

TWO MILLION PCR REACTIONS GENERATED FROM DIFFICULT FORENSIC SAMPLES

F.A. Iman Muharam

Richard Hodgson

Angela van Daal

Cooperative Research Centre for Diagnostics

School of Life Sciences

Queensland University of Technology

GPO Box 2434

Brisbane, Australia 4001

Tel.: +61 7 3864 2502

Fax.: +61 7 3864 1534

E-mail: a.vandaal@qut.edu.au

Poster Abstract

Limiting DNA samples are an inherent problem in fields such as forensics and molecular archaeology. We have used a DNA amplification method to overcome problems with difficult forensic samples such as single shed hairs and touched objects. Amplification of single human cells and archival buccal swabs/bloodspots was also carried out. We were able to amplify limiting samples by up to 200,000-fold compared to the original input DNA, and obtained sufficient template for 2,000,000 PCR assays from as little as picogram quantities of input DNA. The amplified product was shown to be highly representative by comparative genomic hybridisation and was suitable for the analysis of both nuclear and mitochondrial DNA. The application of this method to limiting DNA samples alleviates the problem of insufficient template material and is suitable for forensic, molecular archaeology and clinical diagnostic applications. The large amount of product generated allows confirmatory testing and extensive downstream analyses.