

FEDERATION CYNOLOGIQUE INTERNATIONALE (AISBL)

Place Albert 1^{er}, 13, B – 6530 Thuin (Belgique), tel : +32.71.59.12.38, internet : <https://www.fci.be>



Use of genomic tools

Position of the FCI

Over the last 25 years, the field of genomic has revolutionised dog breeding, offering to dog owners, breeders and organisations a multiplicity of tools to breed and monitor their animals. This document presents the position of the FCI regarding the potential and limits of genomic tools for a sustainable management of dog breeds.

Genetic identification and parentage testing is one of the most widely used tool for dog breeding. Using international norms, it should be encouraged and generalised by breeding organisations and by the FCI. This would guarantee the reliability of pedigrees, which is crucial for the integrity of purebred dog breeding. Genetic identification and parentage testing can help to eliminate errors and fraud in pedigrees and provide a more accurate record of a dog's ancestry.

Genetic tests for inherited disorders or phenotypic traits can also be of wide interest for breeding. If well-used, those tests may help to monitor and select against health issues. They can be used to identify carriers of these genetic disorders, and to avoid breeding affected or at-risk dogs. This can help to reduce the incidence of these disorders in the breed, and to improve the health and welfare of the dogs. However, it is important to consider and prioritize tests that are reliable and relevant for a given breed in a given country, and to ensure that the tests used are reliable (Pegram et al. 2019). This means that the tests should be reviewed by experts and published in a scientific paper. Their applicability should be also validated for the population of interest. Indeed, a test relevant and reliable for a given dog population in a given country may be not necessarily relevant or reliable for the same breed in another country. The use of such tools should be integrated in breeding programmes considering the overall health, demographic, economic and governance challenge that the breed is confronted with.

Finally, genomics may support genetic monitoring of genetic diversity both at individual and breed level. Since medium and high-density marker sets have been made available, it is possible to assess genetic relationships and admixture among populations, while measuring genetic variability at individual and breed level, which may be useful to investigate the situation of a breed regarding genetic variability in relation to its health and its history (Donner et al. 2023) and need for potential actions to be taken.

To conclude, the FCI wants to underline that if adequately used, the use of genomic tools in purebred dog breeding can have significant benefits for the health, welfare, and sustainability of breeding programs. The FCI should encourage the use of genetic identification and parentage testing. With regard to genetic testing for hereditary disorders and phenotypic traits, as well as the monitoring of genetic variability, their use should only be encouraged after careful evaluation of the suitability of a given test for a targeted national breed population, taking into account its specific situation in terms of health and welfare, genetic variability and overall breed objectives.

By doing so, the FCI could help to improve the integrity of pedigrees, reduce the incidence of genetic disorders, and promote responsible and sustainable breeding programs.

Approved by the FCI General Committee in Amsterdam, September 2024, based on the recommendation of the FCI Scientific Commission.

References:

Donner, J., Freyer, J., Davison, S., Anderson, H., Blades, M., Honkanen, L., ... & Chodroff Foran, R. (2023). Genetic prevalence and clinical relevance of canine Mendelian disease variants in over one million dogs. *PLoS Genetics*, 19(2), e1010651.

Pegram, C.L., Bonnett, B.N., Skarp, H. et al. Moving from information and collaboration to action: report from the 4th international dog health workshop, Windsor in May 2019. *Canine Genet Epidemiol* 7, 4 (2020). <https://doi.org/10.1186/s40575-020-00083-x>