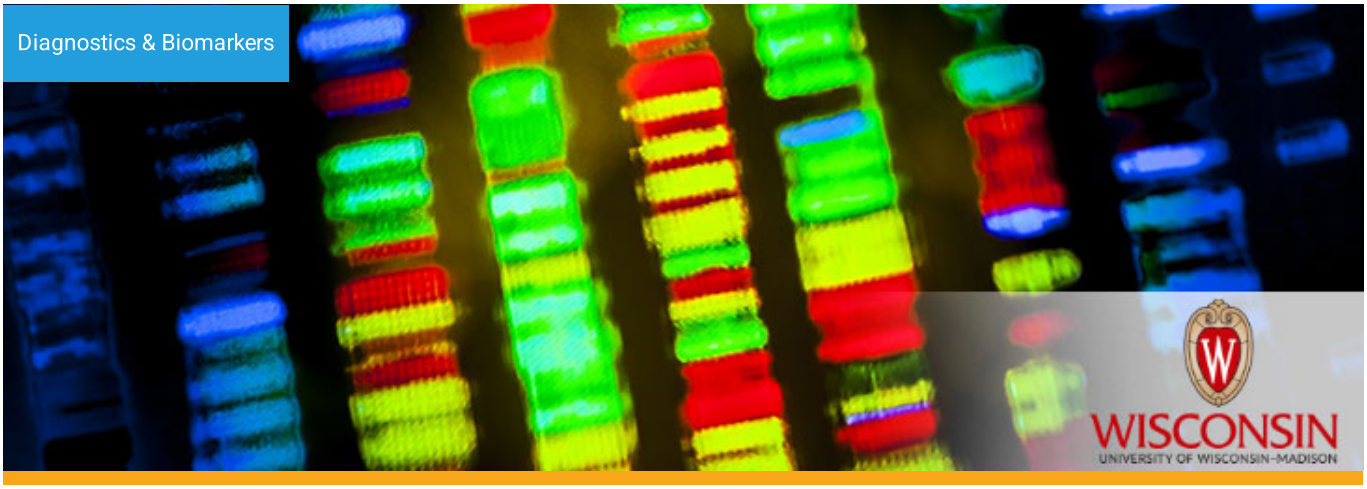

Methods for Identifying Cross-Contamination Among Sequential Nucleic Acid Amplification Reactions

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Inventors: Muhammed Murtaza, Bradon McDonald, Kirsten Dennison, Amanda Schussman

The Invention

UW-Madison researchers have developed a tagged primer system for identifying nucleic acid contamination in genetic sequencing experiments that involve serial PCR amplification steps. The system relies on multiple versions of the same primer set, molecularly tagged on the 5'-end with a short, known oligonucleotide sequence. Each tag is used in each of the amplification steps with the different forward primers (no tag on the reverse primers). The amplification products from each of these primers contains the different tag sequences. Tag1 would be used in the first amplification round, tag2 is used in the second, and tag3 in the third amplification round. Upon sequencing, and sequences after the 2nd round of amplification that have tag1 sequences would be discarded as carryover contamination from the round one primers that remain in the sample. After round 3, and tag1 or tag2 sequences would be discarded.

Additional Information

For More Information About the Inventors

- Muhammed Murtaza

Tech Fields

- Diagnostics & Biomarkers : Diagnostics

For current licensing status, please contact Rafael Diaz at rdiaz@warf.org or 608-960-9847