Bs En 12449 Pdf 17 ##HOT##

A different Sarcocystidae was detected in the two contrasting environments of Tioman Island. Water samples captured between 2014 and 2015 from the eastern (PCI) and northern (SSP/SMP) region of the Island, respectively, were analysed using the 285 RF28S RB Deg R primer set. A total of 16 of the 32 water samples, as well as two out of the 25 soil samples, were positive for Sarcocystidae based on the presence of the 285 rRNA gene. Analysis by amplicon sequencing of the 285 gene variable region detected only two Sarcocystidae species, S. singaporensis and S. nesbitti, in the two contrasting regions and also in both soil samples. Each of the sequences that were detected in this study was named according to the genus, the host sample it was obtained from, the region from where the sample was acquired, the sample date and the country and publication reference. Severe acute sarcocystosis occurred in summer 2012 among visitors of the Tioman Island in south Malaysia. The confirmation of the causal agent was attempted only by the 185 rRNA gene sequencement of the 285 rRNA gene sequences was pre-determined. In this study, a new primer set (285 R7F285 RB Deg R) was designed and used to amplify the partial 285 rRNA gene in 11 cases, in which only a single species was found. The detection rate was 100% (11/11). Sequences were named by GenBank accession number and the species, region of origin, sampling time and sampling reference. Of the 11 new sequences generated, 10 matched a sequence detected in S. in singaporensis (97.7%) and one matched a sequence detected in S. nesbitti (90.9%). The latter sequence was also obtained from soil and was named Sarcocystis sp. YLL-2013.



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A different Sarcocystidae was detected in the two contrasting environments of Tioman Island. Water samples captured between 2014 and 2015 from the eastern (PCI) and northern (SSP/SMP) region of the island, respectively, were analysed using the 28S R7F28S R8 Deg R primer set. A total of 16 of the 32 water samples, as well as two out of the 25 soil samples, were positive for Sarcocystidae based on the presence of the 28S rRNA gene. Analysis by amplicon sequencing of the 28S gene variable region revealed seven distinct Sarcocystidae sequences. The sequence generated from the 18S rRNA gene V9 hypervariable region detected only two Sarcocystidae species, S. singaporensis and S. nesbitti, in the two contrasting regions and also in both soil samples. Each of the sequences that were detected in this study was named according to the genus, the host sample it was obtained from, the region from where the sample was acquired, the sampling date and the country and publication reference. Severe acute sarcocystosis occurred in summer 2012 among visitors of the Tioman Island in south Malaysia. The confirmation of the causal agent was attempted only by the 18S rRNA gene sequencing, since the development of an in-house developed method of PCR-RFLP on the 544 bp of the 28S rRNA was not yet successful. Additionally, for the early identification of species, the nomenclature of the 28S rRNA gene sequences was pre-determined. In this study, a new primer set (28S R7F28S R8 Deg R) was designed and used to amplify the partial 28S rRNA gene in 11 cases, in which only a single species was found. The detection rate was 100% (11/11). Sequences were named by GenBank accession number and the species, region of origin, sampling time and sampling reference. Of the 11 new sequences generated, 10 matched a sequence detected in S. singaporensis (97.7%) and one matched a sequence detected in S. nesbitti (90.9%). The latter sequence was also obtained from soil and was named Sarcocystis sp. YLL-2013. 5ec8ef588b

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