

邵晨, 李耀琪, 罗奥, 王志恒, 席祯翔, 刘建全, 徐晓婷 (2021) 不同生活型被子植物功能性状与基因组大小的关系. 生物多样性, 29, 575–585. <http://www.biodiversity-science.net/CN/10.17520/biods.2020450>

附录 1 基因组大小数据收集参考文献

Appendix 1 References of genome size data

- Bai CK, Alverson WS, Follansbee A, Waller DM (2012) New reports of nuclear DNA content for 407 vascular plant taxa from the United States. *Annals of Botany*, 110, 1623–1629.
- Baziz K, Benamara-Bellagha M, Pustahija F, Brown SC, Siljak-Yakovlev S, Khalfallah N (2014) First karyotype analysis, physical rDNA mapping, and genome size assessment in 4 North African *Astragalus* taxa (Fabaceae). *Turkish Journal of Botany*, 38, 1248–1258.
- Bose B, Kumaria S, Choudhury H, Tandon P (2017) Insights into nuclear DNA content, hydrogen peroxide and antioxidative enzyme activities during transverse thin cell layer organogenesis and ex vitro acclimatization of *Malaxis wallichii*, a threatened medicinal orchid. *Physiology and Molecular Biology of Plants*, 23, 955–968.
- Brem MC, Coulleri JP, Volponi CR, Volponi CR, Ferrucci MS (2018) Genome size, karyotypic features and pollen size in Argentinian species of *Spergula* (Caryophyllaceae). *Boletín de la Sociedad Argentina de Botánica*, 53, 255–266.
- Cao Z, Deng ZN, McLaughlin M (2014) Interspecific genome size and chromosome number variation shed new light on species classification and evolution in *Caladium*. *Journal of the American Society for Horticultural Science*, 139, 449–459.
- Carović-Stanko K, Liber Z, Besendorfer V, Javornik B, Bohanec B, Kolak I, Satovic Z (2010) Genetic relations among basil taxa (*Ocimum* L.) based on molecular markers, nuclear DNA content, and chromosome number. *Plant Systematics and Evolution*, 285, 13–22.
- Carta A, Moretti M, Nardi FD, Siljak-Yakovlev S, Peruzzi L (2015) Seed morphology and genome size in two Tuscan *Crocus* (Iridaceae) endemics: *C. etruscus* and *C. ilvensis*. *Caryologia*, 68, 97–100.
- Castro S, Romeiras MM, Castro M, Duarte MC, Loureiro J (2013) Hidden diversity in wild *Beta* taxa from Portugal: Insights from genome size and ploidy level estimations using flow cytometry. *Plant Science*, 207, 72–78.
- Chae WB, Hong SJ, Gifford JM, Rayburn AL, Sacks EJ, Juvik JA (2014) Plant morphology, genome size, and SSR markers differentiate five distinct taxonomic groups among accessions in the genus *Miscanthus*. *Global Change Biology Bioenergy*, 6, 646–660.
- Chen JJ, Liu XL, Zhu LY, Wang Y (2013) Nuclear genome size estimation and karyotype analysis of *Lycium* species (Solanaceae). *Scientia Horticulturae*, 151, 46–50.
- Chen SC, Cannon CH, Kua CS, Liu JJ, Galbraith DW (2014) Genome size variation in the Fagaceae and its implications for trees. *Tree Genetics and Genomes*, 10, 977–988.
- Chen WH, Kao YL, Tang CY, Tsai CC, Lin TY (2013) Estimating nuclear DNA content within 50 species of the genus *Phalaenopsis* Blume (Orchidaceae). *Scientia Horticulturae*, 161, 70–75.
- Chen ZY, Xiong ZJ, Pan XY, Shen SQ, Geng YP, Xu CY, Chen JK, Zhang WJ (2015) Variation of genome size and the ribosomal DNA ITS region of *Alternanthera philoxeroides* (Amaranthaceae) in Argentina, the USA, and China. *Journal of Systematics and Evolution*, 53, 82–87.
- Chiarini FE, Santíaque FF, Urdampilleta JD, Las Peñas ML (2014) Genome size and karyotype diversity in *Solanum* sect. *Acanthophora* (Solanaceae). *Plant Systematics and Evolution*, 300, 113–125.
- Chumová Z, Krejčíková J, Mandáková T, Suda J, Trávníček P (2015) Evolutionary and taxonomic implications of variation in nuclear genome size: Lesson from the grass genus *Anthoxanthum* (Poaceae). *PLoS ONE*, 10, e0133748.
- Collevatti RG, Dornelas MC (2016) Clues to the evolution of genome size and chromosome number in *Tabebuia alliance* (Bignoniaceae). *Plant Systematics and Evolution*, 302, 601–607.
- Coulleri JP, Urdampilleta JD, Ferrucci MS (2014) Genome size evolution in Sapindaceae at subfamily level: A case study of independence in relation to karyological and palynological traits. *Botanical Journal of the Linnean Society*, 174, 589–600.
- Du WW, Wang XN, Duan Q, Jia WJ, Ma LL, Cui GF, Wang JH (2018) Genome size comparison in 34 *Begonia* L. species. *Journal of Plant Genetic Resources*, 19, 370–376. (in Chinese with English abstract) [杜文文, 王祥宁, 段青, 贾文杰, 马璐琳, 崔光芬, 王继华 (2018) 34 种秋海棠基因组大小比较与分析. 植物遗传资源学报, 19, 370–376.]
- Dudáš M, Fabianová J, Mártonfióvá L, Mártonfi P (2019) *Petasites kablikianus* (Asteraceae) in the Slovak Carpathians: Distribution, chromosome number and genome size. *Botanica Serbica*, 43, 23–30.
- Elansary M, Winkelmann T (2014) Preparing interspecific hybridization in the genus *Lobelia*—Nuclear DNA contents, pollen handling, and localization of crossing barriers. *European Journal of Horticultural Science*, 79, 290–299.
- Fan HJ, Chai Z, Yin FD, Huang HY, Chen LL (2019) Estimation of genome size of *Forsythia suspensa* (Thunb.) vahl by flow cytometry. *Lishizhen Medicine and Materia Medica Research*, 30, 758–760. (in Chinese with English

邵晨, 李耀琪, 罗奥, 王志恒, 席祯翔, 刘建全, 徐晓婷 (2021) 不同生活型被子植物功能性状与基因组大小的关系. 生物多样性, 29, 575–585. <http://www.biodiversity-science.net/CN/10.17520/biods.2020450>

- abstract) [樊慧杰, 柴智, 殷福栋, 黄浩楹, 陈乐乐 (2019) 连翘基因组大小的流式细胞仪测定. 时珍国医国药, 30, 758–760.]
- Frajman B, Rešetnik I, Weiss-Schneeweiss H, Ehrendorfer F, Schönswetter P (2015) Cytotype diversity and genome size variation in *Knautia* (Caprifoliaceae, Dipsacoideae). *BMC Evolutionary Biology*, 15, 1–18.
- Frajman B, Závěská E, Gamisch A, Moser T, The STEPPE Consortium, Schönswetter P (2019) Integrating phylogenomics, phylogenetics, morphometrics, relative genome size and ecological niche modelling disentangles the diversification of Eurasian *Euphorbia seguieriana* s. l. (Euphorbiaceae). *Molecular Phylogenetics and Evolution*, 134, 238–252.
- Fridley JD, Craddock A (2015) Contrasting growth phenology of native and invasive forest shrubs mediated by genome size. *New Phytologist*, 207, 659–668.
- García S, Hidalgo O, Jakovljević I, Siljak-Yakovlev S, Vigo J, Garnatje T, Vallès J (2013) New data on genome size in 128 Asteraceae species and subspecies, with first assessments for 40 genera, 3 tribes and 2 subfamilies. *Plant Biosystems*, 147, 1219–1227.
- Gouja H, García-Fernández A, Garnatje T, Raies A, Neffati M (2014) Genome size and phylogenetic relationships between the Tunisian species of the genus *Calligonum* (Polygonaceae). *Turkish Journal of Botany*, 38, 13–21.
- Gschwend AR, Wai CM, Zee F, Arumuganathan AK, Ming R (2013) Genome size variation among sex types in dioecious and trioecious *Caricaceae* species. *Euphytica*, 189, 461–469.
- Gomes SSL, Saldanha CW, Neves CS, Trevizani M, Raposo NRB, Notini MM, Oliveira Santos M, Campos JMS, Otoni WC, Viccini LF (2014) Karyotype, genome size, and in vitro chromosome doubling of *Pfaffia glomerata* (Spreng.) Pedersen. *Plant Cell, Tissue and Organ Culture (PCTOC)*, 118, 45–56.
- Gomes SSL, Vidal JD, Neves CS, Zorzatto C, Campacci TVS, Lima AK, Koehler S, Viccini LF (2018) Genome size and climate segregation suggest distinct colonization histories of an orchid species from Neotropical high-elevation rocky complexes. *Biological Journal of the Linnean Society*, 124, 456–465.
- He XX, Zhong Q, Zhong YL, Jie YC (2019) Determination of ramie (*Boehmeria nivea*) genome size by flow cytometry. *Molecular Plant Breeding*, 17, 99–103. (in Chinese with English abstract) [何鑫玺, 钟启, 钟英丽, 揭雨成 (2019) 流式细胞术测定苧麻基因组大小. 分子植物育种, 17, 99–103.]
- Hidalgo O, García S, Garnatje T, Mumbrú M, Patterson A, Vigo J, Vallès J (2015) Genome size in aquatic and wetland plants: Fitting with the large genome constraint hypothesis with a few relevant exceptions. *Plant Systematics and Evolution*, 301, 1927–1936.
- Hoang PTN, Schubert V, Meister A, Fuchs J, Schubert I (2019) Variation in genome size, cell and nucleus volume, chromosome number and rDNA loci among duckweeds. *Scientific Reports*, 9, 3234.
- Hoshi Y, Azumatani M, Suyama C, Adamec L (2017) Determination of ploidy level and nuclear DNA content in the Droseraceae by flow cytometry. *Cytologia*, 82, 321–327.
- Huang H, Tong Y, Zhang QJ, Gao LZ (2013) Genome size variation among and within *Camellia* species by using flow cytometric analysis. *PLoS ONE*, 8, e64981.
- Ilhan E, Ozgur S, Tuna GS, Eren AH, Karahan F, Tuna M, Erayman M (2017) Nuclear DNA content variation among *Glycyrrhiza* taxons collected from East Mediterranean. *Fresenius Environmental Bulletin*, 26, 3251–3256.
- Jian H, Zhang T, Wang Q, Yan H, Qiu XQ, Zhou N, Li SB, Chen M, Zhang H, Tang KX (2014) Nuclear DNA content and 1Cx-value variations in genus *Rosa* L. *Caryologia*, 67, 273–280.
- Jiang Y, Xu S, Han X (2017) Investigation of nuclear DNA contents of *Lycoris* species (Amaryllidaceae) with different chromosome number by flow cytometry. *Pakistan Journal of Botany*, 49, 2197–2200.
- Jordan GJ, Carpenter RJ, Koutoulis A, Price A, Brodribb TJ (2015) Environmental adaptation in stomatal size independent of the effects of genome size. *New Phytologist*, 205, 608–617.
- Kang M, Tao JJ, Wang J, Ren C, Qi QW, Xiang QY, Huang HW (2014) Adaptive and nonadaptive genome size evolution in karst endemic flora of China. *New Phytologist*, 202, 1371–1381.
- Kaur N, Datson PM, Murray BG (2012) Genome size and chromosome number in the New Zealand species of *Schoenus* (Cyperaceae). *Botanical Journal of the Linnean Society*, 169, 555–564.
- Krahulcová A, Trávníček P, Krahulec F, Rejmánek M (2017) Small genomes and large seeds: Chromosome numbers, genome size and seed mass in diploid *Aesculus* species (Sapindaceae). *Annals of Botany*, 119, 957–964.
- Kolář F, Lučanová M, Vít P, Urfus T, Chrtěk J, Fér T, Ehrendorfer F, Suda J (2013) Diversity and endemism in deglaciated areas: Ploidy, relative genome size and niche differentiation in the *Galium pusillum* complex (Rubiaceae) in Northern and Central Europe. *Annals of Botany*, 111, 1095–1108.
- Koçyiğit M, Tuna M (2016) Taxonomic remarks on the genus *Sternbergia* L. (Amaryllidaceae) in Turkey based on leaf

邵晨, 李耀琪, 罗奥, 王志恒, 席祯翔, 刘建全, 徐晓婷 (2021) 不同生活型被子植物功能性状与基因组大小的关系. 生物多样性, 29, 575–585. <http://www.biodiversity-science.net/CN/10.17520/biods.2020450>

- anatomy, karyosystematic analysis and nuclear DNA content. *Phytotaxa*, 265, 238–250.
- Kumar PP, Turner IM, Nagaraja Rao A, Arumuganathan K (2011) Estimation of nuclear DNA content of various bamboo and rattan species. *Plant Biotechnology Reports*, 5, 317–322.
- Lattier JD, Ranney TG, Fantz PR, Avent T (2014) Identification, nomenclature, genome sizes, and ploidy levels of *Liriope* and *Ophiopogon* taxa. *HortScience*, 49, 145–151.
- Lee YI, Chung MC, Kuo HC, Wang CN, Lee YC, Lin CY, Jiang H, Yeh CH (2017) The evolution of genome size and distinct distribution patterns of rDNA in *Phalaenopsis* (Orchidaceae). *Botanical Journal of the Linnean Society*, 185, 65–80.
- Leitch IJ, Kahandawala I, Suda J, Hanson L, Ingrouille MJ, Chase MW, Fay MF (2009) Genome size diversity in orchids: Consequences and evolution. *Annals of Botany*, 104, 469–481.
- Li WW, Liu LQ, Pamier A, Wang YN, Cheng G, Liao K (2019) Identification of chromosomal ploidy and DNA content in Xinjiang *Armeniaca vulgaris* by flow cytometry. *Journal of Agricultural Biotechnology*, 27, 542–550. (in Chinese with English abstract) [李雯雯, 刘立强, 帕米尔·艾尼, 王亚楠, 程功, 廖康 (2019) 利用流式细胞术鉴定新疆野杏染色体倍性 DNA 含量. 农业生物技术学报, 27, 542–550.]
- Lin F, Xiao YE, Zhou XY, Tang Y, Gao BH (2018) Estimation of genomic C value of 25 samples of *Iris* plants by flow cytometry. *Acta Agrestia Sinica*, 26, 985–990. (in Chinese with English abstract) [林峰, 肖月娥, 周翔宇, 唐颖, 高步红 (2018) 25 份鸢尾属植物基因组 DNA C 值的流式测定. 草地学报, 26, 985–990.]
- Lipnerová I, Bureš P, Horová L, Šmarda P (2013) Evolution of genome size in *Carex* (Cyperaceae) in relation to chromosome number and genomic base composition. *Annals of Botany*, 111, 79–94.
- Lysak MA, Koch MA, Beaulieu JM, Meister A, Leitch IJ (2009) The dynamic ups and downs of genome size evolution in Brassicaceae. *Molecular Biology and Evolution*, 26, 85–98.
- Mandák B, Krak K, Vít P, Pavlíková Z, Lomonosova MN, Habibi F, Wang L, Jellen EN, Douda J (2016) How genome size variation is linked with evolution within *Chenopodium* sensu lato. *Perspectives in Plant Ecology, Evolution and Systematics*, 23, 18–32.
- Matz F, Hammer K, Schubert I (2003) Coevolution of apomixis and genome size within the genus *Hypericum*. *Sexual Plant Reproduction*, 16, 51–58.
- Meiners J, Debener T, Schweizer G, Winkelmann T (2011) Analysis of the taxonomic subdivision within the genus *Helleborus* by nuclear DNA content and genome-wide DNA markers. *Scientia Horticulturae*, 128, 38–47.
- Mishiba KI, Yamane K, Nakatsuka T, Nakano Y, Yamamura S, Abe J, Kawamura H, Takahata Y, Nishihara M (2009) Genetic relationships in the genus *Gentiana* based on chloroplast DNA sequence data and nuclear DNA content. *Breeding Science*, 59, 119–127.
- Moja S, Guitton Y, Nicolè F, Legendre L, Pasquier B, Upson T, Jullien F (2016) Genome size and plastid *trnK-matK* markers give new insights into the evolutionary history of the genus *Lavandula* L. *Plant Biosystems*, 150, 1216–1224.
- Müller LLB, Zotz G, Albach DC (2019) Bromeliaceae subfamilies show divergent trends of genome size evolution. *Scientific Reports*, 9, 1–12.
- Nani TF, Mesquita AT, Bustamante FDO, Barbosa S, Barbosa JVC, Davide LC (2015) Variation of karyotype and nuclear DNA content among four species of *Plectranthus* L' Héritier, 1788 (Lamiaceae) from Brazil. *Comparative Cytogenetics*, 9, 549–563.
- Ni JJ, He B, Wang WJ, Yu K (2015) Flow cytometric analysis of genome size in *Atractylodes lancea*. *Journal of Chinese Medicinal Materials*, 38, 1153–1156. (in Chinese with English abstract) [倪金菁, 贺彬, 汪文杰, 余坤 (2015) 流式细胞法测定茅苍术基因组大小. 中药材, 38, 1153–1156.]
- Ng CH, Lee SL, Tnah LH, Ng KKS, Lee CT, Madon M (2016) Genome size variation and evolution in Dipterocarpaceae. *Plant Ecology & Diversity*, 9, 437–446.
- Obae SG, West TP (2010) Nuclear DNA content of *Hydrastis canadensis* L. and genome size stability of in vitro regenerated plantlets. *Plant Cell, Tissue and Organ Culture (PCTOC)*, 102, 259–263.
- Omondi EO, Debener T, Linde M, Abukutsa-Onyango M, Dinssa FF, Winkelmann T (2017) Mating biology, nuclear DNA content and genetic diversity in spider plant (*Cleome gynandra*) germplasm from various African countries. *Plant Breeding*, 136, 578–589.
- Palma-Rojas C, Jara-Seguel P, Von Brand E (2012) Nuclear DNA content in Chilean species of *Phycella* and *Rhodolirium* (Amaryllidaceae). *Gayana Botanica*, 69, 184–185.
- Pan YZ, Zhang YC, Gong X, Li FS (2014) Estimation of genome size of four *Panax* species by flow cytometry. *Plant Diversity and Resources*, 36, 233–236. (in Chinese with English abstract) [潘跃芝, 张亦弛, 龚洵, 李富生 (2014)

邵晨, 李耀琪, 罗奥, 王志恒, 席祯翔, 刘建全, 徐晓婷 (2021) 不同生活型被子植物功能性状与基因组大小的关系. 生物多样性, 29, 575–585. <http://www.biodiversity-science.net/CN/10.17520/biods.2020450>

4 种人参属植物基因组大小的测定. 植物分类与资源学报, 36, 233–236.]

- Pang HB, Gao Q, Li YY, Ma CY, Liu HX, Yang CY, Lü RX (2016) Genome size estimation of *Bidens bipinnata* L. by using flow cytometry. *Genomics and Applied Biology*, 35, 1800–1804. (in Chinese with English abstract) [逢洪波, 高秋, 李玥莹, 马纯艳, 刘宏鑫, 杨成瑶, 吕瑞雪 (2016) 利用流式细胞仪测定鬼针草基因组大小. 基因组学与应用生物学, 35, 1800–1804.]
- Parris JK, Ranney TG, Knap HT, Baird WV (2010) Ploidy levels, relative genome sizes, and base pair composition in *Magnolia*. *Journal of the American Society for Horticultural Science*, 135, 533–547.
- Pellicer J, Kelly LJ, Magdalena C, Leitch IJ (2013) Insights into the dynamics of genome size and chromosome evolution in the early diverging angiosperm lineage Nymphaeales (water lilies). *Genome*, 56, 437–449.
- Pellicer J, Kelly LJ, Leitch IJ, Zomlefer WB, Fay MF (2014) A universe of dwarfs and giants: Genome size and chromosome evolution in the monocot family Melanthiaceae. *New Phytologist*, 201, 1484–1497.
- Peruzzi L, Nardi FD, Siljak-Yakovlev S (2015) Genome size estimates for nine species of *Gagea salisb.* (Liliaceae) from the Mediterranean region. *Caryologia*, 68, 347–350.
- Poggio L, Realini MF, Fourastié MF, García AM, González GE (2014) Genome downsizing and karyotype constancy in diploid and polyploid congeners: A model of genome size variation. *AoB Plants*, 6, plu029.
- Prančl J, Kaplan Z, Trávníček P, Jarolímová V (2014) Genome size as a key to evolutionary complex aquatic plants: Polyploidy and hybridization in *Callitriche* (Plantaginaceae). *PLoS ONE*, 9, e105997.
- Razafinarivo NJ, Rakotomalala JJ, Brown SC, Bourge M, Hamon S, Kochko A, Poncet V, Dubreuil-Tranchant C, Couturon E, Guyot R, Hamon P (2012) Geographical gradients in the genome size variation of wild coffee trees (*Coffea*) native to Africa and Indian Ocean Islands. *Tree Genetics and Genomes*, 8, 1345–1358.
- Róis AS, Castro S, Loureiro J, Sádio F, Rhazi L, Guara-Requena M, Caperta AD (2018) Genome sizes and phylogenetic relationships suggest recent divergence of closely related species of the *Limonium vulgare* complex (Plumbaginaceae). *Plant Systematics and Evolution*, 304, 955–967.
- Rothleutner JJ, Friddle MW, Contreras RN (2016) Ploidy levels, relative genome sizes, and base pair composition in *Cotoneaster*. *Journal of the American Society for Horticultural Science*, 141, 457–466.
- Sadhu A, Bhadra S, Bandyopadhyay M (2016) Novel nuclei isolation buffer for flow cytometric genome size estimation of Zingiberaceae: A comparison with common isolation buffers. *Annals of Botany*, 118, 1057–1070.
- Sakhanokho HF, Islam-Faridi N (2013) Nuclear DNA content, base composition, and cytogenetic characterization of *Christia obcordata*. *Journal of the American Society for Horticultural Science*, 138, 205–209.
- Sakhanokho HF, Islam-Faridi MN, Rajasekaran K, Pounders CT (2018) Diversity in nuclear DNA content and ploidy level of *Hedychium* species and hybrids. *Journal of Crop Improvement*, 32, 431–439.
- Sakhanokho HF, Rinehart TA, Stringer SJ, Islam-Faridi MN, Pounders CT (2018) Variation in nuclear DNA content and chromosome numbers in blueberry. *Scientia Horticulturae*, 233, 108–113.
- Sakhanokho HF, Babiker EM, Smith BJ, Drackett PR (2019) High-frequency somatic embryogenesis, nuclear DNA estimation of milkweed species (*Asclepias latifolia*, *A. speciosa*, and *A. subverticillata*), and genome size stability of regenerants. *Plant Cell, Tissue and Organ Culture (PCTOC)*, 137, 149–156.
- Samoluk SS, Chalup L, Robledo G, Seijo JG (2015) Genome sizes in diploid and allopolyploid *Arachis* L. species (section *Arachis*). *Genetic Resources and Crop Evolution*, 62, 747–763.
- Schneider JV, Paule J, Gitaí J, Dressler S, Gusmão CLS, Benko-Iseppon AM (2015) Divergent genome sizes reflect the infrafamilial subdivision of the Neotropical woody Marcgraviaceae. *Botanical Journal of the Linnean Society*, 177, 1–14.
- Shearer K, Ranney TG (2013) Ploidy levels and relative genome sizes of species, hybrids, and cultivars of dogwood (*Cornus* spp.). *HortScience*, 48, 825–830.
- Šlenker M, Zozomová-Lihová J, Mandáková T, Kudoh H, Zhao YP, Soejima A, Yahara T, Skokanová K, Španiel S, Marhold K (2018) Morphology and genome size of the widespread weed *Cardamine occulta*: How it differs from cleistogamic *C. kokaiensis* and other closely related taxa in Europe and Asia. *Botanical Journal of the Linnean Society*, 187, 456–482.
- Štubňová E, Hodálová I, Kučera J, Mártonfiová L, Svitok M, Slovák M (2017) Karyological patterns in the European endemic genus *Soldanella* L.: Absolute genome size variation uncorrelated with cytotype chromosome numbers. *American Journal of Botany*, 104, 1241–1253.
- Suda J, Kyncl T, Jarolímová V (2005) Genome size variation in Macaronesian angiosperms: Forty percent of the Canarian endemic flora completed. *Plant Systematics and Evolution*, 252, 215–238.
- Suda J, Krahulcová A, Trávníček P, Rosenbaumová R, Peckert T, Krahulec F (2007) Genome size variation and species

邵晨, 李耀琪, 罗奥, 王志恒, 席祯翔, 刘建全, 徐晓婷 (2021) 不同生活型被子植物功能性状与基因组大小的关系. 生物多样性, 29, 575–585. <http://www.biodiversity-science.net/CN/10.17520/biods.2020450>

- relationships in Hieracium sub-genus *Pilosella* (Asteraceae) as inferred by flow cytometry. *Annals of Botany*, 100, 1323–1335.
- Sun HG, Wei CX, Yang MX, Gao F, Zhou YJ (2019) Estimation of genome sizes of *Astragalus membranaceus* based on flow cytometry and K-mer analysis. *Chinese Traditional and Herbal Drugs*, 50, 1448–1452. (in Chinese with English abstract) [孙会改, 韦春香, 杨旻啸, 高飞, 周宜君 (2019) 基于流式细胞术和 K-mer 分析的黄芪基因组大小估测. *中草药*, 50, 1448–1452.]
- Tanaka H, Chotekajorn A, Kai S, Ishigaki G, Hashiguchi M, Akashi R (2016) Determination of genome size, chromosome number, and genetic variation using inter-simple sequence repeat markers in *Lotus* spp. *Cytologia*, 81, 95–102.
- Timbó ALO, Pereira RC, Souza Sobrinho F, Davide LC (2014) Nuclear DNA content and chromosome number in *Brachiaria* spp. genotypes. *Revista Ciência Agronômica*, 45, 62–67.
- Trávníček P, Ponert J, Urfus T, Jersáková J, Vrána J, Hřibová E, Doležel J, Suda J (2015) Challenges of flow-cytometric estimation of nuclear genome size in orchids, a plant group with both whole-genome and progressively partial endoreplication. *Cytometry*, 87, 958–966.
- Tyagi A, Sandhya, Sharma P, Saxena S, Sharma R, Amitha Mithra SV, Solanke AU, Singh NK, Sharma TR, Gaikwad K (2019) The genome size of clusterbean (*Cyamopsis tetragonoloba*) is significantly smaller compared to its wild relatives as estimated by flow cytometry. *Gene*, 707, 205–211.
- Veleba A, Bureš P, Adamec L, Šmarda P, Lipnerová I, Horová L (2014) Genome size and genomic GC content evolution in the miniature genome-sized family Lentibulariaceae. *New Phytologist*, 203, 22–28.
- Veleba A, Šmarda P, Zedek F, Horová L, Šmarda J, Bureš P (2017) Evolution of genome size and genomic GC content in carnivorous holokinetics (Droseraceae). *Annals of Botany*, 119, 409–416.
- Veselý P, Bureš P, Šmarda P, Pavlíček T (2012) Genome size and DNA base composition of geophytes: The mirror of phenology and ecology? *Annals of Botany*, 109, 65–75.
- Vižintin L, Kosovel V, Feoli Chiapella L (2012) Genetic characterization of *Genista sericea* Wulfen (Cytiseae – Fabaceae) as revealed by nuclear DNA content and ITS nrDNA region analysis. *Acta Botanica Croatica*, 71, 195–205.
- Voronkova M, Banaev E, Tomoshevich M, Ak-Lama T (2018) Variation of nuclear DNA content in seeds of *Nitraria schoberi* L. *BIO Web of Conferences*, 11, 00046.
- Wang CY, Zhang K, Liang F, Cui B, Ma RL (2015) Estimation of genome size of *Cymbidium faberi* Rolfe. *Northern Horticulture*, 11, 86–90. (in Chinese with English abstract) [汪琛颖, 张坤, 梁芳, 崔波, 马润林 (2015) 蕙兰 (*Cymbidium faberi* Rolfe) 基因组大小测定. *北方园艺*, 11, 86–90.]
- Wang GY, Yang YP (2016) The effects of fresh and rapid desiccated tissue on estimates of Ophiopogoneae genome size. *Plant Diversity*, 38, 190–193.
- Wang GY, Meng Y, Yang YP (2017) Genome size variation among and within Ophiopogoneae species by flow cytometric analysis. *Brazilian Journal of Botany*, 40, 529–537.
- Wang X, Chen HZ, Li YF, Han R, Chen H (2018) Determination of genome size of *Halocnemum strobilaceum*. *Journal of Biology*, 35, 100–102. (in Chinese with English abstract) [王霞, 陈慧泽, 李永峰, 韩榕, 陈惠 (2018) 盐节木基因组大小的测定. *生物学杂志*, 35, 100–102.]
- Wang X, Zhou JY, Sun HG, Yu RM, Gao F, Zhou YJ (2018) Genomic survey sequencing and estimation of genome size of *Ammopiptanthus mongolicus*. *Journal of Plant Genetic Resources*, 19, 143–149. (in Chinese with English abstract) [王雪, 周佳熠, 孙会改, 禹瑞敏, 高飞, 周宜君 (2018) 新疆沙冬青基因组调查测序与基因组大小预测. *植物遗传资源学报*, 19, 143–149.]
- Wang YP, Xiao BY, Xiong WB, Wu SD, Ji AJ, Duan LX (2018) Genome size analysis for *Morinda officinalis* how using flow cytometry. *Traditional Chinese Drug Research and Clinical Pharmacology*, 29, 657–660. (in Chinese with English abstract) [王云鹏, 肖博允, 熊文波, 吴世丹, 季爱加, 段礼新 (2018) 流式细胞术测定巴戟天基因组大小. *中药新药与临床药理*, 29, 657–660.]
- Wolf DE, Steets JA, Houliston GJ, Takebayashi N (2014) Genome size variation and evolution in allotetraploid *Arabidopsis kamchatica* and its parents, *Arabidopsis lyrata* and *Arabidopsis halleri*. *AoB Plants*, 6, plu025.
- Wong C, Murray BG (2012) Variable changes in genome size associated with different polyploid events in *Plantago* (Plantaginaceae). *Journal of Heredity*, 103, 711–719.
- Yan HH, Martin SL, Bekele WA, Latta RG, Diederichsen A, Peng YY, Tinker NA (2016) Genome size variation in the genus *Avena*. *Genome*, 59, 209–220.
- Ye LJ, Zhang ZR, Sun ZX, Tian S, Zhang ZY (2015) The determination of nuclear DNA content (2C-value) on some

邵晨, 李耀琪, 罗奥, 王志恒, 席祯翔, 刘建全, 徐晓婷 (2021) 不同生活型被子植物功能性状与基因组大小的关系. 生物多样性, 29, 575–585. <http://www.biodiversity-science.net/CN/10.17520/biods.2020450>

- representative genus and species of Magnoliaceae. *Plant Diversity and Resources*, 37, 605–610. (in Chinese with English abstract) [叶林江, 张志荣, 孙志霞, 田双, 张志勇 (2015) 木兰科主要属种核 DNA 含量(2C-值)的检测. *植物分类与资源学报*, 37, 605–610.]
- Yin YY, Zhong PS, Zhang GQ, Chen LJ, Zeng SJ, Li MH, Liu ZJ (2016) Morphological, genome-size and molecular analyses of *Apostasia fogangica* (Apostasioideae, Orchidaceae), a new species from China. *Phytotaxa*, 277, 59–67.
- Younis A, Ryu KB, Co VT, Hwang YJ, Jee SO, Kim MS, Kim CK, Lim KB (2013) Analysis of chromosomes and nuclear DNA content in nine genotypes of *Cymbidium*. *Korean Society for Floricultural Science*, 21, 158–161.
- Žabka M, Ďurišová L, Eliáš P, Baranec T (2018) Genome size and ploidy level among wild and cultivated *Prunus* taxa in Slovakia. *Biologia*, 73, 121–128.
- Zahradníček J, Chrtek J, Ferreira MZ, Krahulcová A, Fehrer J (2018) Genome size variation in the genus *Andryala* (Hieraciinae, Asteraceae). *Folia Geobotanica*, 53, 429–447.
- Zhang J, Wang Y, Ma XJ, Tan F, Li M, Li YJ (2018) Determination of chromosome ploidy and genome size of *Salix matsudana* based on flow cytometry. *Jiangsu Agricultural Sciences*, 46(22), 40–43. (in Chinese) [张健, 王莹, 马祥建, 谈峰, 李敏, 李玉娟 (2018) 基于流式细胞术的旱柳染色体倍性与基因组大小测定. *江苏农业科学*, 46(22), 40–43.]
- Zhang LL, Cao B, Bai CK (2013) New reports of nuclear DNA content for 66 traditional Chinese medicinal plant taxa in China. *Caryologia*, 66, 375–383.
- Zhang NN, Yang J, Sun WB (2014) Genome size estimation of *Viburnum* (Adoxaceae) species by using flow cytometry. *Plant Diversity and Resources*, 36, 730–736. (in Chinese with English abstract) [张宁宁, 杨静, 孙卫邦 (2014) 利用流式细胞仪测定荚蒾属植物的基因组大小. *植物分类与资源学报*, 36, 730–736.]
- Zhu M, Wang YP, Xiong WB, Luo YG, Duan LX, Lu XY (2018) Genome size estimation for three Iridaceae plants by using flow cytometry. *Journal of Chinese Medicinal Materials*, 41, 2306–2310. (in Chinese with English abstract) [朱敏, 王云鹏, 熊文波, 罗盈光, 段礼新, 陆幸妍 (2018) 流式细胞仪测定三种鸢尾科植物基因组的大小. *中药材*, 41, 2306–2310.]
- Zonneveld BJM (2015) Nuclear genome sizes of 343 accessions of wild collected *Haworthia* and *Astroloba* (Asphodelaceae, Aloooideae), compared with the genome sizes of *Chortolirion*, *Gasteria* and 83 *Aloe* species. *Plant Systematics and Evolution*, 301, 931–953.