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# CHARACTERIZATION OF GENETIC VARIATION AND BASIS OF INFLAMMATORY BOWEL DISEASE IN THE TOLL-LIKE RECEPTOR 5 GENE OF THE RED WOLF AND THE MANED WOLF

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**ABSTRACT** Characterizing Toll-like receptors across taxa can lead to an increasingly accurate documentation of the evolutionary processes acting within this receptor class, as well as a greater understanding of the diseases associated with these receptors. This study examines two sequenced portions of the Toll-like receptor 5 protein coding gene in two imperiled canid species: the near threatened maned wolf (*Chrysocyon brachyurus*) and the critically endangered red wolf (*Canis rufus*), to characterize genetic variation and investigate the presence of single nucleotide polymorphisms (SNPs) previously associated with canine inflammatory bowel disease (IBD). Both maned and red wolves suffer from inflammatory bowel disease, threatening the sustainability of their crucial *ex situ* populations. Here we report novel polymorphic positions found in maned and red wolf TLR5, differences in variation with regard to nucleotide polymorphisms and resulting amino acid variation between maned wolves, red wolves, gray wolves and domestic dogs. Domestic dog SNPs associated with IBD were not found to be polymorphic in maned wolves and red wolves. Samples of both focal species and gray wolves lack the protective alleles present in many dog breeds, suggesting a potential genetic predisposition for IBD in these two wild canid species and a possible development of these protective alleles post domestication. This potential predisposition informs *ex situ* management practices and treatment for IBD.

**KEY WORDS** maned wolf; red wolf; Toll-like receptor 5; Inflammatory Bowel Disease

With the perils of habitat fragmentation, hunting and disease threatening *in situ* populations, the viability of *ex situ* populations is becoming increasingly relevant to the survival of many species. This study focuses on two canid species: the critically endangered North American red wolf (*Canis rufus*) and the near threatened South American maned wolf (*Chrysocyon brachyurus*) (IUCN 2016). The red wolf, a canid that was once endemic to the southeastern United States, was considered extinct in the wild in 1980 due to habitat loss, hunting and the introgression of coyote genes (Fredrickson & Hedrick 2006). Due to this introgression, the taxonomic status of red wolves is highly controversial with many studies indicating that the red wolf is a hybrid species between gray wolves and coyotes while others insist it is a distinct species (Gese et al. 2015). The *in situ* population of red wolves was recovered with an intensive reintroduction program in North Carolina beginning in 1987, that has resulted in a population of approximately 75 individuals residing within the current 6,000 $km^2$ reintroduction area (Harrison 2014). The maned wolf faces many of its own challenges (Ratter et al. 1997, Deem & Emmons 2005, Maia & Gouveia 2002) and as of 2008 the highly fragmented *in situ* maned wolf population was estimated at only 17,000 mature individuals and is predicted to decline by at least 10% in the next ten years (Paula et al. 2008).

Though the importance of viable *ex situ* populations for both maned and red wolves is becoming increasingly apparent, both species suffer health (Phillips & Scheck 1991, Gilioli & Silva 2000) and reproductive difficulties (Rabon 2011, Ginsberg 1994, Rodden et al. 1996, Johnson et al. 2014). Gastrointestinal disease is a major factor in mortalities in both red and maned wolves and has a high prevalence in both *ex situ* populations (Acton et al. 2000, Maia & Gouveia 2002, Stirling et al. 2008, Seeley et al. 2016).

Inflammatory bowel disease (IBD), a common diagnosis in both species, is characterized by inflammation of the gastrointestinal tract (Craven et al. 2004). IBD is a multifaceted disorder (German et al. 2003) that has both microbial (Simpson & Jergens 2011, Inness et al. 2007, Xenoulis et al. 2008) and genetic bases (Cario & Podolsky 2000, Himmel et al. 2008) in other species. In the domestic dog (*Canis familiaris*), the disease is linked to single nucleotide polymorphisms (SNPs) in the Toll-like receptor 4 (TLR4) and Toll-like receptor 5 (TLR5) genes (Kathrani et al. 2010), with two protective alleles against IBD identified in TLR5 across 38 different breeds (Kathrani et al. 2011).

Toll-like receptors (TLRs) are pattern recognition receptors essential to the functioning of the innate immune system that belong to a large family of interleukin 1 receptors (Akira 2003). These transmembrane receptors consist of a cytoplasmic Toll-interleukin 1 receptor (TIR) domain, responsible for downstream signal transduction, transmembrane domains and leucine rich repeat (LRR) extracellular domains (Kawai & Akira 2010). These extracellular LRR motifs form a ligand-binding horseshoe shaped solenoid-like structure that recognizes pathogen associated molecular patterns (PAMP) (Leulier & Lemaitre 2008, Bell et al. 2003) on the surface of bacterial cells and helps to initiate an appropriate immune response through the production of cytokines (Akira et al. 2001). The pathogen recognition capability of TLRs make them an important component of the innate immune system and indicates a greater specificity for this system (Kawai & Akira 2010). Six TLR families have been identified in vertebrates, with each family recognizing a specific class of PAMP (Roach et al. 2005). Receptors within the TLR5 family are responsible for detecting bacterial flagellin and mammalian TLR5 recognizes flagellin from both Gram-negative and Gram-positive bacteria (Hayashi et al. 2001).

Phylogenetic analysis places the origin of TLRs at 700 mya (Leulier & Lemaitre 2008). Studies attempting to identify the applicable model of evolution for these immune genes have oscillated between claiming that vertebrate TLRs are highly conserved because of the functional constraint of PAMPs (Roach et al. 2005) or that they are experiencing positive selection as a result of their constant interaction with rapidly evolving pathogens (Areal et al. 2011). Signatures of positive selection have been found in all mammalian TLRs across carnivores, lagomorphs, rodents, primates and artiodactyla, with non-viral TLRs having higher rates of positive selection than viral TLRs (Areal et al. 2011). In all species where adaptive selection has been identified, selective pressure is focused on the LRR extracellular domain because of its interaction with PAMPs (Areal et al. 2011) while a large portion of the TLR domain remains relatively conserved (Akira 2003). In TLR5, evidence of adaptive evolution has been found in the LRR pattern recognition extracellular domain (Wlasiuk et al. 2009, Smith et al. 2012) and a specific signature of adaptively evolving codons within this domain identified in domesticated mammals (Smith et al. 2012).

Toll-like receptors, because of their important role in the innate immune system, have been associated with many maladies. Mutations in TLRs, or their associated signaling pathways, have been linked to pneumococcal disease, systemic lupus erythematosus, chagas cardiomyopathy, malaria and tuberculosis in humans (Netea et al. 2012). Of particular interest to the present study, TLRs have also been implicated in the pathogenesis of gastrointestinal disorders (Netea et al. 2012). A healthy gut is characterized by its ability to regulate its immune response to food antigens and commensal bacteria while maintaining the ability to respond to pathogens. When this balance is disrupted, it can lead to inflammation and IBD. TLRs play an important role in maintaining this balance (Fukata & Abreu 2008). In humans, polymorphisms in

the TLR2 gene as well as the TLR4 gene are more likely to be present in patients with colorectal cancer, and a TLR9 polymorphism has been associated with Crohn's disease. SNPs in TLR1, 2 and 6 associate with both ulcerative colitis and Crohn's disease (Fukata & Abreu 2008), and genomic methods implicate TLR7 and 8 in celiac susceptibility (Netea et al. 2012). In mice, individuals that lack TLR2, 4, 5 or 9 are more likely to develop colitis and have a higher mortality risk (Maloy & Powrie 2011, Vijay-Kumar et al. 2007). Polymorphisms in the TLR5 gene are significantly associated with IBD in domestic dogs (Kathrani et al. 2010), with two protective SNPs identified across many different dog breeds (Kathrani et al. 2011).

Our aims in the present study were: 1) to characterize polymorphisms within two selected regions of the TLR5 gene in maned and red wolves; and 2) to determine the role of previously identified genetic markers for IBD in these two disease-prone species. We report novel polymorphisms in these previously unsampled threatened species and differing variability in TLR5 among four canid species: the maned wolf, red wolf, gray wolf and domestic dog. We also demonstrate a potential role for IBD SNPs in the pathogenesis of IBD within maned wolves and red wolves.

## METHODS

Thirty one maned wolves (24 *ex situ* and 7 *in situ)* and fifteen red wolves were sampled for this study. Due to the opportunistic collection of samples an IACUC was not required by either the Smithsonian Conservation Biology Institute's IACUC committee or George Mason University's IACUC committee. *Ex situ* maned wolf samples were collected from individuals housed at the Smithsonian Conservation Biology Institute in Front Royal, VA and at four other Association of Zoos and Aquariums (AZA) accredited institutions. Maned wolf *in situ* samples represent populations situated in Bolivia (N=5), Argentina (N=1) and Brazil (N=1). Red wolf *ex*

155 *situ* samples were collected from individuals at the Point Defiance Zoo and Aquarium in Tacoma,
156 WA. For extant *ex situ* individuals of both species, blood was collected opportunistically during
157 routine veterinary examinations. For deceased *ex situ* individuals, necropsy samples of liver were
158 collected. *In situ* maned wolf samples were obtained from DNA extracted for previous studies
159 investigating maned wolf genetic variability throughout their range (Gonzalez et al. 2015).
160 Samples from Argentina and Brazil are from samples stored at the Conservation Genetics
161 Laboratory at Departamento de Biodiversidad y Genética-IIBCE-Uruguay. Bolivian samples
162 were obtained from populations in Noel Kempff Mercado National Park (Emmons et al. 2012).
163 DNA was extracted from whole blood and tissue using a Qiagen DNeasy blood and tissue
164 kit (QIAGEN). For extraction from whole blood Qiagen tissue lysis buffer was substituted for
165 phosphate buffered saline (PBS) and DNA eluted in 100 µl buffer AE with no repeat elution. For
166 tissue samples a 1g tissue sliver was used for extraction, incubated at 56 ºC overnight for
167 thorough lysis and eluted in 100 µl buffer AE with no repeat elution. DNA concentration and
168 quality was measured using a Nanodrop 1000 Spectrophotometer (Thermo Scientific).
169 Two fragments surrounding the three IBD associated SNPS in domestic dogs (Kathrani et
170 al. 2010) were selected for amplification (Fig. 1). Both fragments are approximately 350bp
171 (trimmed) with one fragment (Frag1) containing SNPs G22A (G727A in this study) and C100T
172 (C805T); and the second fragment (Frag2) containing SNP T1844C (C2549T). Primers (Supp
173 Fig. 1) were designed to amplify these fragments using the Primer3 software (Untergasser et al.
174 2012) against domestic dog TLR5 (Genbank accession NW_0119176 and Ensembl accession
175 ENSCAFT00000018059). AmpliTaq Gold Taq and buffer (Applied Biosystems) were used for
176 all polymerase chain reactions (PCR) but cycling conditions varied between fragments (Supp Fig.
177 2). All reactions were run on a Biorad DNA engine Peltier thermal cycler tetrad (Bio-Rad). To

178 inspect products for specific binding, and for the quality and quantity of amplified DNA, PCR
179 products were run on a 1.5% agarose gel using GelRed dye (Biotium), a BioRad PowerPac Basic
180 gel box and Tris-Acetate (TAE) buffer. Gels were visualized using a MultiDoc-it Digital
181 Imaging System (UVP).

182 Effective purification methods varied based on fragment and species due to the variation
183 in size of nonspecific bands appearing in PCR products. For maned wolf samples nonspecific
184 bands were typically less than 100 bp, and fragments were purified using 2 µl of EXOsapIT
185 (Affymetrix) per 7 µl of PCR product and incubated at 37 ºC for 25 min followed by 80 ºC for
186 15 min. In red wolves, where contaminating products were typically larger than 100 bp, products
187 were purified with solid phase reversible immobilization using carboxyl coated magnetic beads
188 (SPRI beads). Samples were incubated for 10 min at room temp, then 5 min on a magnetic
189 separation plate, subsequently washed with 100% ethanol and eluted with Qiagen Elution Buffer
190 (QIAGEN) and 20% Tween (EBT) (CSH protocol).

191 Purified products were sequenced using Big Dye Terminator v3.1 (Applied Biosystems).
192 Samples were heated to 96º C for 2 min, followed by 24 cycles of 96 ºC for 10 sec, 50 ºC for 10
193 sec and 60 ºC for 4 min. Sequenced fragments were cleaned using a Sephadex G50 (GE
194 Healthcare) column. After the application of water to dry Sephadex powder and the subsequent
195 solidification of the powder, sequencing products were applied to the column, and centrifuged at
196 2500 RPM for 5 min in an Allegra X-15R plate centrifuge (VWR). Ten microliters of Hi-Di
197 Formamide (Life Technologies) was added to each well of sample and the plate was sequenced
198 on an ABIPRISM3100 genetic analyzer (Life Technologies). All fragments were sequenced on
199 both the forward and reverse strands to confirm polymorphic positions.

Sequenced fragments were aligned using the software program Sequencher 5.3 (Gene Codes) and inspected manually for the presence of polymorphic positions. Subsequent contigs were aligned with available published domestic dog sequences for TLR5 (Genbank accession NW_0119176 and Ensembl accession ENSCAFT00000018059). SNP position was reported in reference to ENSCAFT00000018059. The number of SNPs in the two amplified regions of red wolf and maned wolf TLR5 were counted and compared to the number of SNPs in the same two regions in domestic dogs (Cusco et al. 2014). Heterozygous positions were identified in Sequencher and corroborated by manual inspection. For heterozygous loci, the gametic phase was determined using the software PHASE (Stephens et al. 2001). Mean heterozygosity was calculated and compared between *ex situ* and *in situ* maned wolf samples using a Mann-Whitney U test and between maned wolves, red wolves and previously published values for domestic dog and gray wolf (Cusco et al. 2014) using a one way ANOVA with a Bonferroni post hoc in SPSS. Nucleotide diversity (Θ) was calculated using a Tajima's test of neutrality in MEGA 5.22 (Tamura et al. 2011). To investigate patterns of selection rates of non-synonymous (dN) and synonymous (dS) substitutions were calculated using both the codon based HyPhy selection model and the Nei and Gojobori (1986) method, with a Jukes- Cantor correction using MEGA software version 5.2.2 (Tamura et al. 2011).

Translation of fragment sequences into amino acids was performed in Sequencher (Genecodes). Amino acid change ratio was calculated by dividing the length of the resulting translation for each fragment by the number of amino acid changes created by non-synonymous SNPs. The amino acid change ratio for each fragment was compared to published data for domestic dog TLR5 (Cusco et al. 2014). Protein domain predictions were made in SMART (Letunic et al. 2014) and used to identify domains encompassed by Frag1 and Frag2 as well as

the domain type for identified SNPs. PROVEAN (Choi & Chan 2015) was used to predict the functional impact of SNPs resulting in non-synonymous mutations by taking into consideration the amino acid sequence surrounding the residue of interest and classifying the mutation as either deleterious or neutral.

**RESULTS**

We detected two polymorphic positions in maned wolves, both in Frag1, and six polymorphic positions in red wolves with four in Frag1 and two in Frag2 (Table 1 & Fig. 1). In contrast, inspection of previously published data (Cusco et al. 2014) revealed that domestic dogs and gray wolves have more SNPs within these two TLR5 regions. Domestic dogs have seven SNPs in Frag1 and three SNPs within Frag2 and gray wolves have 5 SNPs in Frag1 and 6 SNPs in Frag2 (Table 2). No polymorphic positions were shared between maned wolves and red wolves. Neither of the SNPs identified in maned wolves were found to be polymorphic in domestic dog and only one red wolf SNP was common to domestic dogs (A729G). A729G was also seen to be polymorphic within the published gray wolf SNP data set in addition to G2274A (Table 1).

In contrast with the finding of more SNPs in TLR5, dogs and gray wolves did not significantly differ from maned and red wolves in mean heterozygosity at these SNPs ($P \geq 0.1$) (Table 2). Tajima's D nucleotide diversity measures for maned and red wolves found a greater average variability in maned wolves ($\Theta = 0.002599$) than in red wolves ($\Theta = 0.0013765$) echoing the trend seen in heterozygosity with more variability in maned wolves than red wolves. Within maned wolves there was no significant difference in mean heterozygosity between *ex situ* and *in situ* samples ($P \geq 0.1$).

A Z-test of selection for each species by fragment revealed no evidence of non-neutral selection for Frag1 in maned wolves and Frag2 in red wolves ($P \geq 0.05$). The ratio of dN/dS could not be calculated for these fragments because of the lack of synonymous mutations in each. In red wolf Frag1, although the codon based Z test of selection showed only neutral selection ($P \geq 0.05$), HyPhy calculated dN/dS at 0.146, indicating a slight evidence of purifying selection (Table 3). Tests of selection were not performed for maned wolf Frag2 due to the lack of synonymous or non-synonymous mutations.

Tests of selection between species found evidence for both purifying and positive selection. The dN/dS ratio for Frag1 between maned and red wolves was 0.3362 indicating purifying selection. The Nei Gojobori method with a Jukes Cantor correction for purifying selection also found purifying selection between these species in Frag1 ($P \leq 0.05$) with the probability at 0.05. For maned wolf and red wolf Frag2, strong evidence was found for positive selection ($P \leq 0.05$) with a codon based Z test of selection using a Nei Gojobori model with Jukes Cantor correction yielding an overall probability of 0.03 (Table 3).

We used an amino acid change ratio to compare the effect of these described polymorphic sites on resulting proteins. Domestic dogs and gray wolves had a higher amino acid change ratio than either maned or red wolves, which may be due to a population bottleneck in red wolves or to a higher level of evolutionary conservation of the TLR5 locus in both threatened species (Table 4).

We predicted protein domain structure for the selected fragments. Frag1 for both maned wolves and red wolves consisted of three unknown domains and two low complexity regions. Frag2 consisted of three leucine rich repeat (LRR) regions, one leucine rich repeat C-terminal (LRR-CT) region and one unknown region. All SNPs in Frag1 in both species were in areas with

268 unknown SMART predictions while both SNPs in red wolf Frag2 were in the LRR region (Table
269 1).

270 Both maned wolf SNPs were non-synonymous compared with two of six red wolf SNPs,
271 five of eleven gray wolf polymorphisms and four of ten domestic dog polymorphisms. All non-
272 synonymous maned wolf and red wolf SNPs were in Frag1 while domestic dog and gray wolf
273 non-synonymous SNPs were more evenly distributed between the two fragments.

274 The functional impact of these non-synonymous SNPs was tested using PROVEAN and
275 all identified red wolf and maned wolf non-synonymous SNPs were shown to have a neutral
276 effect on protein function (Table 1). Comparatively, three non-synonymous domestic dog SNPs
277 and four gray wolf non-synonymous SNPs present within Frag1 and Frag2 were reported to have
278 a probably or possibly damaging impact on protein function (Cusco et al. 2014). One of these
279 SNPs is T1844C, a SNP previously associated with domestic dog IBD (Kathrani et al. 2010),
280 which was shown to be deleterious (Cusco et al. 2014). All identified domestic dog and gray
281 wolf SNPs (Cusco et al. 2014) with a potential functional impact are not present as polymorphic
282 positions in maned or red wolves.

283 The SNPs identified as associated with domestic dog IBD (G727A, C805T and C2549T)
284 were not polymorphic in maned or red wolves. However, both red wolves and maned wolves
285 lacked the protective T allele in C805T and C2549T and the risk allele A in G727A (Fig. 2).
286 Gray wolves also lack these protective alleles (Cusco et al. 2014) indicating that the non-
287 protective C is potentially ancestral. Provean predictions show that the deleterious impact of the
288 leucine to serine amino acid change in the C2549T SNP is retained in maned wolves and red
289 wolves (Table 5).

290 **DISCUSSION**

291 Toll-like receptors are increasingly becoming a target of research due to their crucial
292 roles as sentinels of the innate immune system and their associations with many common and
293 debilitating diseases in both humans and in animal models (Netea et al. 2012). Our
294 characterization of the TLR5 locus is the first description of polymorphism in this locus in two
295 threatened canid species in need of careful captive management. A greater understanding of the
296 genetic diversity of these immune genes should contribute to maintaining healthy *ex situ*
297 populations.
298 The larger number of SNPs in domestic dog and gray wolf and the lack of significant
299 difference between mean heterozygosity in all four species implies that these regions may be
300 more variable in gray wolf and domestic dog but that heterozygosity has been maintained over
301 evolutionary time. This would suggest a role for balancing selection in this system, which has
302 been implicated in the evolution of innate immunity in humans (Ferrer-Admetlla et al. 2008).
303 The higher amino acid change ratio in domestic dogs and gray wolves indicates that the observed
304 genetic variation results in changes in amino acid composition within the two TLR5 regions.
305 Future studies should screen for variation across a larger number of canid species and individuals
306 to confirm levels of variation across this family.
307 Consistent with reports that identify the leucine-rich repeat region of TLR5 as a site
308 under adaptive selection due to its direct interaction with evolving pathogens (Areal et al. 2011),
309 signatures of adaptive selection were detected within the LRR here between maned and red
310 wolves, indicating that this ligand binding pocket is potentially adapting to compete with
311 evolving microbes, as in other mammalian species. However this hypothesis needs to be further
312 tested by conducting comparative microbiome analyses in maned and red wolves. The higher
313 number of SNPs in both gray wolf and domestic dog and their higher propensity to be non-

synonymous and damaging, is suggestive of deleterious allele accumulation in this region of TLR5. Deleterious allele accumulation is seen in domestic dogs and gray wolves and could be a result of a previously documented bottleneck in domestic dogs and in the European population of wolves referenced in this study (Cusco et al. 2014, Cruz et al. 2008, Pilot et al. 2014). Some of the non-damaging mutations found in maned and red wolves could be products of adaptation to different microbial and dietary environments that require a species-specific function of TLR5 (Bergman et al. 2010). The complete lack of overlap in variable sites between all four canid species and the conservation of just one polymorphic position between red wolves, gray wolves and domestic dogs further suggests a potential species-specific function for TLR5 in maned wolves and red wolves, as is seen in other species (Werling et al. 2009).

The finding of less variation in maned and red wolf TLR5 fragments than in domestic dog and gray wolf is supported by: (1) the low SNP number in maned wolves and red wolves compared to domestic dogs and gray wolves, (2) the neutral functional impact of observed non-synonymous SNPs, (3) the low amino acid change ratio and the low number of SNPs in both Frag1 and the putatively variable LRR region in Frag2. This potential within-species conservation supports previous studies that identify TLRs as a conserved class of proteins (Roach et al. 2005). The finding of distinct variation between species, especially in the ligand binding site, points to a potential specificity of function of TLR5 in maned wolves and red wolves, likely influenced by differences in their microbial environments (Takeda et al. 2003). The implications of these findings for studies of the adaptive nature of TLR5 are limited by the lack of a robust demographic analysis that would incorporate the distinct recent evolutionary histories of these four species. That said, we chose samples that capture the full range of

336 diversity in the current red wolf and maned wolf populations, especially through the inclusion of
337 *in situ* maned wolf samples.
338 Within these two now characterized fragments lie the three SNPs previously associated
339 with domestic dog IBD (G727A, C805T and C2549; Kathrani et al. 2010). The non-polymorphic
340 nature of these SNPs in maned wolves and red wolves makes them unsuitable as diagnostic
341 markers for inflammatory bowel disease. However, all sampled *ex situ* and *in situ* maned wolves
342 and red wolves lacked the protective thymine present in the alleles validated across all dog
343 breeds (C805T and C2549T; Kathrani et al. 2011), suggesting that both taxa may carry a genetic
344 predisposition to IBD. The high prevalence of IBD in captive populations of both species, and
345 the retention of the deleterious effect of the C2549T SNP, are further evidence for this
346 predisposition. A large population of gray wolves also lacks the protective allele T in both
347 C805T and C2549T, indicating that the non-protective allele C is ancestral and that the T allele
348 emerged in domestic dogs (Cusco et al. 2014). The lack of the domestic dog protective alleles in
349 these threatened canids is not enough to prove a genetic predisposition to IBD. Future work is
350 needed to correlate standardized molecular and pathological markers of disease status with these
351 genetic findings.
352 Recent work on dog domestication has identified a host of genes containing a signature of
353 domestication, typically in mutations that allow dogs to better adapt to association with humans
354 (Wang et al. 2013). Adaptation to a starch-based diet plays an essential role in domestication and
355 provides a relevant link to IBD (Axelsson et al. 2013). Since TLR5 recognizes bacterial flagellin,
356 a shift in gut microbiome composition as a result of diet change (Middelbos et al. 2010) can
357 result in an inappropriate hypo- or hyper- activation of the TLR pathway and lead to

358 inflammation (Cario 2010). It is possible that the T allele in domestic dog C805T and C2549T
359 developed as a protection against this type of inflammation.
360 *Ex situ* maned and red wolves in the United States are primarily fed artifical starch based
361 diets (Songsasen 2014, Harrison 2014) in contrast to their *in situ* omnivorous and carnivorous
362 diets respectively (Aragona & Setz 2001, Paradiso & Nowak 1972). Differences in diet between
363 captive and wild individuals can result in changes to the intestinal microbial community
364 (Turnbaugh et al. 2009). Feeding *ex situ* wild canids diets developed for domestic dogs may
365 promote the development of microbial communities more similar to those of domestic animals
366 than to those of their *in situ* conspecifics (De Jesús-Laboy et al. 2011). Since Toll-like receptor 5
367 specifically recognizes bacterial flagellin, a dog-like microbiome interacting with a maned or red
368 wolf Toll-like receptor evolutionarily adapted to the native microbiome of these species could
369 result in a hypo- or hyper-activation of this portion of the innate immune system. While dogs
370 have had about 10,000 years (Wang et al. 2013, Freedman et al. 2014) since the domestication of
371 grains to adapt to a starch based diet, maned and red wolves have been managed by species
372 survival plans in captivity for only 30 and 35 years respectively. Adaptation to starch based diets
373 should not be a goal of captive breeding programs and should be avoided at all costs for any *ex*
374 *situ* programs that may eventually result in reintroduction. With further investigation, this
375 relationship between putative genetic predisposition, and inappropriate diet in combination with
376 the resulting foreign microbial community could explain the high prevalence of IBD in *ex situ*
377 maned and red wolves.

378 Future studies should focus on documenting and correlating the gastrointestinal
379 microbiome compositions of *ex situ* and *in situ* maned wolves and red wolves with clinical,
380 histopathological and serum markers of IBD. Further characterizations of the full sequence of

TLR5 for these sampled populations of maned and red wolves, in addition to other canid species, could inform the evolutionary nature of toll like receptors within the Canis genus. Additionally, with more research on the accurate diagnosis of maned and red wolf IBD, future work can focus on correlating the TLR5 SNPs identified in domestic dogs with a definitive IBD diagnosis in maned and red wolves.

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## Figures and Tables

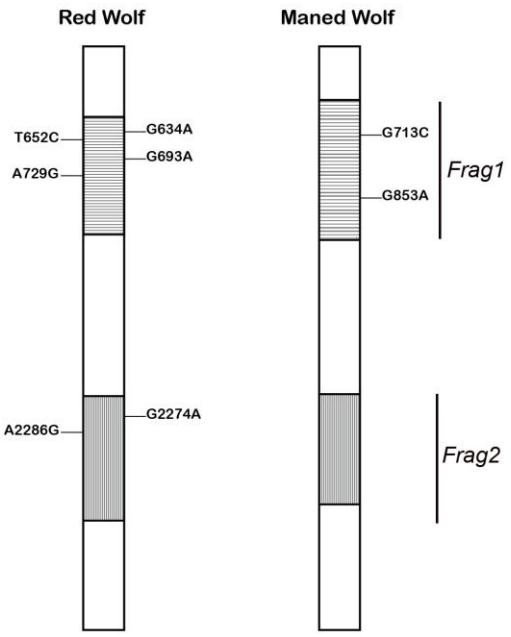


Figure 1: Single nucleotide polymorphisms identified in TLR5 in 29 maned wolves and 15 red wolves within the indicated Fragment 1 and 2 regions.

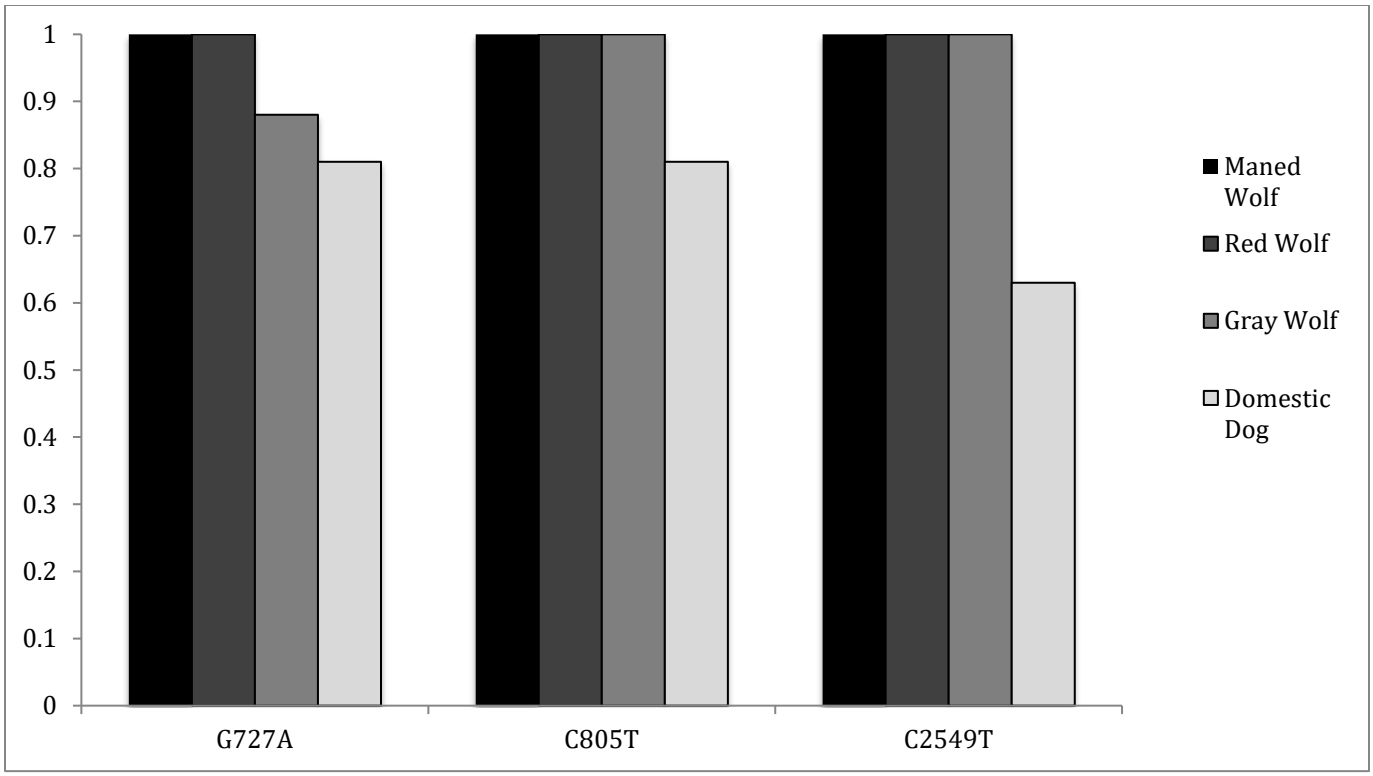


Figure 2: Observed allele frequency for IBD associated SNPs (A in G727A, C in C805T and C2549T) in maned wolves and red wolves. Allele frequencies for gray wolf and domestic dog IBD SNPs provided by Cusco et al. 2014.

Table 1: Polymorphic sites in TLR5 in 29 maned wolves and 15 red wolves

| Position | SNP ID | Codon | | Aa Subst[a] | Protein Domain[b] | Provean Output[c] | Allele Freq | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Allele 1 | Allele 2 | | | | Maned Wolf | Red Wolf | Gray Wolf[d] | Domestic Dog[d] |
| 634 | G634A | **G**TC | **A**TC | val/ile* | ncp[1] | neutral | G(1) | G(.86) | | G(1) |
| 652 | T652C | **T**GG | **C**GG | trp/arg* | ncp | neutral | T(0) | T(.73) | | T(1) |
| 693 | G693A | CC**G** | CC**A** | pro/pro | ncp | | G(1) | G(.91) | | G(1) |
| 713 | G713C | C**G**C | C**C**C | arg/pro* | ncp | neutral | G(.75) | G(1) | | G(1) |
| 729 | A729G | GC**A** | GC**G** | ala/ala | ncp | | A(0) | A(.82) | A(.4) | A(.39) |
| 853 | G853A | **G**TC | **A**TC | ile/val* | ncp | neutral | G(.54) | G(0) | | G(0) |
| 2274 | G2274A | CG**G** | CG**A** | arg/arg | LRR[2] | | G(1) | G(.92) | G(.76) | G(1) |
| 2286 | A2286G | GC**A** | GC**G** | ala/ala | LRR | | A(0) | A(.92) | | A(0) |

SNP position is in reference to ENSCAFT00000018059 and SNP ID includes the most frequent allele first, followed by the position and the least frequent allele.

[a] Amino acid substitution * non-synonymous aa change

[b] Protein domain predicted by SMART [1] ncp, no confident prediction [2] LRR, leucine rich repeat region

[c] Provean function prediction of non-synonymous SNPs only

[d] Gray wolf and red wolf allele frequencies provided by Cusco et al. 2014

Table 2: Comparison of SNP number and SNP heterozygosity in maned wolves, red wolves, gray wolves and domestic dogs

| Species[a] | Number of SNPs | | | Mean Heterozygosity[d] |
|---|---|---|---|---|
| | Syn[b] | Non-Syn[c] | Σ | |
| Maned Wolf | 0 | 2 | 2 | 0.44 ± 0.09* |
| Red Wolf | 4 | 2 | 6 | 0.23 ± 0.10* |
| Gray Wolf | 6 | 5 | 11 | 0.27 ± 0.17* |
| Domestic Dog | 6 | 4 | 10 | 0.26 ± 0.15* |

Differences in mean heterozygosity between species were tested for significance by a one way ANOVA with a Bonferroni post hoc
* $P \geq 0.10$
[a] Mean heterozygosity for gray wolf and domestic dog extrapolated from data published in Cusco et al. 2014
[b] Synonymous
[c] Non-synonymous
[d] Mean ± SD

Table 3: Tests for Neutral, Purifying and Positive Selection and dN/dS for maned wolves (MW) and red wolves (RW)

| Species/Frag[a] | dN/dS[b] | Selection Test[c] | | | | | |
|---|---|---|---|---|---|---|---|
| | | Neutral Selection | | Purifying Selection | | Positive Selection | |
| | | Probability[d] | Test Statistic[e] | Probability[f] | Test Statistic | Probability[g] | Test Statistic |
| MW[1] Frag1 | | 0.17 | 1.39 | 1.00 | -1.35 | 0.08 | 1.43 |
| RW[2] Frag1 | 0.146 | 0.27 | 1.11 | 0.13 | 1.15 | 1.00 | -1.14 |
| RW Frag2 | | 0.14 | 1.48 | 1.00 | -1.40 | 0.07 | 1.45 |
| MW and RW Frag1 | 0.3362 | 0.09 | 1.73 | **0.05** | -1.67 | 1.00 | -1.69 |
| MW and RW Frag2 | | 0.07 | -1.81 | 1.00 | -1.76 | **0.03** | 1.88 |

MW Frag2 not included due to lack of variable sites, significant values in bold
[a]Species abbreviations [1] Maned Wolf [2] Red Wolf
[b] dN/dS for fragments with both non-synonymous and synonymous changes only
[c] Codon-based Z test of Selection, Nei-Gojobori method with Jukes-Cantor correction
[d] Probability of rejecting the null hypothesis of dN=dS
[e] Test statistic= dN-dS
[f] Probability of rejecting the null hypothesis of dN=dS for dN<dS
[g] Probability of rejecting the null hypothesis of dN=dS for dN>dS

Table 4: Comparison of amino acid change ratio in maned wolf, red wolf, gray wolf and domestic dog TLR5

| Species[a] | Protein length (aa) | AA change ratio[b] |
|---|---|---|
| Maned Wolf | 288 | 1/144 |
| Red Wolf | 279 | 1/139.5 |
| Gray Wolf | 288 | 1/57.6 |
| Domestic Dog | 288 | 1/72 |

[a] Amino acid change ratio for gray wolf and domestic dog extrapolated from data published in Cusco et al. 2014
[b] Amino acid ratio: amino acid changes caused by nsSNPs divided by the protein length

Table 5: Polymorphic sites associated with Inflammatory Bowel Disease in maned wolves, red wolves, gray wolves and domestic dogs

| Position | SNP ID | Codon | | AA Subst[a] | Protein Domain[b] | Provean Output[c] | Allele Freq | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Allele 1 | Allele 2 | | | | Maned Wolf | Red Wolf | Gray Wolf[d] | Domestic Dog[d] |
| 727 | G727A | **G**CG | **A**CG | ala/thr* | ncp[1] | neutral | G(1) | G(1) | G(.88) | G(.81) |
| 805 | C805T | **C**GC | **T**GC | arg/cys* | ncp | neutral | C(1) | C(1) | C(.99) | C(.81) |
| 2549 | C2549T | T**C**G | T**T**G | ser/leu* | LRR CT[2] | deleterious | C(1) | C(1) | C(.98) | C(.63) |

SNP position is in reference to ENSCAFT00000018059 and SNP ID includes the most frequent allele first, followed by the position and the least frequent allele.

[a] Amino acid substitution * non-synonymous aa change

[b] Protein domain predicted by SMART [1] ncp, no confident prediction [2] LRR CT, leucine rich repeat C-terminal region

[c] Provean function prediction of non-synonymous SNPs only

[d] Gray wolf and red wolf allele frequencies provided by Cusco et al. 2014

## Supplement

**Supp. Fig. 1**

| Primer | Manufacturer | Direction | Primer sequence |
|---|---|---|---|
| TLR5 Fragment 1 | Eurofins MWG (Huntsville, USA) | Forward | 5'-GTT TCT CAA GGA CCC AGC AC-3' |
| | | Reverse | 5'-TCC TGA AGG CTT CTC TGT CG-3' |
| TLR5 Fragment 2 | Eurogins MWG (Huntsville, USA) | Forward | 5'-GCT GCA CCT GAA CCA CAA C-3' |
| | | Reverse | 5'-TGA AGA GGG AGA ACG TGA GG-3' |

**Supp. Fig. 2**

| Frag1 cycling conditions | | |
|---|---|---|
| Cycle Number | Settings: | |
| 1 | 95°C | 10 minutes |
| 35 | 95°C | 1 minute |
| | 57°C | 1 minute |
| | 72°C | 2 minutes |
| 1 | 72°C | 7 minutes |
| Frag2 cycling conditions | | |
| Cycle Number | Settings: | |
| 1 | 95°C | 8 minutes |
| 2 | 95°C | 30 seconds |
| | 64°C | 30 seconds |
| | 72°C | 1 minute |
| 2 | 95°C | 30 seconds |
| | 62°C | 30 seconds |
| | 72°C | 1 minute |
| 2 | 95°C | 30 seconds |
| | 60°C | 30 seconds |
| | 72°C | 1 minute |
| 2 | 95°C | 30 seconds |
| | 58°C | 30 seconds |
| | 72°C | 1 minute |
| 2 | 95°C | 30 seconds |
| | 56°C | 30 seconds |
| | 72°C | 1 minute |
| 1 | 72°C | 15 minutes |

**Supp. Fig.3**

DD ATGGGAGGAGAGCGTGCGTGCAGAGGAAGCAGCACGTGCCAAGTCCCAGC 50
MW
RW

DD CCTGGAAGTGCGTGGAGAGGCGGCCGGAGCCCCCGTGTTGCACCCCCCGC 100
MW
RW

DD CTCCCCGCTGGGCCTCCTTCCTTTGCATCCCTGGGGCCCCTGGATGTCAT 150
MW
RW

DD CGAGTCATCGGGGGCCTTCCTGGCCACTCTGGCCGCTGCCGCCTGCCCCA 200
MW
RW

DD GGACGTGCGCCCCAGCTGGCCCGTGTGTCCAGCCCCTGCTGCACCCTGTG 250
MW
RW

DD CACAGAGCGGACGTGTGGCACTTGTCCAGATGACGGGCGCCCTGAGCCGC 300
MW
RW

DD GCCGCGCTCGCCCCCACAGGCCTGGGCAGGGGGTGGGAGGGGGATGCACT 350
MW
RW

DD GACCCGTCAGGCTGGGCGCTTCGCGGATGGTGGCCCGAAGGACCAGCGTG 400
MW
RW

DD TGCGTGCTGACCCGGGCCGTGTGTGGAGCGCGCAGGGGGCGGAGGGGCGG 450
MW
RW

DD GCCCCCGGCACTGGGCGGGGGCGGCACCAGTATCCTCCGCCTGCCATTTT 500
MW
RW

DD CCCCGAAGCCCTGCACGCATCCCGATTGAGTGACGGCAAACAGACTCTCC 550
MW

```
RW

DD    TCAAGGTAAGTGTTTCTCAAGGACCCAGCACGGCGCTGAGTGCGCGTCCC 600
MW                             ----------------
RW

DD    GCCGGGCGCACGTGTGGGGGGAGGCAGGTGCCCGTCCAGGGGCCCCCGTC 650
MW    ---A---C-------------------------------------A--
RW            ----------------------R----------------

DD    CTGGGCCCCGGGGTGGCGTTGGGCTTGCACGGCTGTGTTTCCGTCCCGCA 700
MW   -C-----------------------------------------------
RW   -Y---------------------------------------R-------

DD    GGATCATGGGCCGCCAGCTGGGCCGCACGCTGGGGCTGCTGCTTGTGGCC 750
MW    -----------S----------T--G----------------------
RW    -------------------------G-R--------------------

DD    GGCGCCGTGGCCGCAGCATCCTGCTGCGTGGCTGACGGCCGGAGGGCCCT 800
MW    -------------G----------------C--T--------------
RW    -------------G----------------------------------

DD    GTACCGCTCCTGCAACCTCAGCCAGGTGCCCCCGGTCCCCAGCACCACCG 850
MW    ---------------------------------------T-------
RW    ------------------------------------------------

DD    AGATCCTCCTGCTGAGCTTCAACTACATCCGGGCCGTCACCCGCGCCTCG 900
MW    --R-------------------------------------------
RW    ------------------------------------------------

DD    TTCCCCCTCCTGGAGCGGCTGCAGCTGCTGGAGCTGGGGACGCAGCAGAC 950
MW    --------------------
RW    ----------------------------------------------

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RW

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MW
RW

DD    CAGGGGCTGCCCCACCTGCAGGAACTCCGGCTGTTCGCCTGTGGCCTCTC 1100
MW
RW
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RW

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RW

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MW
RW

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MW
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MW
RW

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MW
RW

DD GGGGGCTGCCCCGGCTCCGGGTGCTGCACCTGAACCACAACTACCTGGCC 2250
MW
RW

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RW                ---R-----------R--------------

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RW    -------------------------------------------------

DD    CCTTGGAGGTGCTGGATGTGTCCAGGAACCAGCTCCTGTCCCTGGACCCC 2400
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RW    -------------------------------------------------

DD    GGGCTGCTCGCCCCGCTCAGAGCCGTGGACCTAACGCACAACAAGTTCAT 2450
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RW    -------------------------------------------------

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RW    ----C-------------------------------------------C-

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MW
RW

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MW
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RW

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MW
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MW
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DD GGGGCGCCGACCTCACTGCACCGGGGCCCCGGGGGCGCTGCTCCTCCGCG 3600
MW
RW

DD GCGGGCGCCCGGGTCCGACAAAGGGCGAGGGCGCGAGCGGTGCGGCGCAG 3650
MW
RW

DD GAGCTCAGGGTCCGCGCGGAGGACCCGGGAGCACACACGGCCCGAGGAGC 3700
MW
RW

DD CGCCCCGCGCCCGCCCCGCCCTCGGTCGCGCCCCCGCCGCAGCCCCAGCC 3750
MW
RW

DD CCCCGCGCCCCCGCCCGGCCCCGCCGCCGCCCCCCGCGGCTGCCCCGACC 3800
MW
RW

DD CTGCCCGCCCTCCGCCCGCGCGGGCTGCCCGGCCCCGCGTCCTTACCCGG 3850
MW
RW

DD TCTCCCGGCCCCGCGGCGCGGGGGGCGGCGGCGGCGGCGGCGGCGGC 3900
MW
RW

DD GGGGCCGGGACGCGTCCACGCAGGAGACAGGCGCCCCCGACGCGCCGGCC 3950
MW
RW

DD CCGATGCGGACCCGGAGCCGGCTTCCGCCTCCCGCCGGAAGGCGTCCCGA 4000

MW
RW

DD GCAGGACCGGAAGTCCCGCCCCGGCGGCTGAGGGGGGCGGCCGGGGGCGG 4050
MW
RW

DD TCGTGTCAGCAGTTCGGCGGGGCGGGGGGTCACACCGACGTCCGTGGGCT 4100
MW
RW

DD GCCCCCGGCCTCGGGCGGGCCGCGTGTTTCTCCGTCCGCCCGCTCCTCGC 4150
MW
RW

DD CAGACCGCCGGGTCGCGGCGGGGGAGGGGGCGGGGCGGGGCGGGACGCAG 4200
MW
RW

DD GAGGGGCGGGGCGTGGGAGAGGCGGGGGCGGGGCGCGAGAGGGGCGGGGC 4250
MW
RW

DD GGGGCGGGGCGTGGGA 4266
MW
RW