Gene expansion shapes genome architecture in the human pathogen *Lichtheimia corymbifera*: an evolutionary genomics analysis in the ancient terrestrial Mucorales (Mucoromycotina).

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Details

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Abstract

Lichtheimia species are the second most important cause of mucormycosis in Europe. To provide broader insights into the molecular basis of the pathogenicity-associated traits of the basal Mucorales, we report the full genome sequence of *L. corymbifera* and compared it to the genome of *Rhizopus oryzae*, the most common cause of mucormycosis worldwide. The genome assembly encompasses 33.6 MB and 12,379 protein-coding genes. This study reveals four major differences of the *L. corymbifera* genome to *R. oryzae*: (i) the presence of an highly elevated number of gene duplications which are unlike *R. oryzae* not due to whole genome duplication

(WGD), (ii) despite the relatively high incidence of introns, alternative splicing (AS) is not frequently observed for the generation of paralogs and in response to stress, (iii) the content of repetitive elements is strikingly low (