
Genetic diversity in *A. flavus*

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Divergent populations in *A. flavus*

- AF-producing & non-producing isolates
 - Vegetative compatibility groups
 - Small & large sclerotial variants
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Differences between *A. flavus* S and L

S

Consistent production of aflatoxins

Smaller and more abundant sclerotia

Fewer conidia on AM media

L

Larger sclerotia

Abundant conidia

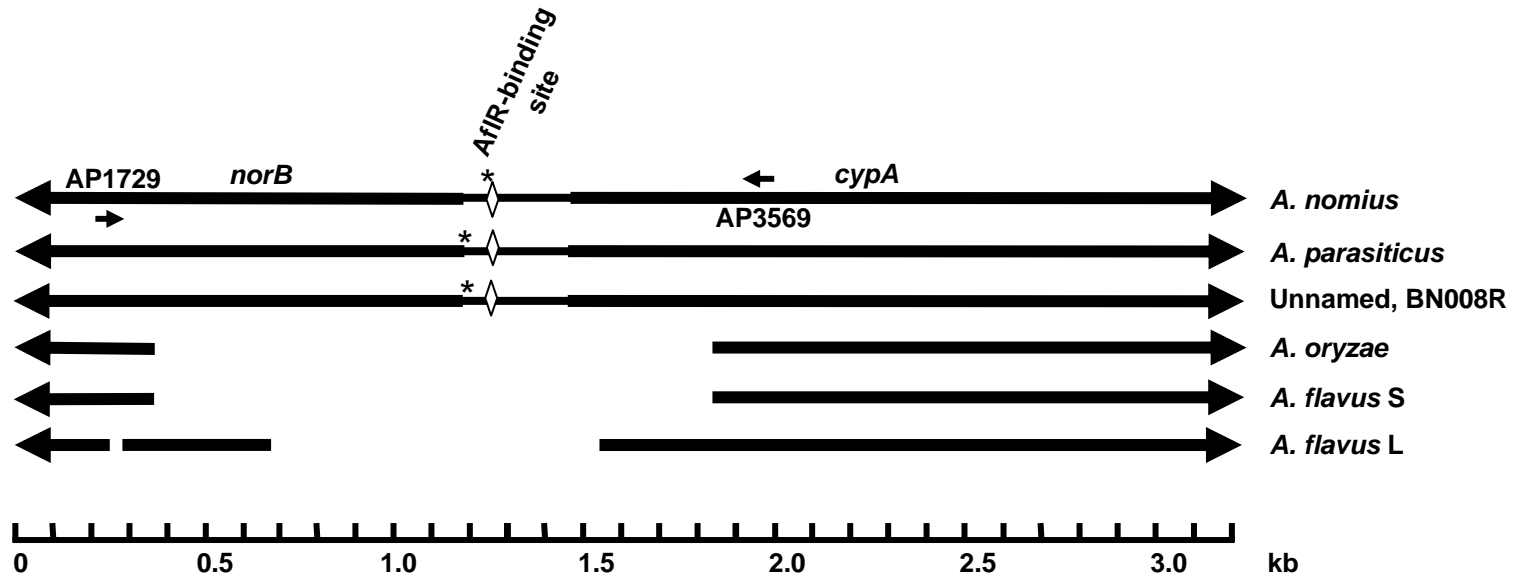
More consistent pectinase production

Comparison of aflatoxin production by closely related strains

Type	AM	NO	UR	Ratio AM to NO
AFL	240	190	102	1.3
AFS	2230	670	1130	3.3
AP	3260	330	5200	9.8
S _{BG}	60	950	1470	0.1

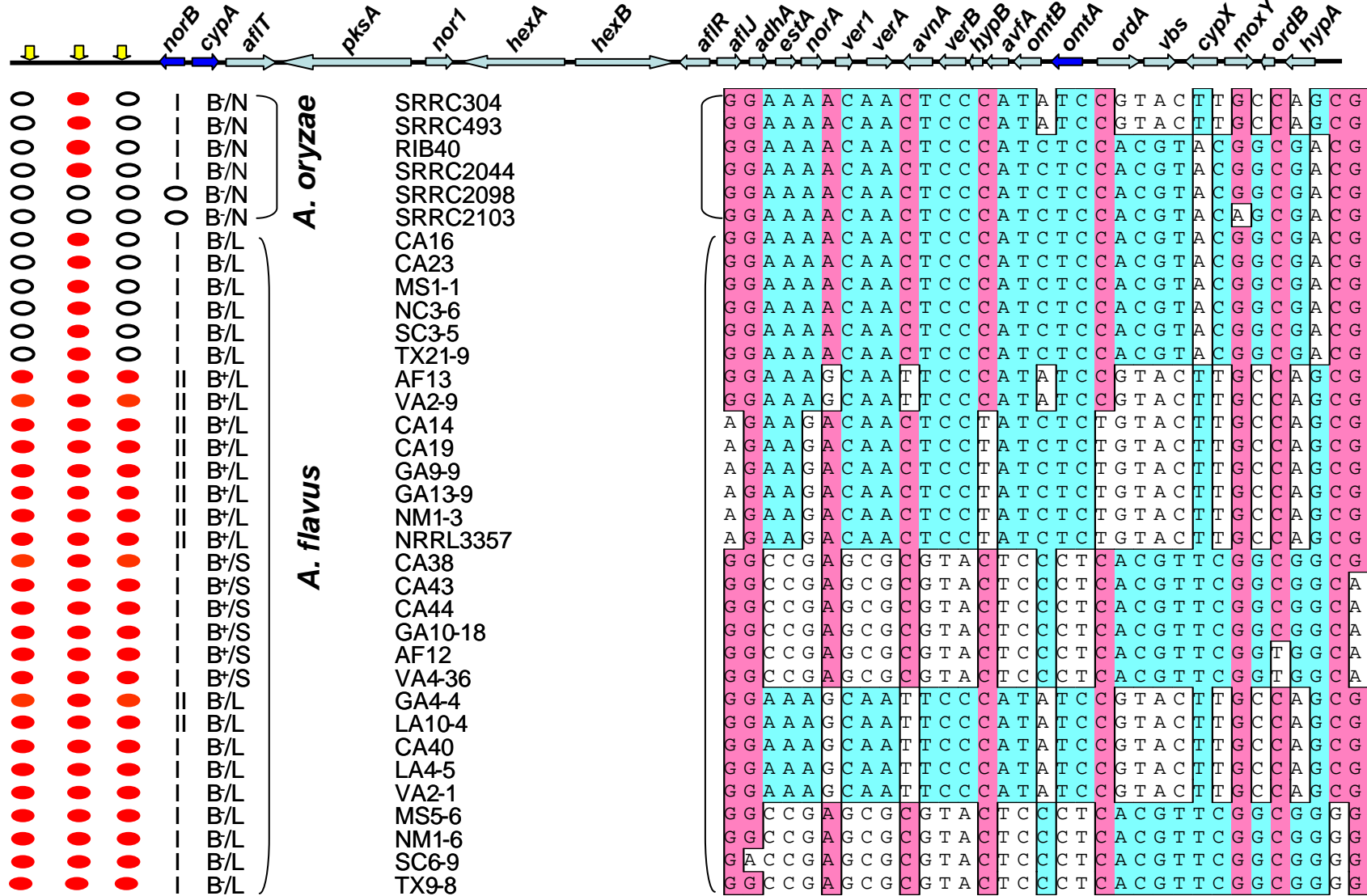
AF yield ug/70 ml culture-4 days

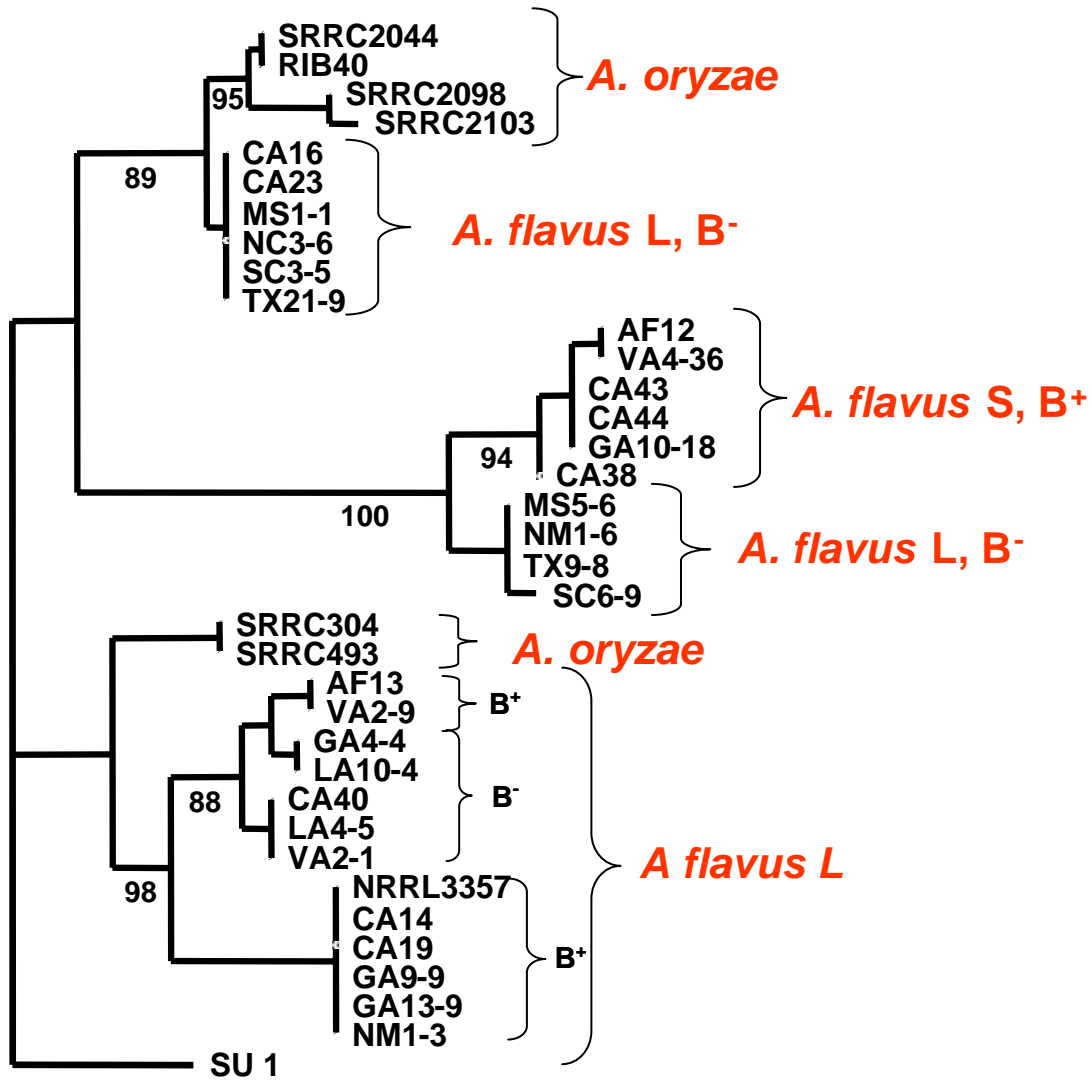
Deletions in the *norB-cypA* intergenic region



Deletions

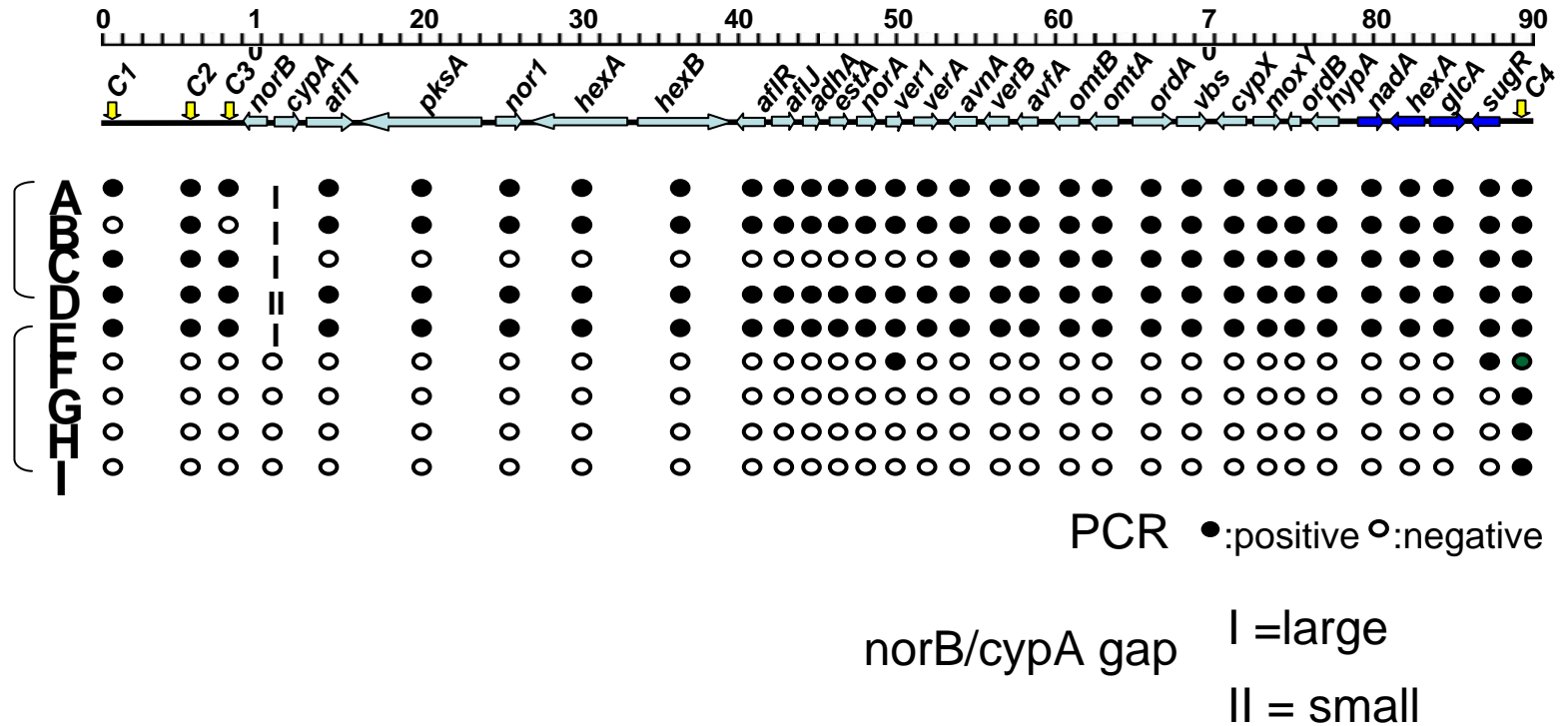
Polymorphisms in *omtA* gene



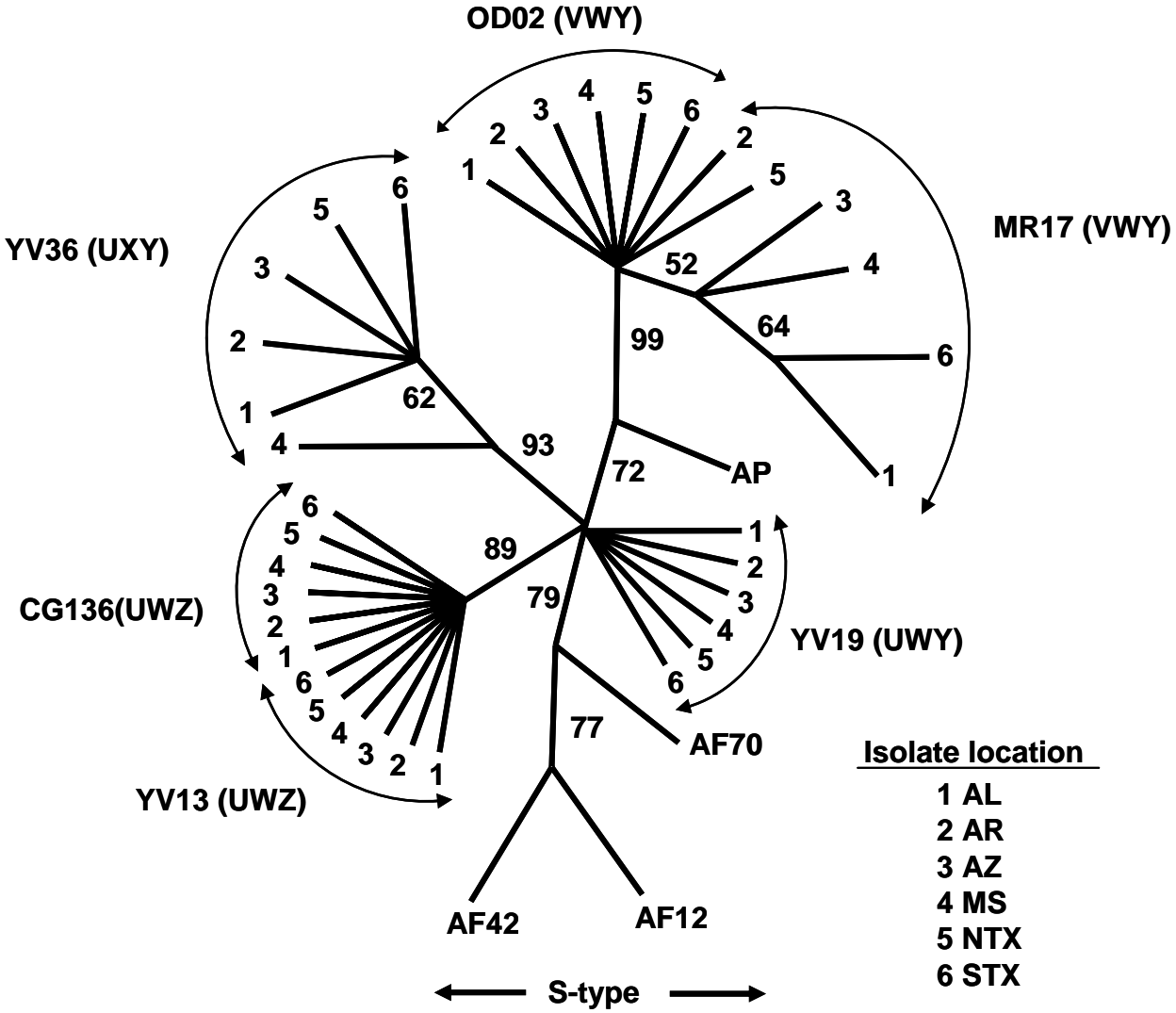


▯ 0.01 substitutions/site

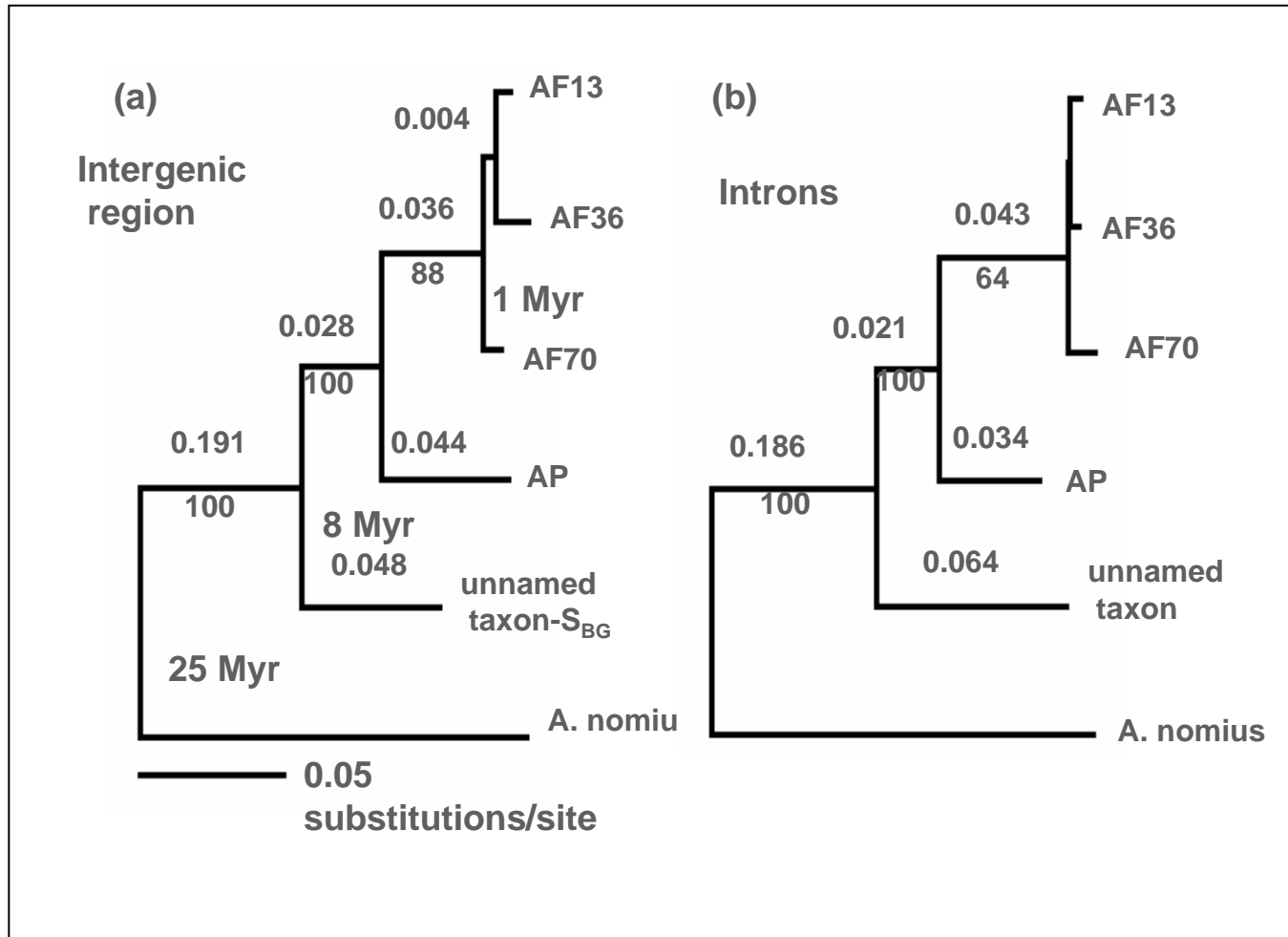
Deletion patterns in *A. flavus* aflatoxin gene clusters



Diversity by Vegetative Incompatibility



Phylogenetic relationships based on AF gene cluster



Strain degeneration

- Position of cluster near the telomere
 - Carbon-rich environment may be conducive to gene loss
 - Stress and AF production
 - Transposon movement
 - Epigenetic changes
 - Recombination
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Implications for bioremediation of aflatoxin contamination

- Suitable competitor strains must compete against both S and L strain *A. flavus*
 - Recombination is not frequent among VCG populations
 - Naturally occurring atoxigenic isolates are more likely to be found in agricultural than in non-agricultural soils.
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Conclusions

- VCG separation is a stimulus to diversification
 - Aflatoxin production is associated with only certain VCGs
 - S morphotype *A. flavus* isolates produce more AF than the L morphotype isolates
 - The *A. flavus* L strain is probably ancestral to the S strain and to *A. oryzae*
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A. flavus S_B

A. flavus L

