Erratum to: Genotypic Characterization of Environmental Isolates of *Cryptococcus gattii* from Puerto Rico

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A number of errors have gone uncorrected in the manuscript. Importantly, mating type assignments were incorrect for the samples initially examined in this study. Mating type determination was repeated by the laboratory at Albany after receiving a note from Drs. Carlos Rios-Velazquez and Alejandro Ruiz about ongoing study of Dr. Edmond J. Byrnes III in the laboratory of Dr. Joe Heitman at Duke University. According to Dr. Byrnes unpublished findings most of the *C. gattii* isolates from Puerto Rico are *MATa*. We have also found similar results after repeating this part of the experiments. We would like to make following corrections:

Yaliz Loperena-Alvarez and Ping Ren contributed equally to this work.

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Yaliz Loperena-Alvarez and Ping Ren contributed
equally to this work.

Abstract, p. 1

Line 9: “*Cryptococcus*” should be italicized as
“*Cryptococcus*”.

Line 14: “MAT strains” should be “majority of
them were *MATa* strains”.

Figure 1, Legend, p. 3

Delete “(arrow indicates sample lesion)”

Delete “the arrows indicate the detritus collected
and the hole sampled”

Mating Type Determination by PCR Pheromone Genes, p. 4

Left column 1st paragraph last sentence (line 9–
13): “PCR ...mating types.” should be “The new
primer pairs of V1823 (5′-CGCGATGTTGGCTGTA
ATGG-3′), V1824 (5′-ATAAAAAGTTCGAGGTTT
CCCAC-3′) and V1825 (5′-TAAGGAGAAAGAGC
GACGTC-3′), V1826 (5′GGCATGTTCAATTGGG
TTGC-3′) were designed for PCR-Sequencing of
MFα1 and *MFα1* gene fragments from *Cryptococcus*
gattii, because previous primer set V191 -192 works

best when it is used only for mating type screening on special gel; we have now confirmed that this primer set is not useful for nucleotide sequencing owing to the small size of the amplicons. The *MATa* sequences were submitted to Gene Bank under the accession numbers HM535310–HM535326.

Results and Discussion, p. 4

Line 2: Number “22” should be “23 with one sample found non-viable subsequently”

Table 1, p. 4

Total number of samples collected should be “710” instead of “705”. Total positive samples should be “23” instead of “22”.

Results and Discussion, p. 5

Left column 2nd paragraph 1st sentence (line 19–21): “Flow cytometry ... being *C. gattii*.” should be read as “Flow cytometry analysis demonstrated that all 22 isolates were haploid. Seventeen isolates were *C. gattii*; subsequent typing showed 16 of the 17 isolates to be *MATa*.” Right column line 5: “similar to” should be “different from”.

Right column line 9–12: “Perhaps, the relative number ... is present in Puerto Rico.” should be “Surprisingly, *MATa* strains were dominant relative to *MATα* in the environment in Puerto Rico area”.

References, pp. 6–7

There are no numbers assigned to references in the bibliography to match with number of cited reference in the text. Corrected list of the references is as follows:

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