

# Pengembangan Metode FINS (Forensically Informative Nucleotide Sequencing) untuk Sampel Forensik Harimau Sumatra (*Panthera tigris sumatrae*, Pocock 1929) dengan Markah Genetik Control Region mtDNA. = FINS (Forensically Informative Nucleotide Sequencing) Method Development for Forensic Samples of Sumatran Tigers (*Panthera tigris sumatrae*, Pocock 1929) with mtDNA Control Region Genetic Markers

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## Abstrak

Sampel forensik harimau sumatra yang umum diperdagangkan secara ilegal di Indonesia dan dunia, di antaranya yaitu kulit, rambut, tulang, gigi, dan tengkorak. Identifikasi molekuler sampel forensik dengan memanfaatkan penanda genetik spesifik dari sampel dapat menggunakan metode Forensically Informative Nucleotide Sequencing (FINS). Teknik FINS memiliki lima tahapan, yakni ekstraksi isolat DNA, amplifikasi menggunakan primer, penentuan urutan basa nukleotida, analisis hasil sekuensing, dan analisis filogenetik. Bahan uji yang digunakan berjumlah 15 sampel forensik harimau sumatra yang diperoleh dari BKSDA Aceh, Taman Nasional Batang Gadis (TNBG), Taman Nasional Bukit Barisan Selatan (TNBBS), dan kasus kejahatan di Garut. Tahapan penelitian yang dilakukan, yaitu desain primer menggunakan Geneious Prime, ekstraksi sampel menggunakan Wizard® Genomic DNA Purification Kit, uji kuantifikasi DNA, Polymerase Chain Reaction, analisis sekuensing, dan analisis filogenetik. Primer "CR\_PTS" berhasil didesain dan memenuhi syarat primer yang baik. Kemurnian dari sampel hasil ekstraksi berkisar antara 1,1–2,3. Sampel yang berhasil tervisualisasi pada gel elektroforesis, yaitu kulit, tulang rusuk, dan tulang kaki dari Aceh, serta kulit dari TNBBS. Hasil analisis pohon filogenetik menunjukkan adanya pengelompokan klade antarsampel. Hasil analisis haplotipe tidak menunjukkan perbedaan wilayah asal pada Hap\_1 yang terbentuk. Penelitian identifikasi sampel forensik menggunakan primer PTS\_CR lebih lanjut perlu dilakukan untuk menguji tingkat spesifitas primer.

.....Forensic samples of Sumatran tigers that are commonly traded illegally in Indonesia and the world, include skin, hair, bones, teeth and skulls. Molecular identification of forensic samples by utilizing specific genetic markers from samples can use the Forensically Informative Nucleotide Sequencing (FINS) method. The FINS technique has five stages, namely extraction of DNA isolates, amplification using primers, determination of the nucleotide base sequence, analysis of the results of the sequencing, and phylogenetic analysis. The test materials used was 15 Sumatran tiger forensic samples obtained from BKSDA Aceh, Taman Nasional Batang Gadis (TNBG), Taman Nasional Bukit Barisan Selatan (TNBBS), and crime cases in Garut. The stages of the research were carried out, namely primer design using Geneious Prime, sample extraction using Wizard® Genomic DNA Purification Kit, DNA quantification test, PCR, sequencing analysis, and phylogenetic analysis. The primer "CR\_PTS" was successfully designed and met the requirements of a good primer. The purity of the extracted samples ranged from 1.1–2.3. Samples that were successfully visualized on gel electrophoresis were skin, ribs, and leg bones from Aceh, and also skin from TNBSS. The results of the phylogenetic tree analysis showed that there was a clade grouping between samples. The results of the haplotype analysis did not show differences in the region of origin on the formed

Hap\_1. Further research on the identification of forensic samples using PTS\_CR primers needs to be carried out to test the specificity of the primers.