2. Factors affecting meiotic stability of the *bufl* gene in *Magnaporthe grisea*

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Meiotic stability of the *bufl* gene in *Magnaporthe grisea* is controlled by interaction with the homologous chromosome. It appears to be correlated with the homologous *bufl* loci having different physical organizations. Two hypotheses were tested that were related to *bufl* instability: Hypothesis 1: *bufl* instability is caused by mis-pairing between the homologous *bufl* loci. Physical mapping was used to identify strains with different physical organizations at their *bufl* loci. Genetic crosses were then used to incorporate these loci into both the *matl-1* and *matl-2* mating type backgrounds. Compatible strains were then mated so that the loci were paired in all possible combinations. Regardless of origin, the *bufl* gene was stable in most crosses involving *bufl* loci with identical organizations. In the one exceptional cross it was lost at a low frequency. Loci that were originally from strains 2539 and Arcadia were perfectly stable in all crosses. However, the loci from ML33 and Guy11, which both suffered deletion in crosses with strain 2539, were stable in crosses with Arcadia. Arcadia has a *bufl* locus structure that is quite different from that of ML33 or Guy11, indicating that mis-pairing *per se* is insufficient to induce instability at the *bufl* locus. Instead, we propose that specific structural differences promote the loss of *bufl*. Hypothesis 2: The frequency of deletion is determined by the physical organization of the *bufl* locus. This was tested by crossing strains with different *bufl* locus structures to the same tester strain and measuring deletion frequency. Surprisingly, the frequency varied significantly between different crosses of the same strains. Furthermore, if the *bufl* gene survived deletion through crosses, it became progressively more stable in each subsequent generation. This suggests that *bufl* deletion frequency is determined primarily by genetic background.

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