

SUPPLEMENTARY TABLE I. Summary of analysis with separate gene running Maximum Likelihood (ML), ML-BS = bootstrapping/no. of taxa

Genes	No. taxa	<i>Beauveria</i> clade	<i>C.</i> <i>locustiphila</i> clade	<i>C.</i> <i>acridophila</i> clade	<i>C.</i> <i>diapheromeriphila</i> clade
<i>nrSSU</i>	99	45/14	100/2	100/6	96/3
<i>nrLSU</i>	98	30/14	100/2	100/6	96/3
<i>EF-1α</i>	105	96/24	94/1	100/6	100/3
<i>RPB1</i>	96	99/26	100/2	100/7	100/3
<i>RPB2</i>	84	100/17	100/1	60/4	—