

Mating type locus-like regions in the homothallic species *Volvox africanus*.

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Abstract:

In the oogamous genus *Volvox*, there are two types of sex determination, heterothallism and homothallism. The former type has genetically determined sexes and each sex produces male or female sexual spheroids (dioecism), whereas the latter has both sexes in a single strain producing monoecious sexual spheroids (containing both eggs and sperm packets) or sometimes dioecious sexual spheroids. Sexual differentiation in heterothallic species of the unicellular and colonial/multicellular volvocine algae is controlled by a sex-determining or mating type locus (*MT*) containing *MID* in the minus or male strain (Ferris and Goodenough 1997; Ferris et al 2010; Hamaji et al 2016). Comparative analyses of *MT* loci in volvocine algae are important to elucidate the molecular and genomic basis of evolution of sexual differentiation.

We recently reported that a *MID* ortholog is present in the homothallic species *V. africanus* which produces both male and monoecious sexual spheroids in a single strain (Yamamoto et al. 2017). In *V. africanus*, monoecious spheroid-specific down regulation of gene expression of the *MID* ortholog was demonstrated (Yamamoto et al 2017). Furthermore, androgonidia (male reproductive cells) in the male strain of heterothallic *V. carteri* develop to be eggs by experimental suppression of *VcMID* expression (Geng et al. 2014). Therefore, we hypothesized that the homothallic species *V. africanus* might have evolved directly from a male strain of the heterothallic ancestor by modification of the regulation system of *MID* expressions in sexual spheroids (Yamamoto et al. 2017).

In order to test our hypothesis of the evolution of homothallic *V. africanus* (Yamamoto et al. 2017), we here generated *de novo* nuclear genome assemblies of a strain of *V. africanus* and male and female strains of its closely related heterothallic species *V. reticuliferus* (Nozaki et al. 2015). Our comparative analyses of these three genomes revealed male and female haplotypes of *V. reticuliferus* *MT*, and *MT*-like regions in the *V. africanus* genome. Male and female haplotypes in *MT* of *V. reticuliferus* measured approximately 1 Mb long and contained a male-specific *MID* ortholog and a female-specific *FUS1*-like sequence. In *V. africanus*, an *MT*-like region measured approximately 1.2 Mb long and harbored a *FUS1*-like sequence. However, *MID* ortholog of *V. africanus* was found in another scaffold, in which five tandemly repeated *MID* sequences and homologs of two gametologs in *V. carteri* (*SPS1* and *MTF1436*) constituted a very small genome region (ca. 50 kb).

References:

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