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AUTHOR CORRECTION

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Author Correction: Genomic epidemiology of the UK outbreak of the emerging human fungal pathogen *Candida auris*

Johanna Rhodes¹, Alireza Abdolrasouli^{2,3}, Rhys A. Farrer¹, Christina A. Cuomo⁴, David M. Aanensen^{1,5}, Darius Armstrong-James², Matthew C. Fisher¹ and Silke Schelenz²

Correction to: *Emerging Microbes & Infections* (2018) 7,43 <https://doi.org/10.1038/s41426-018-0045-x>; published online 29 March 2018

Upon publication of the original article¹ the authors were contacted by Dr. Trevor Bedford who has provided invaluable methods to improve the temporal analysis work presented in this paper. Due to conversations with Dr. Bedford the authors improved the calculation of the time to most recent common ancestor (TMRCA) and the clock rate of evolution within *Candida auris*, to take into account the whole genome, not just the variable sites.

This author correction provides an updated Fig. 2 and an updated paragraph related to this new information. The updated information has been indicated in **bold** in the below paragraphs.

- Fitting root-to-tip regression showed there was a linear relationship between sampling time (measured in days) and the expected number of nucleotide substitutions along the tree, demonstrating clock-like evolution across the timescale of the outbreak (Fig. 2). There was a **good** association between genetic distances and sampling dates ($R^2 = 0.3737$), showing that the dataset has a reasonable temporal signal for further molecular clock analysis. **Given 0.5757 substitutions per site per year in variable sites, which represent 0.01% of total sites across the genomes, the evolutionary rate of *C. auris* nuclear DNA equates to 5.7×10^{-5} substitutions per site per year, which is comparable to nuclear DNA of other fungal species,**

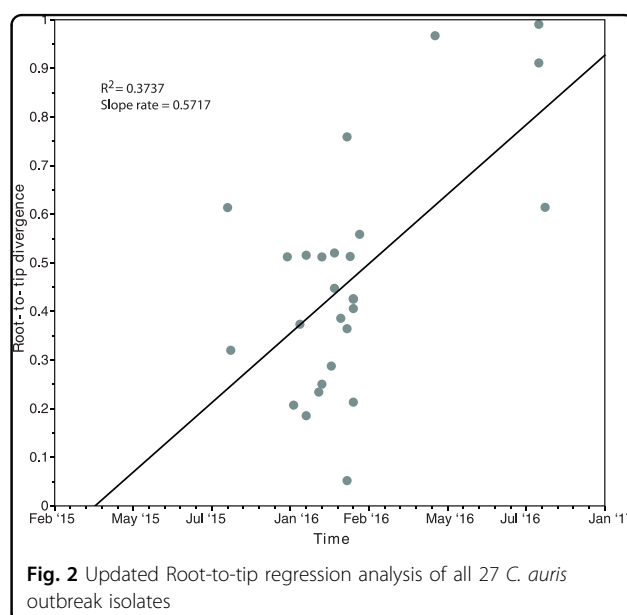


Fig. 2 Updated Root-to-tip regression analysis of all 27 *C. auris* outbreak isolates

such as *Schizosaccharomyces pombe* beer strains (3.0×10^{-3} ²⁸) and *Saccharomyces cerevisiae* (5.7×10^{-3} ²⁹). The time to the most recent common ancestor (TMRCA) was estimated to be late **March 2015**, weeks prior to the first patient identified with a *C. auris* infection.

- Future alignments will require clade-specific references due to the large evolutionary distances between the South American/African and Indian/Pakistani clades. Although the mode of introduction into the UK is unknown, temporal analysis of the outbreak isolates placed the most recent common ancestor as **late March 2015**, which correlates closely to the first confirmed infection within the hospital **weeks later**, suggesting a recent introduction into the UK.

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