Erratum

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Transcriptional control of sexual development in *Cryptococcus neoformans*

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In the article by Mead and Hull published in Journal of Microbiology 2016; 54, 339–346, the following references should be cited as below.

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In addition to Mat2, two other sequence-specific High Mobility Group Domain proteins exist in *C. neoformans* (Hgr1 and Hgr2) and both more closely resemble PRFs from other systems than Mat2 (Kruzel, 2011; Mead, 2015; Mead *et al.*, unpublished data). While neither protein is the PRF in *C. neoformans*, both play roles in sexual development. *HGR1* is required for wild type levels of filamentation and spore formation; that is, crosses between *hgr1Δ* strains exhibit fewer, shorter filaments than wild type crosses, fewer numbers of spores, and a lower frequency of spore germination (Kruzel, 2011; Mead, 2015; Mead *et al.*, unpublished data). In addition, *HGR1* interacts genetically with the filament regulators *STE12a* and *STE12α* (Kruzel, 2011; Mead *et al.*, unpublished data). *HGR2* is required for wild type levels of spore production and normal frequencies of spore germination (Mead, 2015; Mead *et al.*, unpublished data). Deletion of both *HGR1* and *HGR2* results in a nearly complete loss of spore production (Mead, 2015; Mead *et al.*, unpublished data).

MAT2, *HGR1*, and *HGR2* form an interconnected network where each gene is required for proper expression of the other two (Mead, 2015; Mead *et al.*, unpublished data). This high level of interdependency suggests that rewiring of the ancestral network occurred, and it resulted in Mat2 assuming the role of a PRF (Kruzel *et al.*, 2012).

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