J Vet Clin Vol. 23, No. 1(Suppl.) May (2006)

Polymorphism of VWF Gene for Genetic von Willebrand Disease Diagnosis in Sapsaree

Mi-Hyun Ha, Chung-Boo Kang, Jong-Uk Shin, Jae-Hyeon Cho[1], Phil-OK Koh[1], Chung-Kil Won[1], Jung-Chul Kim[2], Sung-Kook Jun[2], Ji-Hong Ha[2], and Kyu-Woan Cho*

Department of veterinary internal medicine, [1]Department of veterinary anatomy, College of veterinary medicine, Gyeongsang national university, [2]Department of genetic engineering, College of natural sciences, Kyungpook national university,

Introduction: Von Willebrand disease(VWD) is the most frequent hereditary bleeding disorder in human and animal, is due to a deficiency or abnormality of the von Willebrand factor (VWF).1 Mutation of the VWF may result in the disruption of complex biosynthetic process to impair the assembly, intracellular targeting, or secretion of VWF multimers.2 Single nucleotide polymorphisms (SNPs) are the available markers of choice for identifying individuals at risk of disease, measuring the variability between populations.3 The Sapsaree is Korean native dog, elimination of the mutated gene by selective breeding is an important goal for the health of this breed. To detect VWD affected or carrier, we genotyped the 8 SNPs of VWF gene in the Sapsarees.

Materials and methods: Genomic DNA samples were provided by Ji-Hong Ha (University of Kyungpook , Taegu, Republic of Korea). The canine VWF gene fragments including SNPs were amplified using five primer sets and PCR. For the genotyping of SNP, we used SNaPshotTM multiplex kit (Applied Biosystems, Foster City, CA, USA) based on the addition of a specific fluorescently labeled ddNTP to extension primers.

Results: We have investigated 8 SNPs of VWF in 170 Sapsarees, found polymorphism in 208G/A in exon 3, rs8769435 and rs8769434 in intron 3, while not found inSandra2005 in exon 4, Rs8946977 in intron 5,Rs8827220 in exon 6, 98Rieln16 in intron 16 and 04KraEx28 in exon 28. Genotypic frequencies of 208G/A in exon 3 in the 163 Sapsarees presented distributions for G/G (n=52), G/A (n=90) and A/A (n=21). Venta et al (Venta PJ 2000) found the G→ mutation in exon 3 in a Scottish Terrier with VWD type 3, but they did not have evidence that it contributes to the VWD phenotype. In this study, A allele frequency is 40.5%, this mutation may not contribute to the VWD. Sapsarees are not VWD trait carrier in this result.

Clinical relevance: We have genotyped the 8 SNPs of VWF gene to detect VWD affected or carriers in 170 Sapsarees. Sapsaree have not polymorphisms of Sandra2005 in exon 4, 98Rieln16 in intron 16 and 04KraEx28 in exon 28 related VWD trait.

*Corresponding author: chokw@gsnu.ac.kr