

Dry Eye, Curly Coat Syndrome (DECC)

Affected breeds: Cavalier King Charles Spaniel

A problem which affects the skin, eyes and nails, is "congenital keratoconjunctivitis sicca and ichthyosiform dermatosis" (CKCSID), and is more commonly referred to as Dry Eye, Curly Coat Syndrome. Affected pups show symptoms early in life and these comprise a rough/curly coat, reduced tear production, and scaly skin.. The foodpads are thick and cracked from an early age, and the nails grow abnormally and slough off regularly, leading to lameness. Affected dogs also often suffer from increased dental disease. Affected dogs are often euthanised on welfare grounds as the control of symptoms is difficult.



The mutation is recessive, which means that dogs which carry the mutation ("CARRIERS") are normal but will pass the mutation on to an average of 50% of their offspring. Puppies which inherit two copies of the mutation are at high risk of Dry Eye, Curly Coat

This test is particularly useful for breeders:

- To identify carriers among their breeding stock so that they can avoid CARRIER X CARRIER mating combinations which would risk AFFECTED puppies.
- To conclusively confirm Dry Eye, Curly Coat

This test will be reported as:

CLEAR : no evidence of the Dry Eye, Curly Coat mutation

CARRIER : carries one copy of the defect, which will be passed to 50% of offspring

AFFECTED : carries two copies of the defect, and is at high risk of Dry Eye, Curly Coat

The genetic status of dogs can be used to predict breeding outcomes when different combinations are mated:

AFFECTED X AFFECTED = 100% AFFECTED

AFFECTED X CARRIER = 50% AFFECTED, 50% CARRIER

AFFECTED X CLEAR = 100% CARRIER

CARRIER X CARRIER = 25% AFFECTED, 50% CARRIER, 25% CLEAR

CARRIER X CLEAR = 50% CARRIER, 50% CLEAR

CLEAR X CLEAR = 100% CLEAR

References

Forman OP, Penderis J, Hartley C, Hayward LJ, Ricketts SL, Mellersh CS. Parallel mapping and simultaneous sequencing reveals deletions in BCAN and FAM83H associated with discrete inherited disorders in a domestic dog breed. PLoS Genet. 2012;8(1):e1002462.