

Alternative splicing in response to fungal niche shift

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Motivation and Aim: Alternative splicing (AS) is a ubiquitous regulatory mechanism of gene expression in eukaryotes since it enables different mRNA and/or protein isoforms to be generated from the same gene [1]. Although AS plays important roles in fungi, how it changes along with fungal niche shift is understudied, especially for the pathogenic fungi [2].

Results: Taking entomopathogenic fungus *Metarhizium robertsii* as an example, we comprehensively investigated the genome-wide changes of AS in response to the niche shift during fungal infecting host. We analyzed 37 RNA-seq datasets of samples collected from three typical niches, including the saprophytic, infecting, and parasitic stages. Thousands of novel splicing events were then identified, but they were generally lowly occurred in comparison with those annotated in the genome. We found the infecting and parasitic stages gave rise to more AS events than the saprophytic stage. We also found that AS could act independently from the expression level through changing the structure of major isoforms and/or the co-splicing patterns. Eventually, a set of AS genes were uncovered as likely to be important in the niche shift during infection.

Conclusion: Together, our study reveals the significant changes and potential roles of AS in mediating pathogenic fungal adaptations to different niches in the process of infection.

References

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