Calculation and user-friendly reporting of anticipated amplicons from (un)specific primer-binding on bisulfite-treated genomes

Seyed Ahmad Salehzadeh *, Ali Mohammadian
Department of Medical Biotechnology, Tarbiat Modares University, Tehran, postal code: 14115-116, Iran
*salehzadeh.a@modares.ac.ir

Abstract: DNA methylation is an epigenetic mechanism of gene regulation. Most wet-lab DNA methylation analyses are based on bisulfite-treated DNA. Bisulfite treatment of DNA converts unmethylated cytosine nucleotides to uracil, while sparing methylated cytosines [1]. Although searching against modified genome is an important step in primer design, NCBI primer blast does not support searching against bisulfite-treated genomes [2]. This search is essential for designing acceptable methylation specific-primers and bisulfite sequencing primers. We developed an R script that takes 2 or more primers, searches unmodified genome and bisulfite modified genome for exact and non-exact matches and returns a tabulated excel file containing the possible amplicons. The information given are: 1- Length of the resulting amplicon with primers 2-Number of mismatches to the left and right primers, 3-, and a visual guide to the places of mismatches of primers.

Keywords: primer; mismatch; bisulfite-treated genome, R script

References

[1] Hernandez, Hernan G., et al. "Optimizing methodologies for PCR-based DNA methylation analysis." Biotechniques 55.4 (2013): 181-197.

[2] Ye, Jian, et al. "Primer-BLAST: a tool to design target-specific primers for polymerase chain reaction." BMC bioinformatics 13.1 (2012): 134.