

## **ANALYSIS AND INTERPRETATION OF THREE- AND FOUR-BANDED PATTERNS AND FALSE HOMOZYGOTIC HUMAN DNA SAMPLES**

Rainer Schubbert, Lars Giesen, Wolfgang Hell  
Medigenomix GmbH  
Fraunhoferstr. 22  
82152 Martinsried, Germany  
[www.medigenomix.de](http://www.medigenomix.de)

Medigenomix is specialized in DNA analytical services for DNA sequencing and genotyping. Our genotyping service includes identity testing in humans and animals, population genetics, gene-mapping, pharmacogenetics and forensic DNA trace-analysis.

In our work for the German National DNA database and screenings for different police departments we found several samples, where three or four alleles per marker could be detected. Because these three- and four banded patterns are present only in one of the eight analysed STR systems of these samples, a contamination could be excluded. Additional samples from the same person showed the same results. We also confirmed these data by analysis of these samples with a second PCR kit from another supplier. After that we have cloned and sequenced the different alleles of the three- and four banded patterns to verify whether the alleles showed different motifs, which would be an indication for a third chromosome or a recombination event, or the same motifs plus one repeat which would be an indication for a mutation during embryogenesis.

These three- and four banded patterns could lead to misinterpretations of DNA samples analysed during casework, especially at mixed samples.

We also found several cases, where samples seemed to be homozygous in one STR system by analysis with one commercial available kit, but were heterozygous by analysis with a kit from another supplier. In one case we found a sample, which seemed to be homozygous by analysis with one kit, but heterozygous with two different alleles by analysis with another kit and three-allelic with the primers originally published.

We have also cloned and sequenced several alleles to detect the reason of these effects.

Different results from the same DNA sample by using different kits may result in missing hits in the database, depending on the design of the DNA database, especially when error-tolerance is not built in.