

**Table S1: Tandem repeats in the *Chlorokybus* mitochondrial genome**

| Repeat unit                  | Size (bp) | No. of units/site <sup>a</sup> | No. of sites | Total no. of units |
|------------------------------|-----------|--------------------------------|--------------|--------------------|
| TGCA                         | 4         | 2–15                           | 249          | 612                |
| ATGCA                        | 5         | 2–39                           | 105          | 383                |
| ATTCC                        | 5         | 2–11                           | 27           | 66                 |
| GGGCT                        | 5         | 2–12                           | 81           | 204                |
| GCACT                        | 5         | 2–34                           | 111          | 356                |
| CAAAG                        | 5         | 2–16                           | 35           | 86                 |
| CCCAA                        | 5         | 2–10                           | 26           | 61                 |
| CCCAAA                       | 6         | 2–13                           | 2            | 15                 |
| GGGCTGCACT                   | 10        | 2–4                            | 11           | 28                 |
| TTCAAATTCAAGAA               | 14        | 6                              | 1            | 6                  |
| TACCACGAAGTGGTAGGATTCGAAGAAT | 28        | 11                             | 1            | 11                 |

<sup>a</sup> The number of units was estimated by allowing one substitution per repeat unit.

**Table S2: Dispersed repeats in the *Chlorokybus* mitochondrial genome**

| Repeat unit | Size (bp) | Copy number   |              |
|-------------|-----------|---------------|--------------|
|             |           | Perfect match | One mismatch |
| AATGCA      | 6         | 520           | 4845         |
| CGGAGA      | 6         | 64            | 1020         |
| TGGCTCT     | 7         | 26            | 410          |
| TGCGCCT     | 7         | 91            | 439          |
| GACCAAG     | 7         | 30            | 338          |
| GTAAGAG     | 7         | 43            | 578          |
| GTGGTAG     | 7         | 216           | 729          |
| GGGCTGC     | 7         | 214           | 1051         |
| TAATCGA     | 7         | 292           | 1851         |
| GCTGCAGC    | 8         | 140           | 1018         |
| GGCTTCCA    | 8         | 29            | 113          |