

# **Human-blind probes and primers for dengue virus identification.**

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Reliable detection and identification of pathogens in complex biological samples, in the presence of contaminating DNA from a variety of sources, is an important and challenging diagnostic problem for the development of field tests. The problem is compounded by the difficulty of finding a single, unique genomic sequence that is present simultaneously in all genomes of a species of closely related pathogens and absent in the genomes of the host or the organisms that contribute to the sample background. Here we describe 'host-blind probe design'- a novel strategy of designing probes based on highly frequent genomic signatures found in the pathogen genomes of interest but absent from the host genome. Upon hybridization, an array of such informative probes will produce a unique pattern that is a genetic fingerprint for each pathogen strain. This multiprobe approach was applied to 83 dengue virus genome sequences, available in public databases, to design and perform in silico microarray experiments. The resulting patterns allow one to unequivocally distinguish the four major serotypes, and within each serotype to identify the most similar strain among those that have been completely sequenced. In an environment where dengue is indigenous, this would allow investigators to determine if a particular isolate belongs to an ongoing outbreak or is a previously circulating version. Using our probe set, the probability that misdiagnosis at the serotype level would occur is approximately 1 : 10(150).

PMID: 16403026 [PubMed - indexed for MEDLINE]