|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Table 2.** Genome size, chromosome number, and ploidy level data for 13 *Scutellaria* species. Genome sizes for 8 species were measured in this study using flow cytometry. Other genome size, and all chromosome number and ploidy level data was collected from literature. *S. wrightii* and *S. suffrutescens* were not included in the flow cytometry procedure, and genome size, chromosome number, nor ploidy level data has been published. Cell colors indicate phylogenetic clade, as shown in Figure 1. | | | | |
| **Species** | **Estimated genome size (Gbp)** | | **Chromosome number** | **Ploidy level** |
| Measured in this study | Published previously | Published previously | Published previously |
| *S. insignis* |  | 0.46 (Lee & Kim, 2017) | 2n = 26 (Lee, 1967) | 2 (Lee, 1967) |
| *S. indica var. coccinea* |  | 0.38 (Lee & Kim, 2017) |  |  |
| *S. barbata* | 0.52 ± 0.03 | 0.35 (Xu et al., 2020) | 2n = 26 (Xu et al., 2020) | 2 (Hsieh & Huang, 1995) |
| *S. racemosa* | 0.44 ± 0.03 | 0.37 (Cole et al., 2008) | 2n = 18 (Cole et al., 2008) |  |
| *S. strigillosa* |  | 0.38 (Lee & Kim, 2017) | 2n = 32 (Sokolovskaya et al., 1986);  2n = 32 (Nishikawa, 1985) | 4 (Sokoloyskaya et al., 1986);  4 (Nishikawa, 1985) |
| *S. dependens* | 0.44 ± 0.01 |  | 2n = 28 (Sawanomukai et al., 2003);  2n = 32 (Probatova, 2006) | 4 (Sawanomukai et al., 2003);  4 (Probatova, 2006) |
| S. *wrightii* |  |  |  |  |
| *S. suffrutescens* |  |  |  |  |
| *S. baicalensis* | 0.54 ± 0.00 | 0.38 (Xu et al., 2020);  0.41 (Zhao et al., 2019);  0.41 (Cole et al., 2008) | 2n = 18 (Xu et al., 2020);  2n = 18 (Zhao et al., 2019) | 2 (Cheng, 2010) |
| *S. altissima* | 0.39 ± 0.02 |  | 2n = 34 (Lövkvist & Hultgard, 1999) | 4 (Lövkvist & Hultgard, 1999) |
| *S. tournefortii* | 0.39 ± 0.01 |  |  |  |
| *S. leonardii* | 0.50 ± 0.02 |  | 2n = 20 (Gill, 1981) | 2 (Gill, 1981) |
| *S. pekenensis var. alpina* | 0.38 ± 0.02 |  |  |  |