Emerging perspectives on hereditary glomerulopathies in canines

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Abstract: Familial glomerulopathies have been described in more than two dozen dog breeds. These canine spontaneous cases of glomerular disease are good models for their human counterparts. The dogs present clinically with protein-losing nephropathy and variable signs of hypertension, thromboembolic events, edema/effusions/nephrotic syndrome, or eventually with signs of renal disease such as anorexia, vomiting, weight loss, and/or polyuria/polydipsia. Laboratory changes include proteinuria, hypoalbuminemia, hypercholesterolemia, and eventually azotemia, hyperphosphatemia, anemia, and isosthenuria. Renal biopsies examined with transmission electron microscopy, immunofluorescence, and thin section light microscopy may show ultrastructural glomerular basement membrane abnormalities, glomerulosclerosis, amyloidosis, non-amyloid fibrillary deposition, or breed-associated predispositions for immune-complex glomerulonephritis. Genome-wide association studies and fine sequencing of candidate genes have led to the discovery of variant alleles associated with disease in some breeds; eg, 1) glomerular basement membrane ultrastructural abnormalities due to defective collagen type IV, caused by different premature stop codons in each of four breeds; ie, in COL4A5 in Samoyeds and Navasota mix breed dogs (X-linked), and in COL4A4 in English Cocker Spaniels and English Springer Spaniels (autosomal recessive); and 2) glomerulosclerosis-related podocytopathy with slit diaphragm protein anomalies of both nephrin and Neph3/filtrim due to non-synonymous single nucleotide polymorphisms in conserved regions of their encoding genes, NPHS1 and KIRREL2, in Soft Coated Wheaten Terriers and Airedale Terriers, with a complex mode of inheritance. Age at onset and progression to end-stage renal disease vary depending on the model. Genetic counseling using DNA testing is available for several breeds but many more inherited canine models of glomerulopathy still need to be characterized. Dog breeds, with their long haplotypes and linkage disequilibrium, represent excellent models to study the underlying molecular basis for protein-losing nephropathy, glomerular function, genetic manipulations, possible environmental triggers, and treatments. Results of studies of genetic canine diseases will help dogs and other species, including man.

Keywords: Alport, glomerulosclerosis, glomerulonephritis, nephrin, NPHS1, podocytopathy

Introduction
Veterinarians have long been diagnosing and managing pet dogs with spontaneous protein-losing nephropathy (PLN). The first sign of glomerular disease, persistent proteinuria, may be occult initially, but eventually discovered along with hypoalbuminemia, hypercholesterolemia, and possibly azotemia, hyperphosphatemia, anemia, and/or isosthenuria, when dogs present with clinical signs due to progressive renal injury (decreased appetite, weight loss, vomiting, polyuria/polydipsia [PU/PD]) or perhaps earlier with dramatic signs due to hypertension (eg, blindness due to retinal
detachment or hemorrhage), thromboembolic events (eg, dyspnea or sudden death due to a pulmonary event, or hind leg lameness due to a distal aortic “saddle” thrombus), or nephrotic syndrome (eg, cavity effusions or edema). If the owner allows, diagnostic tests are done to localize proteinuria to the kidney, search for any underlying cause, and plan a management regime.\(^1\)\(^{-}\)\(^6\) Standard treatment of canine PLN includes angiotensin-converting enzyme (ACE) inhibitors (and possibly other inhibitors of the renin-angiotensin-aldosterone system), modified low protein/low phosphorus diets, antithrombotics, antihypertensives, omega-3 fatty acid supplementation, and treatments as needed for renal failure.\(^3\)

Immunosuppressive protocols are recommended for PLN cases with an immune-mediated basis.\(^1\)\(^{,}\)\(^6\)

In some instances the owner/breeder knows of similarly affected canine relatives. Pedigree analysis and banked DNA samples from sick dogs and their relatives have been very useful for study. More than two dozen breeds have shown familial PLN,\(^1\)\(^7\) but only recently, with the advent of better tools to define genotypes and better characterize phenotypes, have specific genetic abnormalities been identified and associated with specific pathologic entities. Genomic tools include databases and computer software to compare the whole canine genome sequence (map) with that of humans, genome-wide association studies (GWAS) with single nucleotide polymorphism (SNP) chip technology, and fine mapping (gene sequencing) of candidate genes using DNA extracted from blood, semen, or tissue samples from well-documented affected animals and properly identified unaffected controls from the same genetic population. Phenotypic characterization of canine PLN subgroups is described with more accuracy currently by diagnostic testing to identify and localize proteinuria and to exclude acquired infectious, toxic, immune-mediated, and neoplastic causes of glomerular disease.\(^1\)\(^{,}\)\(^6\)

Cortical renal samples (surgical wedge or percutaneous ultrasound-guided needle-core biopsies) may now be obtained from properly chosen candidates by trained personnel, submitted properly in special media, and interpreted by experienced veterinary nephropathologists using transmission electron microscopy (TEM), immunofluorescence (IF), and thin section (3 \(\mu\)m) light microscopy (LM), in order to better define the ultrastructural detail of the glomerular basement membrane (GBM) and foot processes, visualize distinctive changes in cells and the extracellular matrix, and to check for the presence of amloid, non-amyloid, and/or immune-complex deposits.\(^8\)

Previously, using LM and standard 5 \(\mu\)m (thickly cut) sections, changes of glomerulosclerosis, glomerulonephritis, and GBM structural abnormalities had similar appearance, but with the introduction of more detailed examinations by TEM, IF, and thin section (3 \(\mu\)m) LM and with special stains, veterinary nephropathologists are now able to differentiate these entities. Among 501 proteinuric field cases studied by TEM/IF/LM,\(^7\) 48% had immune-complex glomerulonephritis (ICGN), 21% had primary glomerulosclerosis (focal segmental glomerulosclerosis [FSGS]), 15% had amyloidosis, 9% had non-immune complex glomerulopathy, 5% had non-immune complex nephropathy, and 2% had primary tubular disease. Of these 501 cases, 47% were from just 12 dog breeds, most of which are suspected of having a genetic predisposition for PLN or renal disease, including Labrador Retrievers (10.4%), Golden Retrievers (7.6%), Yorkshire Terriers (5.8%), Beagles (3.0%), Miniature Schnauzers (3.0%), Shetland Sheepdogs (2.8%), Boxers (2.6%), Dobermans (2.6%), Cocker Spaniels (2.6%), Soft Coated Wheaten Terriers (SCWT) (2.6%), English Bulldogs (2.2%), and Standard Poodles (2.0%).

Once a phenotypic entity is well-defined, a search on the Online Mendelian Inheritance in Man resource at \(\text{http://www.ncbi.nlm.nih.gov/pubmed/}\) may indicate possible candidate genes associated with that phenotype. If the phenotypic disorder or syndrome is complex, possibly involving a wide variety of pathogenetic mechanisms involving basic biochemical and/or physiologic pathways with a myriad of candidate genes, the field of study may be narrowed by comparing genomes of affected cases with related unaffected control/geriatric cases via GWAS, to search for statistically significant differences of linked SNPs, pointing to intervals of interest on one or more chromosomes, containing fewer candidate genes for study.

A GWAS may find linked markers (SNPs) and one or more candidate genes within an interval which may be associated with risk for affection. Gene sequencing of candidate genes from affected and control dogs may show that a mutation exists, such as a deletion, addition, or even a single non-synonymous SNP that is associated with affection. The identification of a variant allele of a candidate gene associated with the trait (PLN) proposes that the underlying molecular basis and pathogenesis for the phenotype includes alteration of the encoded protein, whose impact may be predicted by PolyPhen-2 software. Understanding the pathogenesis may suggest specific treatment. Customized Taqman genotyping assays (Illumina Inc., San Diego, CA, USA) for the discovered variant allele may then be developed as a “DNA test” to help identify individuals at risk for disease, in order to closely monitor them and initiate intervention earlier to hopefully slow disease progression, and to help breeders...
Identify which dogs are best to breed with one another to decrease the production of dogs at risk, while maintaining genetic diversity in the breed, through genetic counseling. Different breeds with similar phenotypes often have different mutations in either the same gene or a different gene, unless the breeds have common ancestral backgrounds; therefore different DNA tests may be necessary to detect at-risk variant allele carrier status in each breed. For human patients, up to 37 PLN candidate genes, including those associated with either Alport syndrome or FSGS, or even 292 genes associated with kidney malformations, may be studied at the same time, by next-generation sequencing and targeted exome sequencing, which may find novel mutations in a family. Such comprehensive panels are species-specific, and development of platforms to capture and evaluate canine exons of these candidate genes is needed.

The development of canine breeds led to their extensive linkage disequilibrium and long haplotypes, making them excellent models for genetic research because relatively few affected cases and controls may yield statistically significant findings. A spontaneous canine model of PLN may genuinely mimic spontaneous disease in man, with similar signs of illness, laboratory and histopathologic changes, and response to medications and diets. In addition, pet dogs which live closely with people are exposed to similar environmental triggers and may have similar comorbidities which realistically portray the nature of complex disease.

**Canine models of GBM defects: collagen IV abnormalities**

The distinctive ultrastructural GBM abnormalities found in some models of canine PLN (ie, extensive longitudinal multilaminar splitting and thickening of the GBM with a basketweave appearance in the lamina densa) and abnormal collagen IV chain content in the GBM, found by immunohistochemical staining with antibodies directed against specific chains, led investigators to sequence the candidate genes involved in human Alport syndrome in these canine cases. Since dogs do not show Alport-associated hearing deficits or ocular changes, the term “hereditary nephropathy” (HN) is used.

Collagen IV is the main structural component of the framework of the GBM which is important for the permselective barrier. Abnormal production, assembly, and repair of the GBM causes proteinuria and then further adaptive changes damage the rest of the nephron (glomerulus and tubules), leading to progressive damage, azotemia, PU/PD, and end-stage renal disease (ESRD). Collagen IV is made up of heterotrimers of six possible collagen chains, numbered α1 through α6, encoded by genes COL4A1 through COL4A6. COL4A1 and COL4A2 are on canine chromosome 22, COL4A3 and COL4A4 are on chromosome 25, and COL4A5 and COL4A6 are on the canine X chromosome. In mature mammalian kidneys, the heterotrimer that is predominant in the GBM is α3α4α5; the chains need to cross-link into a network via sulfilimine bonds of adjacent conserved methionine and lysine residues. A short or abnormally folded chain that cannot cross-link properly in the network would interfere with the 3-dimensional nanostructure of this important network and cause the laminar splitting that is seen ultrastructurally by TEM. The main candidate genes to investigate in dogs with suspected HN are COL4A5 (for an X-linked mode of inheritance) and COL4A3 and COL4A4 (for an autosomal mode of inheritance).

In 1994, the first characterization of the genetic basis for an inherited canine glomerulopathy was described in Samoyed dogs. The mode of inheritance is X-linked; affected hemizygous males show proteinuria quite early (3–6 months of age) and progress to ESRD by 6–24 months of age. Heterozygous carrier female Samoyeds (mosaics) also show proteinuria early but typically do not show ESRD until past 5 years of age. Ultrastructural GBM changes suggested HN, and as an X-linked form of HN (XLHN), a COL4A5 mutation was suspected, further supported by immunostaining with monoclonal anti-α5 antibodies which showed decreased α5 chains present in the GBM of affected dogs compared with controls. Upon sequencing the gene COL4A5, a non-synonymous SNP was found in exon 35, changing a G to a T (c.3079G>T), causing a premature stop codon and truncated α5 chain. An allele-specific polymerase chain reaction (PCR) test for this mutation is available (http://www.vetgen.com; http://www.pawprintgenetics.com) thus carrier dogs are removed from the gene pool, curtailing PLN among pet Samoyed dogs.

Another model of XLHN was found in a family of mixed breed dogs from Navosota, TX. In these dogs, carriers of both sexes show early onset of proteinuria by 6 months and ESRD at 6–18 months of age. Sequencing of the COL4A5 gene showed a 10 base-pair deletion in exon 9 (c.689_699delTAATCCAGGA) which caused a frame shift and a premature stop codon in exon 10 in this dominant form of XLHN. It is not unusual to find different mutations associated with the same phenotype. In humans, more than 1,100 unique variants have been found in COL4A5, of which 40% are missense and 50% nonsense mutations. Glycine substitutions occur most frequently; Gly-X-Y is an important
repeating triplet in the triple chain helical structure of collagen in the GBM.\textsuperscript{10}

The generation of closed colonies of XLHN carrier and affected dogs has been an important resource for study.\textsuperscript{17} These models have been useful to study microalbuminuria development,\textsuperscript{22} daily variation of proteinuria,\textsuperscript{23} urinary biomarkers,\textsuperscript{24,25} the development of the GBM network from fetal (α1α1α2) to adult type (α3α4α5) collagen IV,\textsuperscript{26} and the effects of ACE inhibition,\textsuperscript{27} prednisone,\textsuperscript{28} diet,\textsuperscript{29,30} and cyclosporine\textsuperscript{31} on this model.

From the mid-1940s until 2007 when a DNA test was developed, English Cocker Spaniels were at risk for “familial nephropathy” and ESRD by 10–24 months of age.\textsuperscript{32–35} The autosomal recessive mode of inheritance made it difficult to eradicate, as normal appearing heterozygote carrier matings occurred. It was not until TEM was utilized that affected dogs (but not carriers) were found to have GBM changes of HN, and an autosomal mutation in either COL4A3 or COL4A4 was suspected.\textsuperscript{34} When sequenced, a COL4A4 non-synonymous SNP was found in exon 3, changing an A to a T (c.115A>T), causing a premature stop codon. The allele-specific PCR DNA test (http://www.optigen.com) allows breeders to avoid breeding normal appearing carrier heterozygotes to one another and thus decrease the production of this autosomal recessive disease.

Most recently another autosomal recessive form of HN was found in two female English Springer Spaniel littersmates at 7 months of age, which progressed to ESRD over 2–3 months. The mutation found was a non-synonymous SNP in exon 30 of COL4A4, changing C to T (c.2712C>T), causing a premature stop codon.\textsuperscript{36} A specific PCR test is available (http://www.pawprintgenetics.com).

Bull Terriers\textsuperscript{17,37–40} and Dalmatians\textsuperscript{41} appear to have autosomal dominant forms of HN, which as in their human counterparts, may show clinical variability.\textsuperscript{42} Onset of ESRD is variable and can be later in life, up to 10 years of age (much later than the XLHN models above) with an average age of onset for Bull Terriers at 3.5 years (range 11 months to 8 years) and for Dalmatians at 18 months (range 8 months to 7 years). Although the mode of inheritance is dominant, normal appearing dogs might be bred unknowingly. With no genetic test available, conscientious breeders screen for proteinuria using microalbuminuria or urine protein/creatinine (UPC) ratio tests to identify dogs at risk (UPC ≥0.3) as early as possible and to start early intervention which may slow progression. Studies in Bull Terriers showed that although the GBM appears as HN by TEM examination (already seen in stillborn and 1-day old pups, compared with 1 month of age in the XLHN model), immunostaining showed normal amounts of collagen IV chains. Functional defects, perhaps due to non-synonymous SNPs, or other genes such as MYH9 or LMX1 may be involved.\textsuperscript{17} Ultrastructural GBM changes suggestive of HN may also be seen in other breeds for which the specific genetic defects still need to be characterized, eg, Doberman Pinschers (<3 years),\textsuperscript{43} Beagles (up to at least 8 years),\textsuperscript{44} and Rottweilers (<1 year).\textsuperscript{45}

### Canine models of podocytopathy and glomerulosclerosis associated with NPHS1 and KIRREL2 variant alleles

**SCWT**

Breeders of SCWT dogs in North America recognized in the 1980s that too many dogs (10%–15%)\textsuperscript{46} were sick or dying prematurely in young to middle-aged adulthood, many with similar clinical signs (vomiting, diarrhea, hyporexia, weight loss, effusions, PU/PD, sometimes sudden death) and laboratory abnormalities (hypoproteinemia, azotemia, low Na+/K+ ratio), which were eventually differentiated as separate or combined renal, intestinal, and/or adrenal diseases, based on blood, urine, and histopathology results. An SCWT DNA bank at the University of Pennsylvania School of Veterinary Medicine (PennVet) began to store hundreds of samples from affected SCWT dogs as well as geriatric (14–18 years old) unaffacted relatives. Beginning in 1997, the SCWT Open Registry listed dogs documented to have PLN (n=722 last update), protein-losing enteropathy (PLE) or inflammatory bowel disease (IBD) (n=501), combined PLE/PLN (n=279), Addison’s disease (n=98), and juvenile renal disease (JRD), also known as renal dysplasia (n=66). Many dogs had combined affection, due to the small foundation stock brought from Europe and popular sires, or a shared molecular pathogenesis. Dogs with PLN had proteinuria, hypoalbuminemia, and hypercholesterolemia, with or without hypertension, thromboembolic events, effusions, or azotemia. PU/PD was a late development associated with secondary tubular damage, as opposed to an early finding in dogs with JRD. Dogs with PLE often had small bowel diarrhea, possibly with effusions or thromboembolic events, and had panhypoproteinemia and hypocholesterolemia. The age of onset was 4.7±2.6 years for PLE, 5.9±2.2 years for PLE/PLN, and 6.3±2.0 years for PLN, but there was no age limit.\textsuperscript{46} The mode of inheritance of PLE/PLN appeared complex; the Open Registry listed affected dogs with long-lived ancestors (suggesting recessive inheritance), but the “Wheagle” colony at the North
Carolina State University College of Veterinary Medicine (developed by breeding an affected SCWT with a Beagle) produced affected dogs in the first generation, suggesting dominant inheritance. In field cases, PLE and/or PLN were reported in more female than male dogs (female: male = 1.4–1.9) however sampling bias may exist because breeders own more females. The pathogenesis of the diseases was unclear; renal histopathology (usually only examined by LM after death) showed changes consistent with glomerulosclerosis or glomerulonephritis and intestinal biopsies showed lymphocytic-plasmacytic IBD and/or lymphangiectasia. Some renal samples examined by TEM, IF, and LM in colony dogs showed glomerulosclerosis in 10% of glomeruli and immune-deposits in 4%, but whether these were causative or passive findings was unknown. There were no early biomarkers to warn of future PLE/PLN in young dogs or breeding stock and many dogs were bred before affectation was apparent. This model of PLN was used to study the onset of microalbuminuria and that averaging a pooled sample over several days was a useful method to determine daily proteinuria by UPC ratio determinations, in view of daily variation.

The main theories of pathogenesis for PLN in SCWT included 1) immunodysregulation, in view of possible breed-associated ICGN, food allergies, IBD, or PLE, presence of pANCA antibodies, possible female predisposition, and Addison’s disease (which may have an immune-mediated basis); and 2) possibly structural, functional, growth/repair factors, or developmental abnormalities causing intestinal, renal, or lymphatic/vascular cell adhesion defects, permeability changes, and loss of proteins, glomerulosclerosis, intestinal lymphangiectasia, and/or JRD with fetal glomeruli and fetal mesenchyme. In other words, there were too many possible gene candidates needing to be sequenced.

In order to narrow the field of study, a GWAS was done at PennVet, which revealed a significantly different region in PLN-affecteds (n=42) compared to related geriatric controls (n=20) on canine chromosome 1, with three statistically significant SNPs (p_{min} ≤ 4.13x10^{-8}, p_{genome} ≤ 0.005) in a region encompassing 65 genes, four of which were considered candidate genes for PLN, based on Online Mendelian Inheritance in Man resources. Fine mapping of the four candidate genes showed novel variant alleles in two of them, NPHS1 and KIRREL2, which are in linkage disequilibrium. These genes encode two cell adhesion proteins of the immunoglobulin superfamily, nephrin and Neph3/filtin, which are part of the complex nanostructure in the slit diaphragm between the podocyte foot processes. Each gene showed a single nonsynonymous SNP not found in other species, associated with PLN in SCWT. Nephrin is the major slit diaphragm protein, and more than 176 different mutations in NPHS1 have been found associated with PLN in people, including infantile, juvenile, and adult-onset forms. No mutations in KIRREL2 are known yet but decreased expression of Nephr3/filtin has been associated with PLN in people. In SCWT with PLN, in exon 22 of NPHS1, G is changed to A (c.3067G>A), altering a glycine residue (conserved among mammals) to an arginine (G1023R), in the FN3 domain of nephrin. In exon 15 of KIRREL2, C is changed to G (c.1877C>G), changing a proline residue in a conserved proline-rich interval to an arginine (P626R). The application of PolyPhen-2 software showed the SCWT NPHS1 variant is “probably damaging” (the highest score) and the KIRREL2 variant is “possibly damaging” (next highest score).

An additional 145 SCWT dogs with known phenotypes were tested for these SNPs, using a customized Taqman assay for the PLN-associated variant alleles. Homozygous positive dogs showed the highest risk, heterozygous dogs showed intermediate risk, and homozygous negative dogs showed lowest risk for development of PLN (2×3 contingency table, P=7.78×10^{-10} in their lifetimes. The odds ratio for affectation was 29.5 (homozygous positive versus [vs] homozygous negative), 6.8 (homozygous positive vs heterozygous), and 9.1 (homozygous positive vs others).

When non-SCWT breeds were tested for these NPHS1 (n=747 dogs of 114 breeds) and KIRREL2 (n=550 dogs of 105 breeds) variant alleles, only three dogs showed these SNPs, including two Airedales (one was homozygous positive for both SNPs and died of PLN, and one was heterozygous for both SNPs) and one Bloodhound, which was heterozygous for the KIRREL2 SNP only.

A worldwide prevalence study of 1,208 samples (n=2,166 most recently) from SCWT of North America, Europe, and Australia, showed 45% (43%) of the dogs are heterozygous, 38% (42%) are homozygous negative, and 17% (15%) are homozygous positive for both variant alleles. The variant allele frequency in the breed is high (40%; recently 37%), therefore culling all carriers would lead to loss of genetic diversity and possibly new genetic diseases. The current recommendation is to test dogs to know an individual’s risk for developing PLN in its lifetime, and to choose mates for dogs in order to avoid producing homozygous positive puppies. Homozygous positive or heterozygous dogs are best bred to homozygous negative
dogs, to reduce variant allele frequency over time and
decrease risk for PLN.

Although retrospective studies show a high statistically
significant relationship of the PLN-associated variant alleles
with disease, not all homozygous positive dogs become
affected. The mode of inheritance of PLN in SCWT is
complex, possibly with multiple genes, variable expres-
sion, incomplete penetrance, and/or environmental triggers.
Prospective studies need to be done to see what percentage
of dogs with each haplotype become affected, and to study
whether modifier genes, comorbidities, or environmental trig-
gers may be involved with expression of phenotype. While
the predominant histopathologic lesion appears as varying
degrees of FSGS, likely due to genetic podocytopathy and
slit diaphragm protein defects, it may be that podocytes of
affected SCWT are weakened and susceptible to further
damage by inflammation or circulating immune complexes
which otherwise normal dogs are able to process.46 Many
SCWT have food allergies, IBD, or PLE, and since dogs
with combined PLE/PLN average higher UPC than dogs with
PLN alone46 the clinical expression of PLN in carriers may
be exacerbated by a multiple hit pathogenesis.

Airedale Terriers

Given that two Airedale Terrier carriers were found in SCWT
studies, including one homozygous positive dog which had
PLN, and that some breeders noticed familial renal disease
as a problem, a broader North American Airedale Terrier
prevalence study was done, which showed a variant allele
frequency of 28% among 221 dogs.51 Recent statistics for
297 Airedale Terriers found 47% were homozygous negative,
44% were heterozygous, and 9% were homozygous positive
for the PLN-associated variant alleles (NPHS1 and KIRREL2)
previously found in SCWT. A genotype-phenotype correlation
study has not yet been done for lack of samples from Airedales
with well-characterized phenotypes. However, among 24 dogs
closely related to Airedale Terriers that had died with kidney
disease (but which themselves were not available for testing),
the allele frequency was higher than in the general Airedale
population (42% vs 28%), suggesting that the presence of
these variant alleles is associated with risk for kidney disease
in Airedale Terriers, as in the SCWT breed.

Abnormal glomerular deposition

Collagen III

A family of mix breed dogs with PLN was found to have
collagenofibrotic glomerulonephropathy.62,63 Test matings
indicated an autosomal mode of inheritance. As in humans,
increased serum levels of the amino-terminal propeptide of
type III procollagen (PIIINP) may be used as a marker of this
defect. Hypocomplementemia, found in a few human cases,
was not observed in the canine model. The COL3A1 gene
did not appear to be involved in dogs. A similar abnormal
glomerular deposition of collagen III fibrils in glomeruli
may have been found in Newfoundland64 dogs but needs
more study.

Amyloidosis

Familial amyloidosis in Chinese Shar Pei,65–67 Beagle,68 and
English Foxhound69 breeds is seen with adult onset. Amyloid
deposition affecting glomeruli causes PLN. In Shar Pei, depo-
sition of amyloid AA is probably due to chronic inflammatory
disease and the fever/hock syndrome, a common comorbidity,
due to an unstable duplication of the HAS2 gene that causes
wrinkling and periodic fever syndrome.67

Immune-complex deposition

Labradors and Golden Retrievers and possibly Shetland
Sheepdogs show a predisposition for Lyme-specific ICGN,
known as “Lyme nephritis”66,70–74 Possibly an unidentified
genetic podocytopathy or immunodysregulatory defect trig-
gers abnormal immune complex handling, since most Lyme-
erositive dogs, even among these predisposed breeds, do
not show proteinuria or Lyme nephritis. Bernese Mountain
Dogs,75–78 found to be more likely Lyme-seropositive than
other breeds with the same lifestyle, were originally thought
to have a predisposition for Lyme nephritis, however their
Lyme-seropositive status is not associated with proteinuria
or lameness and their membranoproliferative glomerulo-
nephritis is familial with an autosomal recessive mode of
inheritance possibly with an X-linked modifier gene, affect-
ing mostly females (female: male =4). Other breeds at risk
for ICGN because of a higher risk for associated infec-
tious diseases or drug sensitivity are American Foxhounds
(Leishmaniasis),79–82 Basenjis (IBD/PLE),83 Doberman
Pinschers (sulfonamides),84–86 German Shepherds (Ehrlichia
canis),87–89 and SCWT (IBD/PLE).90–92 A colony of Brittany
Spaniel dogs was found to have type 1 membranoproliferative
glomerulonephritis secondary to complement C3 deficiency,
due to a deletion mutation in the gene encoding C3.91,92

More breeds with familial
glomerulopathies

Other breeds with familial glomerulopathies that need more
characterization are listed in Table 1. Renal proteinuria may
also be seen with familial nephropathies, not to be confused
with glomerulopathies, including JRD in numerous breeds with altered renal development and distinctive fetal glomeruli/mesenchyme, reflux nephropathy in Boxer and Gordon Setter dogs, autosomal dominant polycystic kidney disease in Bull Terriers (PKDI, c.9772G>A),106 Fanconi syndrome in Basenjis, polycystic disease in Cairn and West Highland White Terriers, multiple renal cystadenocarcinomas in German Shepherds, and telangiectasia in Pembroke Welsh Corgis.1,7 New reports of familial PLN are likely to occur due to inbreeding, small foundation stock, popular sires, and

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<td>Note: *See <a href="http://www.wsava.org/HereditaryDefects.htm">http://www.wsava.org/HereditaryDefects.htm</a>.</td>
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Abbreviations: A, autosomal; CX, complex; D, dominant; GBM, glomerular basement membrane; GN, glomerulonephritis; GS, glomerulosclerosis; HN, hereditary nephritis; IBD/PLE, inflammatory bowel disease/protein-losing enteropathy; ICGN, immune-complex glomerulonephritis; JRD, juvenile renal disease; MPGN, membranoproliferative glomerulonephritis; R, recessive; SIIPD, small intestinal immunoproliferative disease.
removal of carriers of other known diseases while trying to perpetuate breed characteristics. Mix breed dogs and their families are also at risk, since the modes of inheritance may be dominant or complex.

**Summary**
In summary, many canine breeds have inherited glomerulopathies which are models for human disease, including GBM defects analogous to Alport syndrome, FSGS, and abnormal glomerular depositions of collagen III, amyloid, or immune complexes. The underlying molecular basis is only known for some breeds, and many more need their genetic defects defined. With GWAS, fine sequencing, and the future development of candidate gene sequencing panels specifically developed for dogs, many more underlying genetic defects will be able to be determined. Screening followed by genetic counseling will help breeders produce fewer dogs carrying at-risk genes while maintaining genetic diversity. Awareness of these animal models may benefit investigators studying the molecular basis for disease, inheritance patterns, progression, and treatment options.

**Disclosure**
The author reports no conflicts of interest in this work.

**References**


