

Investigation of Microsatellite Polymorphisms in Chimpanzees

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In order to investigate species specificity, allelic variability, sequence composition and phylogenetic sequence changes, PCR-amplification of the Short Tandem Repeat (STR)- polymorphisms HUMFIBRA, HUMFES/FPS, HUMTH01, HUMVWA, HUMF13A01, HUMF13B, HUMCD4, ACTBP2, D12S391 and DYS19 was performed on DNA samples of 39 chimpanzees (*Pan troglodytes*). Detection was carried out by silver staining on native polyacrylamide gels or laser fluorescence detection on an A.L.F. DNA sequencer (D12S391, HUMF13A01). Additionally, sex was determined using the amelogenin locus. Solid phase, single stranded sequence analysis was also done on the A.L.F. sequencer.

Although typing of these STR polymorphisms was established in human DNA samples amplification products were obtained for all STR-systems except for DYS19. At different loci, chimpanzee alleles migrated either faster than the human specific allelic ladder, within the human allele range or were detected both within the allelic range of humans and off the allelic ladder. In general, less variability was found in chimpanzee allele sizes with the majority of the alleles being shorter than known for humans.

Sequence analysis showed that the repeat motifs reported for *Homo sapiens* also exist in these non-human primates, but mostly contain less reiterations in the regions drawn for human nomenclature. Especially at the hypervariable loci HUMFIBRA, D12S391 and ACTBP2, which show a complex sequence composition in humans, these regions seem to be more simple in chimpanzees. Additionally, base differences as well in the repeat regions as in the flanking regions were found in some of the investigated microsatellites.

Despite evaluation of evolutionary divergences interpretation of such data might first and foremost give hints which lead to a better understanding of phylogenetic development of repeated sequences.