An update on sequenced chloroplast genomes of Bryophytes

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Abstract

The sequencing of complete chloroplast genome of Marchantia polymorpha paved the way to know the structure and organization of chloroplast genomes of other plants. Since then ~747 chloroplast genomes have been sequenced. However, in comparison to the tracheophytes, a small number of complete chloroplast genome sequences of bryophytes are available (only 4 liverworts, 6 mosses and 2 hornwort). This review represents an update on sequenced chloroplast genomes of bryophytes.

Keywords

Bryophytes; hornworts; liverworts; mosses; chloroplast genome

Introduction

Bryophytes are the earliest and the simplest land plants. The extant lineages of bryophytes are classified into hornworts, liverworts, and mosses. Phylogenetic analysis based on chloroplast and mitochondrial genome sequences confirmed paraphyletic origin of bryophytes (Shanker, 2013a; 2013b; 2013c). Green plants contain chloroplasts as an intracellular organelles which have their own autonomously replicating genome. It encode a number of components for the process of photosynthesis (Sugiura, 1989). Among all land plants the first chloroplast genome sequenced was that of a bryophyte, Marchantia polymorpha (Ohyama et al., 1986; Ohyama et al., 1988). However, the chloroplast genome sequencing of bryophytes was outpaced by other plants. Consequently only 12 chloroplast genomes of bryophytes are available in public repositories among 747 total chloroplast genome sequences of green plants (Kapil et al., 2014). These chloroplast genome sequences belong to algae, bryophytes, pteridophytes, gymnosperms, and angiosperms.

Previously a review on sequenced chloroplast genomes of bryophytes including 3 liverworts: Aneura mirabilis, Marchantia polymorpha, Ptilidium pulcherrimum; 2 Mosses: Physcomitrella patens, Syntrichia ruralis, and 1 Hornwort: Anthoceros formosae was published (Shanker, 2012). Since then only 6 new chloroplast genome sequences (3 published and 3 unpublished) have been added in public repository at National Center for Biotechnology Information (NCBI). A list of available chloroplast genomes of bryophytes is given in Table 1. The present review is an update on newly sequenced chloroplast genome of bryophytes (1 each of liverwort, moss, and hornwort).

Pellia endiviifolia (Dicks.) Dumort. (Marchantiophyta)

The chloroplast genome of Pellia endiviifolia consist of 120546 base pairs (bp) with 123 genes, detected based on orthologous relationship from other chloroplast genomes. A strong conservation in the gene content, gene order and overall arrangement was observed in comparison to the chloroplast genome of
Marchantia polymorpha. Moreover, the sequences on the borders of inverted repeats, small single copy, and large single copy were also conserved. The overall A/T content of 64.11% was reported. Pellia endiviifolia possess more compact inverted repeat regions, a 301 bp long non-coding region at the border between inverted repeat b and 3’ rps12, and a 550 bp deletion in the coding region of ycf2. Apart from these differences, 21 introns were also identified in the chloroplast genome of Pellia endiviifolia (Grosche et al., 2012).

**Tetraphis pellucida** Hedw. (Bryophyta)

The chloroplast genome sequence of four-toothed moss, *Tetraphis pellucida*, comprises of 127489 bp and its genome structure was found similar with other available organellar genomes. It possess inverted repeat regions of 9564 bp separated by a small single copy region (18927 bp) and a large single copy region (89434 bp). The GC content was 29.4% which is similar to chloroplast genomes of bryophytes, however, 34-40% lesser than found in seed plants.

Common with *Syntrichia ruralis*, the chloroplast genome of *Tetraphis pellucida* lacks the petN and rpoA genes and the inversion of around 71 kb in the large single copy region. Moreover, the gene content in the inverted repeats of both these species were found identical. Due to an increased total length of intragenic spacer regions in the large single copy region of the *Tetraphis pellucida* chloroplast genome, it is ~5 kb longer than those of *Syntrichia ruralis* and *Physcomitrella patens* (Bell et al., 2014).

**Nothoceros aenigmaticus** (R.M. Schust.) J.C. Villarreal & K.D. McFarland (Anthocerotophyta)

Earlier only a single chloroplast genome sequence of the hornwort *Anthoceros formosae* was available (Kugita et al., 2003). In comparison to other

### Table 1. Sequenced chloroplast genomes of bryophytes available at NCBI.

<table>
<thead>
<tr>
<th>S. No.</th>
<th>Organism Name</th>
<th><em>Accession No.</em></th>
<th>Genome Size (bp)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>1.</td>
<td><em>Aneura mirabilis</em></td>
<td>NC_010359</td>
<td>108007</td>
<td>Wickett et al. 2008</td>
</tr>
<tr>
<td>2.</td>
<td><em>Marchantia polymorpha</em></td>
<td>NC_001319</td>
<td>121024</td>
<td>Ohyama et al. 1986</td>
</tr>
<tr>
<td>4.</td>
<td><em>Ptilidium pulcherrimum</em></td>
<td>NC_015402</td>
<td>119007</td>
<td>Forrest et al. 2011</td>
</tr>
<tr>
<td>5.</td>
<td><em>Nyholmiella obtusifolia</em></td>
<td>NC_026979</td>
<td>122895</td>
<td>NCBI</td>
</tr>
<tr>
<td>6.</td>
<td><em>Orthotrichum rogeri</em></td>
<td>NC_026212</td>
<td>123363</td>
<td>NCBI</td>
</tr>
<tr>
<td>7.</td>
<td><em>Physcomitrella patens</em></td>
<td>NC_005087</td>
<td>122890</td>
<td>Sugiura et al. 2003</td>
</tr>
<tr>
<td>8.</td>
<td><em>Sanionia uncinata</em></td>
<td>NC_025668</td>
<td>124374</td>
<td>NCBI</td>
</tr>
<tr>
<td>9.</td>
<td><em>Syntrichia ruralis</em></td>
<td>NC_012052</td>
<td>122630</td>
<td>Oliver et al. 2010</td>
</tr>
<tr>
<td>10.</td>
<td><em>Tetraphis pellucida</em></td>
<td>NC_024291</td>
<td>127489</td>
<td>Bell et al. 2014</td>
</tr>
<tr>
<td>11.</td>
<td><em>Anthoceros formosae</em></td>
<td>NC_004543</td>
<td>161162</td>
<td>Kugita et al. 2003</td>
</tr>
<tr>
<td>12.</td>
<td><em>Nothocerosaenigmaticus</em></td>
<td>NC_020259</td>
<td>153208</td>
<td>Villarreal et al. 2013</td>
</tr>
</tbody>
</table>

*Chloroplast genome sequence at NCBI will be accessed using this number.
bryophytes it possess an expanded inverted repeat and a type I intron in the 23S ribosomal RNA gene. Recently shotgun sequencing of genomic DNA was used to sequence the chloroplast genome of another hornwort, *Nothoceros aenigmaticus*, and it was found co-linear with chloroplast genome sequences of other bryophytes (Villarreal et al., 2013). The chloroplast DNA of this hornwort contains 153208 bp out of which 11732 bp belongs to each inverted repeat. It contains a total of 124 genes (88 codes for proteins, 32 transfer RNAs and 4 ribosomal RNAs). The bases were found in the following proportion: 32.7% (A), 17.1% (G), 17.9% (C), and 32.3% (T) with a GC content of ~35%. The genes trnL CAU and trnV GAC are the terminal genes of the inverted repeat. The maturase K gene (matK), annotated as a pseudogene in the chloroplast genome of *Anthoceros formosae*, was found as seemingly functional. Three structural differences were observed when the chloroplast genome sequence of *Nothoceros aenigmaticus* was compared with that of *Anthoceros*. Many genes found within the inverted repeat in *Anthoceros* were located in the large single copy region in *Nothoceros*. Moreover, the rpl2 gene was found as a pseudogene and there is a lack of an intron in the rrrn23 gene (Villarreal et al. 2013).

As a concluding remark, despite the importance of bryophytes in the early evolution of land plants their complete nuclear, chloroplast and mitochondrial (Kumar et al., 2014) genomes are poorly represented in public databases. Therefore, efforts are required for the genome sequencing of these early land plants which will in turn help to further solve the mystery of plants adaptation on land.

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**References**


