Anisogamy evolved with the reduced sex-determining region

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Abstract:

Volvocine green algae shape a model lineage for the evolutionary analysis in emergence of anisogamy and oogamy [1-3]. They diverged from a single-celled, isogamous *Chlamydomonas*-like ancestor 2 MYA to give rise to a wide variety of organisms including *Chlamydomonas reinhardtii*, 8- or 16-celled isogamous *Gonium*, 32-celled isogamous *Yamagishiella*, 32-celled anisogamous *Eudorina*, and >500-celled oogamous *Volvox*, enabling experimental comparisons [3]. Charlesworth [4] theoretically predicted close linkage between gamete size-determining genes and the mating type locus (*MT*, sex-determining chromosomal region) for the emergence of anisogamy. However, the molecular basis for the origin of anisogamy has been still unknown even based on the recent comparative genome analyses of *MT* of the isogamous and oogamous volvocine algae (*Chlamydomonas*, *Gonium* and *Volvox*) [5,6]. To approach the molecular basis of the evolution of anisogamy, we here focus on two closely related volvocine algae that phylogenetically link isogamy to anisogamy: advanced isogamous *Yamagishiella* and ancestral anisogamous *Eudorina*. We generated *de novo* nuclear genome assemblies of both sexes of *Yamagishiella* and *Eudorina*. The resultant assemblies contained sex dimorphic haplotype regions that corresponded to their *MT*. In contrast to the large and complex *Volvox carteri MT* which exceeds 1 Mb in size [5], *Yamagishiella unicocca* and *Eudorina* sp. *MT* were small and simple with only two sex-specific genes, *minus* dominance gene (*MID*) and gamete recognition gene (*FUS1*) that were localized in *minus*/male and *plus*/female *MT*, respectively. There were no other sex specifically-predicted gene models. *Eudorina* sp. female and male *MT* haplotypes were highly reduced, measuring 90 and 7 kb in size, respectively. Since sizes of female gametes of *Eudorina* and isogametes of *Yamagishiella* are almost identical to those of their vegetative cells [7], the emergence of anisogamy from isogamy in the *Yamagishiella*- or *Eudorina*-like ancestor might have been mainly based on the evolution of formation of small male gametes or sperm. While *MID* is a master gene determining the mating type *minus* in isogamous *C. reinhardtii* [9], the ortholog of oogamous *Volvox carteri MID* (*VcMID*) determines formation of sperm packets (bundles of sperm or male gametes) by successive divisions of reproductive cells in sexual spheroids [10]. Since both *Eudorina* and *Volvox* perform similar sperm packet formations [7], *Eudorina* sp. *MID* and *VcMID* are assumed to have essentially the same function to initiate the spermatogenesis. Thus, the changes in regulatory mechanisms under the existence of *MID* should be responsible for the emergence of spermatogenesis in the *Eudorina*-like ancestor.

References: (optional)

1. Charlesworth, D. and Charlesworth, B. (2010). Curr. Biol. *20*, R519–R521.
2. Umen, J.G. (2011). Curr. Opin. Microbiol. *14*, 634–641.
3. Hiraide. R., Kawai-Toyooka, H., *et al*. (2013). Mol. Biol. Evol. *30*, 1038–1040.
4. Charlesworth B. (1978). J. Theor. Biol. *73*, 347–357.
5. Ferris, P., Olson, B.J.S.C., *et al*. (2010). Science *328*, 351–354.
6. Hamaji, T., Mogi, Y., *et al*. (2016). G3 (Bethesda) *6*, 1179–1189.

7. Nozaki, H. (1996). J. Plant Res. *109*, 353–361.
8. De Hoff, P.L., Ferris, P., *et al*. (2013) PLoS Genet. *9*, e1003724.
9. Ferris, P.J. and Goodenough, U.W. (1997). Genetics *146*, 859–869.
10. Geng, S., De Hoff, P. and Umen J.G. (2014). PLoS Biol. *12*, e1001904.