IN SILICO ANALYSIS OF SPECIFIC PRIMERS OF CRYPTOSPORIDIUM BAILEYI

(ANÁLISE IN SILICO DE INICIADORES ESPECÍFICOS PARA CRYPTOSPORIDIUM BAILEYI)

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Cryptosporidiosis influenza is a relevant disease due to the ability to cause respiratory and/or gastrointestinal diseases, with high morbidity and mortality rates. Samples isolated from animals or the environment can be characterized using molecular methods, broadening the knowledge about the distribution and biology of these parasites. The PCR technique is a useful tool to identify Cryptosporidium species. The use of good primers is critical to the success of the technique. This study aimed at performing in silico analysis of primers for Cryptosporidium baileyi identification using the OligoAnalyser 3.1 software. We selected five genes of C. baileyi and designed five primer pairs (forward/reverse) for each gene. In silico analysis was performed based on the evaluation of the annealing temperature, the GC ratio, initiator size, similarity with C. baileyi and genetic distancing compared to other species of Cryptosporidium and other species that can be found in chicken droppings or environmental water samples. Of the 25 primer pairs tested, 23 were found to have satisfactory quality standards. Two primers were considered inadequate due to high GC concentration. Twenty-three primers showed similarity greater than 95% with other species of Cryptosporidium. Two pairs of primers showed 100% similarity with C. bayleyi, but similarity around 85 % with other species of the genus. The design of primers for PCR is the key step for a successful reaction, being a simple procedure when the sequence of the target DNA to be amplified is known. In the present work it was found that the lack of complete C. baileyi sequencing makes it difficult to select good initiators, resulting in high identity with other gene sequences. Given these results it is concluded that it is necessary to continue the in silico analysis to obtain a set of primers with high probability of being effective.

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