

Publication

A phylogenetically informed search for an alternative; *Macrostomum*; model species, with notes on taxonomy, mating behavior, karyology, and genome size

JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)**ID** 4530427**Author(s)** Schärer, Lukas; Brand, Jeremias N.; Singh, Pragya; Zadesenets, Kira S.; Stelzer, Claus-Peter; Viktorin, Gudrun**Author(s) at UniBasel** [Schärer, Lukas](#) ;**Year** 2020**Title** A phylogenetically informed search for an alternative; *Macrostomum*; model species, with notes on taxonomy, mating behavior, karyology, and genome size**Journal** Journal of Zoological Systematics and Evolutionary Research**Volume** 58**Number** 1**Pages / Article-Number** 41-65**Keywords** *Macrostomum*; Systematics; Karyology

The free-living flatworm *Macrostomum lignano* is used as a model in a range of research fields-including ageing, bioadhesion, stem cells, and sexual selection-leading to the recent establishment of genome assemblies and transgenics. However, the *Macrostomum* community has run into a roadblock following the discovery of an unusual genome organization in *M. lignano*, which could impair the development of essential resources and tools. Briefly, *M. lignano* has undergone a whole-genome duplication, followed by rediploidisation into a $2n=8$ karyotype (distinct from the canonical $2n=6$ karyotype in the genus). Although this karyotype appears visually diploid, it is in fact a hidden tetraploid (with rarer $2n=9$ and $2n=10$ individuals being pentaploid and hexaploid, respectively). Here we report on a phylogenetically-informed search for close relatives of *M. lignano*, aimed at uncovering alternative *Macrostomum* models with the canonical karyotype and a simple genome organization. We taxonomically describe three new species: the first, *Macrostomum janickei* n. sp., is the closest known relative of *M. lignano*, and shares its derived genome organization; the second, *Macrostomum mirumnovem* n. sp., has an even more unusual genome organization, with a highly variable karyotype based on a $2n=9$ base pattern; and the third, *Macrostomum cliftonensis* n. sp., does not only show the canonical $2n=6$ karyotype, but also performs well under standard laboratory culture conditions and fulfils many other requirements. *M. cliftonensis* is a viable candidate for replacing *M. lignano* as the primary *Macrostomum* model, being outcrossing and having an estimated haploid genome size of only 231 Mbp.

Publisher Wiley**ISSN/ISBN** 1439-0469**edoc-URL** <https://edoc.unibas.ch/75725/>**Full Text on edoc** No;**Digital Object Identifier DOI** 10.1111/jzs.12344**ISI-Number** WOS:000503198100001**Document type (ISI)** Article