S2 Text. Note on bdelloid genome sizes

Mark Welch & Meselson (2003) [1] conducted fluorometric DNA quantitation in oocytes to assess genome size in a number of bdelloid species, including A. vaga and A. ricciae (then called "Adineta sp.1" [2]). The total oocyte DNA content was estimated to be ca. 0.49 pg (479 Mb) for A. ricciae and ca. 0.74 pg (724 Mb) for A. vaga (Table 3 of [1]). However, when these values were imported to the Animal Genome Size Database [3] (www.genomesize.com), they were accidentally switched (and then divided by two to derive "haploid" C-values, which is arguably inapplicable to the asexual bdelloids). Between December 2003 and January 2018, this online resource erroneously reported a C-value of 0.36 pg for A. ricciae (352 Mb), and of 0.25 pg for A. vaga (244 Mb). This last value was cited by Flot et al. [4] when validating the assembly of A. vaga; by coincidence, the database entry appeared to confirm their size estimate of ca. 250 Mb (based on assembly span and coverage analysis). The transposition error in the online database has been corrected as of February 2018 (T. Ryan Gregory, pers comm.) and it is now clear that the fluorometric measurements of absolute genome size [1] differ substantially from assembly size, both as estimated previously [4] and in this work. Even in relative terms, the fluorometric data [1] suggest that A. ricciae has a markedly smaller genome than A. vaga (\sim 66%), which is not reflected in the relative assembly sizes. The reason for these substantial discrepancies between fluorometric and bioinformatic results is unclear (David Mark Welch, pers comm.). Owing to these uncertainties, cytological measures of genome size were not used to validate the A. ricciae assembly or to interpret other patterns in these data.

References

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