Leishmaniasis is a disease caused by more than 20 different species of protozoan parasites of the genus Leishmania which are transmitted from host to host through the bite of sand flies. Visceral leishmaniasis is caused mainly by L. infantum and it is the most severe form of human leishmaniasis, with an estimated incidence of 0.5 million new cases each year and more than 50,000 deaths a year. Dogs are the main reservoir of L. infantum all around the world and this parasite causes Canine Leishmaniasis to them.

**OBJECTIVE OF THE REVIEW:** Identifying the genetic factors that determine whether a dog is susceptible or resistant to Canine Leishmaniasis.

**Background**

- Resistance / susceptibility to leishmaniasis
- Regulation of the intrafagasomal parasite replication within macrophages
- Activation of macrophages
- Pleiotropic effects of antigen presentation

**Solute Carrier family 11 member 1**

- Chromosoma 37
- Total 9 kb
- 15 exons
- Microsatellite at intron 1

**Promoter variations**

- 3 SNPs = 3 haplotypes
  - TAA, TGA, CGA
  - 3 transcription factors binding sites
  - Alter the expression of Slc11a1

**Rich G’s region**

- Polymorphism
- From 7-9 G’s (8 is the most common)
- No independent association

**Microsatellite in intron 1**

- 5 different alleles according to number of repetitions:
  - 133, 137, 139, 141 and 145
- No independent association

**Most frequent haplotypes**

- TAG-8:141 → Heterozygosity = Susceptibility in Boxers (50% of cases)
- TAG-9:145 → Homozygosity = Resistance in Boxers (80% of controls)

**The promoter of this gene plays a main role in the immune response against infection by Leishmania parasites. This region has binding sites for cytokines (INF-y) that regulate gene expression of Slc11a1 during the activation of macrophages.**

**GWAS**

- Two haplotypes of Protection (CFA 11: CFA 20)
- Two haplotypes of Risk (CFA 4)

**Heritability of the Character (Resistance / susceptibility)**

\[ h^2 = 60\% \]

**CONCLUSIONS**

- Slc11a1 canine gene analysis showed the association between haplotype 8-141-TAG and disease susceptibility in Boxer dogs, whereas homozygous haplotype 9-145-TAG seems to provide resistance.
- GWAS studies have reported an association of chromosomes 1, 4 and 20 with the disease and the presence of four different haplotypes, two involved in the development of resistance (chromosomes 1 and 20) and two in susceptibility (chromosome 4).
- Although, studies have failed establishing a single major gene causing the disease, due to its great biological complexity.
- It is necessary to review the evidence found on this studies, because the populations used in the case control studies are often small.

**BIBLIOGRAPHY**

