Erratum: Genome sequencing of Sporisorium scitamineum provides insights into the pathogenic mechanisms of sugarcane smut

Youxiang Que1*, Liping Xu1*, Qibin Wu1, Yongfeng Liu1, Hui Ling1, Yanhong Liu2, Yuye Zhang1, Jinlong Guo1, Yachun Su1, Jiebo Chen3, Shanshan Wang1 and Chengguang Zhang2

Erratum to: BMC Genomics 2014, 15:1184
doi:10.1186/1471-2164-15-1184

Following publication of this article it came to our attention that we neglected to acknowledge the inspiration for figure four (Figure 1 here) and text associated with the figure provided by Guus Bakkeren and colleagues http://dx.doi.org/10.1016/j.fgb.2008.04.005 (9). We have included text to replace that appropriated from the review article by Bakkeren and colleagues. We sincerely apologise for the oversight.

Results and discussion
Characterization of mating type loci in S. scitamineum

For mating to occur, two haploid cells of different mating-type need to recognize each other and fuse to form the infectious dikaryon. Mating is regulated by two loci, a and b, which harbor conserved genes. At the a locus, these genes encode pheromones and pheromone receptors while at the b locus two subunits of a heterodimeric transcription factor are encoded [1].

The bipolar species S. scitamineum and U. hordei as well as the tetrapolar species U. maydis and S. reilianum possess one divergently transcribed gene pair that encode the homeodomain proteins bE (HD1) and bW (HD2). The MAT-1 locus, gene order, orientation, as well as the genomic context are conserved in the b mating-type genes except for the U. hordei MAT-2 locus figure four (Figure 1 here). Interestingly, both bE and bW mating-type genes are present in the genomes of Ustilaginaeae including the two genera of Ustilago and Sporisorium.

In addition to the b mating-type complexes, smut fungi contain genes necessary for cell–cell recognition which are located in the a mating type loci. The detailed structure of these loci has been determined for both the MAT-1 alleles of S. scitamineum and U. hordei, an allele of U. maydis, and for all three alleles of S. reilianum figure four (Figure 1 here). Both U. maydis and U. hordei have two alleles of an a mating system with one pheromone receptor (pra) and one functional pheromone gene (infra) per locus.

In S. scitamineum and U. hordei which have a bipolar mating system, the a and b loci are linked and the mating-type locus (MAT) segregates as one locus. However, in tetrapolar species such as S. reilianum and U. maydis, these genetic loci segregate independently [2]. In S. scitamineum, the a locus encodes a lipopeptide with pheromone and pheromone membrane receptor functions responsible for cell recognition and compatible hyphal fusion, whereas the b locus encodes transcription factors that control the expression of genes responsible for the maintenance of the dikaryotic hyphal growth in plants figure four (Figure 1 here). During their life cycle, Sporisorium presents two distinct monokaryotic and dikaryotic stages. The monokaryotic stage is marked by haploid cells that grow sapropathically and are not able to cause disease, while in the second phase, dikaryotic hyphae are formed by mating (sexual crossing) and are able to infect the host. The induction of the pathogenic program in S. scitamineum implies not only strong morphological changes (from yeast-like to hyphal) but also genetic changes (haploid to dikaryotic transition).

Evolution of bipolar mating in S. scitamineum may have been beneficial for the fungus because it promoted inbreeding and stabilization of the genome. The same process has been proved to be beneficial for the transposon elements (TEs). A study concluded that inbreeding helped fix TEs within a population in U. hordei [10]. In tetrapolar species, such as U. maydis and S. reilianum, outcrossing increases heterozygosity [2].
Overall, sequence analysis and comparison of the mating-type regions of tetrapolar and bipolar smut fungi revealed that they are not fundamentally different. Bipolar and tetrapolar smuts as well as related species contain the genes for these \(a\) and \(b\) mating-type complexes. In the bipolar species \(S. scitamineum\) and \(U. hordei\), these mating-type complexes are encoded on the same chromosome and in a recombination-suppressed region ensuring genetic linkage.

**References**

1. Bakkeren G, Kämper J, Schirawski J. Sex in smut fungi: structure, function and evolution of mating-type complexes. Fungal Genet Biol. 2008;45 suppl 1:15–21.

2. Laurie JD, Ali S, Linning R, Mannhaupt G, Wong P, Güldener U, et al. Genome comparison of barley and maize smut fungi reveals targeted loss of RNA silencing components and species-specific presence of transposable elements. Plant Cell. 2012;24(5):1733–45.