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Phylogenetic Analysis and Nonsynonymous Mutations in an Env Gene Fragment of FIV A in Colombian Cats

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ABSTRACT

Introduction: The feline immunodeficiency virus (FIV) is a retrovirus that infects domestic cats. The genetic variability of FIV, particularly in the V4–V5 region of the envelope (*env*) gene, may lead to specific amino acid changes that influence viral pathogenicity and the emergence of seven distinct subtypes. Consequently, this study aimed to determine the circulating genotype and identify nonsynonymous mutations by analyzing a fragment of the *env* gene in a sample of domestic cats from Colombia.

Methods: Blood samples were collected from 151 domestic cats. Total DNA was extracted, and an 859 bp fragment of the *env* gene was amplified. The evolutionary history of the sequences was reconstructed using both Maximum Likelihood and Bayesian phylogenetic methods. Furthermore, nonsynonymous mutations in the translated amino acid fragment of the *env* gene were analyzed using a predictive tool.

Results: A molecular prevalence of 5.29% (8/151) was observed in the sampled population. Genotype A was identified as the circulating genotype; however, the sequences clustered into distinct clades within this genotype. Twelve nonsynonymous amino acid substitutions were identified, among which H86R ($p < 0.857$), N88K ($p < 0.777$), E41V ($p < 0.773$), and K91D ($p < 0.743$) showed a high probability of being deleterious.

Conclusions: These findings highlight the genetic diversity within FIV genotype A and underscore the potential impact of specific nonsynonymous mutations on viral pathogenicity.

Keywords: deleterious, PCR, sanger sequencing, amino acids.