Unusual ITS Sequence Heterogeneity in the Luminous Mushroom Neonothopanus nambi from Vietnam

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Abstract:

Mushrooms from Binh Phuoc and Binh Duong provinces of Vietnam were identified as Neonothopanus nambi (Speg.) R.H. Petersen & Krisai from morphological observations and sequences of the rDNA internal transcribed spacer regions (ITS1-2). DNA was isolated from tissues cultured from a single basidiome, and amplified ITS fragments were cloned. 38 different ITS sequences were obtained from 98 clones, with 14 nt step. differences across the entire spectrum of clone sequences. There were ten 'hallmark' sequence characteristics (snp's or 1-2 base indels) that grouped the clones into three different sequence patterns. The predominant nuclear condition in the basidiomycete fruit body is a dikaryon, and the two predominant sequence patterns could represent the monokaryons. The uncommon sequence pattern appeared to represent one of two possible diploid phases or recombinants existing in the lamellae, basidia or spores of the original basidiome; the second possible recombinant pattern was not observed. Even in this scenario there were still 10 ITS sequence variants in one monokaryon with an additional snp in the 18S region and two in the 5.8S, 11 ITS variants for the second monokaryon with an additional snp in the 28S region and two in the 5.8S, and two ITS sequence variants for the presumed recombinant. All ten 'hallmark' regions were also detected in four other ITS sequences for Neonothopanus in Genbank, although in varying combinations not consistent with the ITS1 hallmarks being inherited together, as would ITS2 hallmarks, due to the crossover in the 5.8S region. Our observations bring to question the amount of genetic variability possible among mating populations of this species - whether this sequence heterogeneity may be attributed entirely to the existence of variants in the multi-copy rDNA regions, or by a multinucleate condition, or even by occurrence of multiple compatible mating strains in the sense that a single basidiome, as studied here, is in fact a community of compatible strains.

Key words: bioluminescence, internal transcribed spacer, multiple mating strains, Neonothopanus, rDNA