)
	C content:	1094 (20.91%)	1094 (20.91%)	1100 (20.96%)	969 (20.81%)	1031 (21.38%)
	G content:	1400 (26.76%)	1403 (26.82%)	1408 (26.83%)	1268 (27.23%)	1314 (27.25%)
	T content:	1191 (22.76%)	1190 (22.75%)	1193 (22.74%)	1073 (23.05%)	1090 (22.6%)
	GC percentage:	47.68	47.74	47.81	48.05	48.63
tRNA	bases (excluding introns):	1801	1801	1801	1826	1795
	bases (including introns):	1801	1801	1801	1826	1795
tRNA sequence composition:	A content:	462 (25.65%)	460 (25.54%)	460 (25.54%)	463 (25.35%)	458 (25.51%)
	C content:	360 (19.98%)	361 (20.04%)	361 (20.04%)	368 (20.15%)	363 (20.22%)
	G content:	478 (26.54%)	480 (26.65%)	480 (26.65%)	485 (26.56%)	477 (26.57%)
	T content:	501 (27.81%)	500 (27.76%)	500 (27.76%)	510 (27.92%)	497 (27.68%)
	GC percentage:	46.53	46.7	46.7	46.71	46.8
Overall sequence composition:	A content:	30,913 (29.59%)	30,743 (29.49%)	30,738 (29.48%)	31,370 (29.77%)	31,162 (28.92%)
	C content:	20,655 (19.77%)	20,720 (19.87%)	20,720 (19.87%)	20,496 (19.45%)	22,098 (20.51%)
	G content:	22,156 (21.21%)	22,228 (21.32%)	22,229 (21.32%)	22,238 (21.11%)	23,720 (22.01%)
	T content:	30,736 (29.42%)	30,548 (29.3%)	30,565 (29.31%)	31,234 (29.65%)	30,750 (28.54%)
	GC percentage:	40.98	41.2	41.2	40.57	42.53

Table S2. RNA editing sites in the *B. rivulare* mitogenome predicted with *P. patens* as a reference

No.	Gene	Number of C→U and U→C editing sites	Positions of C→U edited sites	Positions of U→C edited sites
1.	atp1	C1 U1	C83573SP	
2.	atp1			U81918SL
3.	atp4	C1	C10361IT	
4.	atp6	U2		U57839SL
5.	atp6			U57996RC
6.	atp8	U1		U10609PS
7.	ccmB	U4		U14137SF
8.	ccmB			U14359PL
9.	ccmB			U14445PS
10.	ccmB			U14632SL
11.	ccmC	C2 U4	C15238VA	
12.	ccmC		C15556VA	
13.	ccmC			U15535SL
14.	ccmC			U15603RC
15.	ccmC			U15613SL
16.	ccmC			U15736PL
17.	ccmFC	C3 U11	C18423LP	
18.	ccmFC		C19973YH	
19.	ccmFC		C19985FL	
20.	ccmFC			U18197LF
21.	ccmFC			U18272PS
22.	ccmFC			U18291SF
23.	ccmFC			U18336SL
24.	ccmFC			U18341HY
25.	ccmFC			U18504SF
26.	ccmFC			U18537SL
27.	ccmFC			U18567SL
28.	ccmFC			U18573SF
29.	ccmFC			U18584LF
30.	ccmFC			U20378RW
31.	ccmFN	C4 U8	C16181FS	
32.	ccmFN		C16744FL	
33.	ccmFN		C17249IT	
34.	ccmFN		C17473FL	
35.	ccmFN			U16154SL
36.	ccmFN			U16913SL
37.	ccmFN			U17147PL
38.	ccmFN			U17152PS

39.	ccmFN			U17156PL
40.	ccmFN			U17158RW
41.	ccmFN			U17527RC
42.	ccmFN			U17554PS
43.	cox1	C1 U4	C1773SP	
44.	cox1			U1796PL
45.	cox1			U2057SL
46.	cox1			U4248SF
47.	cox1			U7721PL
48.	cox2	U5		U64920HY
49.	cox2			U65032SL
50.	cox2			U65035SL
51.	cox2			U65094RW
52.	cox2			U66497HY
53.	cox3	U2		U68672RW
54.	cox3			U69881RW
55.	nad1	U2		U72571RC
56.	nad1			U72626SL
57.	nad2	U3		U53184PL
58.	nad2			U53256PL
59.	nad2			U53592SF
60.	nad3	U2		U84811SL
61.	nad3			U84817SL
62.	nad4	U6		U49980PL
63.	nad4			U50006LF
64.	nad4			U50916SL
65.	nad4			U50925SF
66.	nad4			U51120SL
67.	nad4			U51501SF
68.	nad4L	U1		U28157SL
69.	nad5	C3 U9	C42710FL	
70.	nad5		C45111SP	
71.	nad5		C45606SP	
72.	nad5			U42650LF
73.	nad5			U43676PL
74.	nad5			U43814SL
75.	nad5			U44032RC
76.	nad5			U44164RW
77.	nad5			U45037SL
78.	nad5			U45598SF
79.	nad5			U45679SF
80.	nad5			U48592RW
81.	nad7	C2 U2	C88268CR	
82.	nad7		C88275MT	
83.	nad7			U90454RC

84.	nad7			U90907RC
85.	ORF533	C2	C47247FS	
86.	ORF533		C47259VA	
87.	ORF622	U1		U6221SF
88.	rpl2	C1 U1	C92399FS	
89.	rpl2			U92387SF
90.	rpl6	U1		U98819PL
91.	rps1	C1	C12074SP	
92.	rps14	U2		U96999SL
93.	rps14			U97107SF
94.	rps2	C2	C13610FL	
95.	rps2		C13626IT	
96.	sdh3	C1 U2	C30231FS	
97.	sdh3			U29317SF
98.	sdh3			U30232LF
99.	sdh4	C2	C28692FL	
100.	sdh4		C28718IT	
101.	tatC	C1 U2	C24916LP	
102.	tatC			U24811SL
103.	tatC			U25150TM

Table S3. Microsatellite content of the *B. rivulare* mitogenome

No.	Start	End	Iterations	Motif	Repeat unit length
1.	65	75	11	T	1
2.	11,017	11,026	10	T	1
3.	13,968	13,978	11	A	1
4.	16,612	16,623	12	A	1
5.	16,630	16,640	11	T	1
6.	18,187	18,196	10	T	1
7.	20,386	20,396	11	A	1
8.	21,893	21,902	10	T	1
9.	26,574	26,583	10	T	1
10.	28,429	28,438	10	T	1
11.	33,043	33,052	10	A	1
12.	40,548	40,557	10	A	1
13.	41,954	41,964	11	T	1
14.	46,747	46,756	10	A	1
15.	46,858	46,867	10	T	1
16.	48,020	48,029	10	T	1
17.	49,248	49,258	11	A	1
18.	50,636	50,646	11	T	1
19.	55,375	55,385	11	A	1
20.	55,500	55,509	10	T	1
21.	57,570	57,579	10	T	1
22.	58,445	58,454	10	T	1
23.	64,421	64,430	10	A	1
24.	66,161	66,170	10	T	1
25.	71,175	71,184	10	A	1
26.	85,458	85,467	10	A	1
27.	86,716	86,725	10	T	1
28.	92,360	92,369	10	T	1
29.	93,725	93,734	10	A	1
30.	96,277	96,286	10	A	1
31.	99,027	99,036	10	A	1
32.	100,933	100,942	10	T	1
33.	103,595	103,604	10	A	1
34.	103,914	103,924	11	G	1
35.	482	491	5	TA	2
36.	11,214	11,225	6	TA	2
37.	14,721	14,732	6	AT	2
38.	20,397	20,406	5	TA	2
39.	26,558	26,573	8	TA	2
40.	28,419	28,428	5	TA	2
41.	28,996	29,005	5	TA	2
42.	30,047	30,056	5	AT	2

43.	33,640	33,649	5	AT	2
44.	41,928	41,937	5	TA	2
45.	41,940	41,953	7	TA	2
46.	55,077	55,088	6	AT	2
47.	55,386	55,395	5	TA	2
48.	57,551	57,564	7	TA	2
49.	59,244	59,253	5	AT	2
50.	74,004	74,015	6	CT	2
51.	74,040	74,059	10	TA	2
52.	99,605	99,618	7	TA	2
53.	104,381	104,392	6	AT	2
54.	40,525	40,539	5	GAA	3
55.	49,167	49,184	6	GAA	3
56.	65,544	65,555	4	GAA	3
57.	11,310	11,321	3	ATAG	4
58.	25,771	25,782	3	ATAA	4
59.	34,606	34,637	8	TAAA	4
60.	54,314	54,325	3	ATAA	4
61.	71,411	71,422	3	ATTT	4
62.	91,313	91,324	3	TAGA	4
63.	84,147	84,164	3	TATATT	6