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Short Communication

Incidence and genetic aspects of patellar luxation in Pomeranian dogs in Thailand

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ABSTRACT

There is a high incidence of patellar luxation (PL) in Pomeranian dogs from Thailand. DNA samples were collected from 59 dogs originating from 15 families. PL was present in 75% of the dogs with a male:female ratio of 1:1.95. Polymorphic microsatellites situated close to the *COL6A1*, *COL6A3*, *COL9A1*, *COL9A2*, and *COL9A3* genes were analyzed for linkage to the phenotype. Sibling-pair analysis revealed that none of the collagen markers analyzed had a high non-parametric linkage score with the highest score, 1.56, for *COL9A2* ($P = 0.07$). The low LOD scores for these collagen genes indicated a non-involvement in the pathogenesis of PL in Pomeranians. An association study with a low density single nucleotide polymorphism (SNP) set indicated the possible involvement of a region on chromosome 7. The association of this region remained indicative when larger groups of 43 cases and 40 controls were compared (Chi square test $P = 0.01$).

Patellar luxation (PL) is one of the most common orthopaedic disorders found in small breed dogs, especially Pomeranians. It has been suggested that the disease is inherited (Hayes et al., 1994). The mode of inheritance is unknown because the phenotype has not been analyzed in large family groups. An insight into the genes involved could be used in breeding programs and aetiology studies of PL.

In Thailand, the prevalence of medial patellar luxation (MPL) and lateral patellar luxation (LPL) in small-breed dogs is 87% and 13%, respectively (Wangdee et al., 2005). Pomeranians are currently also the highest ranking breed for PL in the USA, with 42.4% of dogs affected.[2] Defects in collagen formation underlie a number of orthopaedic diseases in humans, and these disorders are often caused by inherited mutations in genes encoding collagen proteins (Salg et al., 2006). As collagen genes are suggested to be involved in PL and hyperextension syndrome in dogs (Temwichitr et al., 2007), we investigated the possible involvement of these candidate genes in PL in Pomeranian dogs.

A total of 238 Pomeranians presented at the Small Animal Hospital, Faculty of Veterinary Science, Chulalongkorn University (SAH Vet CU) during 2006–2008 were screened for PL. The incidence of PL in Pomeranian dogs is shown in Table 2. Of the 238 Pomeranians investigated, 177 (75%) had PL. The ratio of male to female cases was 1:1.95. This is in accordance with Hayes et al. (1994) who found in dogs with PL a male-to-female ratio of 1:1.5. Of the 330 affected joints, 318 (96%) had MPL and only 12 (4%) LPL. Luxation was bilateral in 153 (86%) and unilateral in 24 (14%) of all PL affected dogs. The distribution of MPL affected dogs according to luxation was bilateral in 148 (87%) and unilateral in 22 (13%) and for LPL was bilateral in 5 (71%) and unilateral in 2 (29%) The pedigrees of the Pomeranian dogs with PL (Fig. 1) did not allow us to draw conclusions about the mode of inheritance.

All dogs were investigated according to a standard orthopaedic protocol using a PL grading system (Brinker et al., 1997). Blood (5 mL) was collected from 45 affected and 14 unaffected Pomeranians originating from 15 families (Fig. 1; selection A). All affected dogs in the genetic study had bilateral MPL. DNA was isolated by the salt extraction method (Miller et al., 1988) and analyzed for co-segregation of the phenotype with five polymorphic microsatellites situated close to five collagen genes: i.e., *COL6A1* (NM_001848), *COL6A3* (NM_004369), *COL9A1* (NM_078485), *COL9A2* (NM_001852), and *COL9A3* (NM_001853) (Table 1). The development of these microsatellite markers and the method of genotyping have been described previously (Temwichitr et al., 2007).

Mlink software in Genehunter was used to calculate the logarithm of the odds (LOD) score for linkage of the phenotype with each of the markers in recessive and dominant inheritance models,

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[2] See: http://www.offa.org/stats_pl.html.

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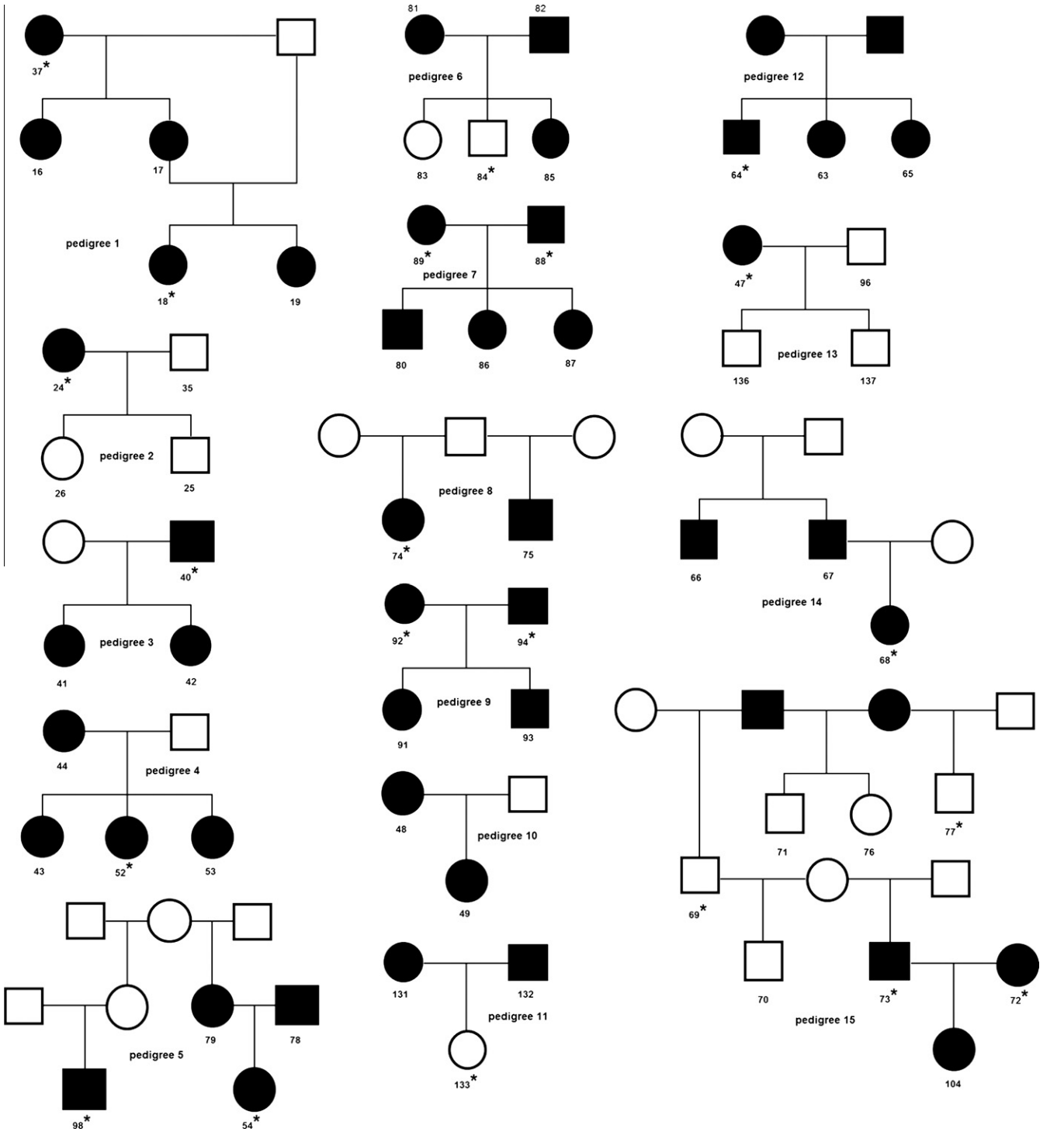

Fig. 1. Pedigrees of Pomeranian dogs with bilateral medial patellar luxation. Circles and squares represent female and male dogs, respectively. Filled symbols indicate dogs with patellar luxation, open symbols represent unaffected dogs. The numbers below the symbols indicate selection A of available DNA samples, asterisks denote selection B.

Table 1
Genomic locations of candidate genes for patellar luxation with known phenotypes in man.

Gene	CFA[a]	Mb[b]	OMIM	Human phenotype of gene mutation
COL6A1	31	39.31	MIM ID 120220	Bethlem myopathy, Ullrich congenital muscular dystrophy
COL6A3	25	48.05	MIM ID 120250	Bethlem myopathy
COL9A1	12	32.81	MIM ID 120210	Multiple epiphyseal dysplasia
COL9A2	15	2.64	MIM ID 120260	Multiple epiphyseal dysplasia
COL9A3	24	46.65	MIM ID 120270	Multiple epiphyseal dysplasia

[a] CFA, *Canis familiaris* chromosome number.
[b] Position in mega base pairs (Mb) of chromosome DNA sequence.