

**Exon 1**  
 AIGGAAGGTAAGTCTGCTATCTCCTGCCCCAGTATCTCCACCTGGCAATCTTCGGCCTTCCGAAAGCTCGCGGCTCGCGGAACGTTCCGGCTGGCGAATACCAGGATGCGGATGCCAAACGGCGGAA  
 M E

**Intron 1**  
 CGATCCCGAGCTTCAGCACATCTCCCTTTCCATCTATCCCGCATCACTGCTATCTGTCCACCGCCTCACTGCTTTGACGCTCACGTTGCCCGGCGAGATGAGCTGAGGACAGATCA

**Exon 2**  
 CATGCTAAACAACGCATTAAAGAAGAGGTTGGCGCCCTGGTTATCGACAATGGGTAAAGCCATCTCGAACCTCATCGGTTACTTCCGTCGCTATCGACCGCGAAATATCCCGCGTGGTCAAGCGGCTTGG

**Intron 2**  
 E E V A A L V I D N G

**Exon 3**  
 ACGGGCTGTCCGAGCCGGGAGTACATGCTAATCTGTCCCTTATAGTTCCGGGTATGTGCAAGGCCGGTTTCGCCGGTGCAGGACGGTCCCTCGTGTCTTCCGTAAGTTTCCACCTCCTCAATCTTTT

**Intron 3**  
 S G M C K A G F A G D D A P R A V F

**Exon 4**  
 GGGCTGTTGAGCTTGCCATTCCGGAGCTACCCGGAGACACGAGCTAACCCACCGCATAGCGTCCATTGTGGTCGGCCCCGTCAICATGGGTGAGTATACGCCGCCCTCCTTTTCGTTCAATTCGGAC

**Intron 4**  
 P S I V G R P R H H G

**Exon 5**  
 CCTCCCCATCCAAAAGAATATGAACGATATCCCAGCTATGAAAATTTCCGCTAAACATTTGGCTATAGCAICATGATCGGTATGGGCCAGAAAGGACTCGTACGTCGGGTGACGAGGCACAGTCCCAAGC

**Lepact-F**  
 I M I G M G Q K D S Y V G D E A Q S K

**Exon 5**  
 GTGGTATCCTCACCGCTTCGGTACCCCAATTGAGCACCGGTGTTGTCAACCACTGGGACGACATGGAGAAATTTGGCACCAACACCTTCTACAACGAGCTGCGTGTGGCTCCCAGGAGGACACCCCAATCC

**Exon 5**  
 R G I L T L R Y P I E H G V V T N W D M E K I W H T F Y N E L R V A P E E H P I

**Exon 5**  
 TGCTCACGGAGGGTCCCATCAATCCCAAGTCCAAACCGTGAAGAGATGACCGCAGATTGTGTTGCGAAACCTTCAACGCAACCGGCCCTTCTACGTCACATCCAGGCCGTGCTGCCCTGTACGGCATCTG

**Exon 5**  
 L L T E A P I N P K S N R E K M T Q I V F E T F N A P A F Y V N I Q A V L S L Y A S

**Exon 5**  
 GTCGTACCACTGGTATCGTTTTGGACTCTGGTGAJGGTGTCACTCACGTCGTGCCCAITTACGAAAGGTTTCGGCTCGCCCGCACGCCAITTCGACGJGTGACAJGGCTGGCCGTGATTTGACCCGACTAC

**Exon 5**  
 G R T T G I V L D S G D G V T H V V P I Y E G F A L P H A I A R V D M A G R D L T D Y

**Exon 5**  
 CTGATGAAGATCTGGCCGAGCGGGTACTCCCTTCTCCACCCTGCGGAGCGGAAAATCGTCCGTCGACATCAAGGAGAAAGCTCTGCTACGTCGCTCTGGACTTTGAGCAGGAGATCCAGACCGGT

**Exon 5**  
 L M K I L A E R G Y S F S T T A E R E I V R D I K E K L C Y V A L D F E Q E I Q T A

**Exon 5**  
 GCCCAGAGCTCCAGCTGGAGAAGTCAACGAGCTCCGGACGGTCAAGTCACTATCGGCAACGAGCGGTTCCGGCCCCCGAGGCTCTGTCCAGCCCTCCGTGCTGGCCCTGGAGAAACGG

**Exon 5**  
 A Q S S L E K S Y E L P D G Q V I T I G N E R F R A P E A L F Q P S V L G L E N G

**Exon 5**  
 CCGTATCCACGTGACCACTTCAACTCGATCATGAAGTGGCATGTCCGGAAGGACCTGTACGGCAACATTTGCTATGTAAAGTGGCGGACAGGCAAGGTGGCGAAACGGGTGACACGGCACA

**Exon 5**  
 G I H V T T F N S I M K C D V D V R K D L Y G N I V M

**Exon 6**  
 ACGGAACTTTCGCTGACACTGCTTTTTTCCCCCACTCTAGTCTGGTGGCACCCACCACTGACCCCGGCCCTGCGGACCGTATGCAGAAAGGAGATCACCGCCCTGGCCCCCTCGTCGATGAAGGTCAC

**Lepact-R**  
 S G G T T M Y P G L S D R M Q K E I T A L A P S S M K V

**Exon 6**  
 AGATCAITGCTCCCCCGAGCGGAAAGTAC TCCGCTCGATCGGTGGCTCTATCTTCCGCTCTGTCGACGTTCCAGCAGATGTGGATCTCGAAGCAGGAGTACGACGAGAGCGGTCTCTCGATCGT

**Exon 6**  
 K I I A P P E R K Y S V W I G G S I L A S L S T F Q Q M W I S K Q E Y D E S G P S I V

**Exon 6**  
 TCACCGCAAGTGTCTTAA  
 H R K C F \*

**Online Resource 1** Annotated map of the complete actin gene of *Grosmannia clavigera* (isolate kw1407), based on the genome sequence (GL629807) by Diguistini et al. (2011). The map was constructed by Yin et al. (2014) and the annotated sequence redeposited in Genbank as KP171180. Primers used for amplification in the study by Yin et al. (2014) are indicated with arrows. \* represents the stop codon.

Diguistini S, Wang Y, Liao NY, et al. (2011). Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont *Grosmannia clavigera*, a lodgepole pine pathogen. PNAS 108:2504-2509.

Yin M, Duong TA, Wingfield MJ, Zhou XD, De Beer ZW (2014). Taxonomy and phylogeny of the *Leptographium procerum* complex, including *L. sinense* sp. nov. and *L. longiconidophorum* sp. nov. Antonie van Leeuwenhoek doi:10.1007/s10482-014-0351-9