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Avian Adenovirus Genotyping Diagnostic Service

Summary

x-OvO Limited has developed a centralised genotyping diagnostic service to facilitate the identification of avian adenovirus from tissue samples taken from commercial poultry flocks. The test will allow the determination of the degree of association between two isolates and thus provide statistically significant evidence of the likelihood of transmission (or not) of any such virus from a source flock to a progeny flock. Association with genotypes known previously to cause significant pathologies is also possible.

x-OvO Limited is pleased to announce the launch of a novel genetic typing analysis service for avian adenovirus infections in domestic poultry.

Although often implicated in sub-optimal performance of breeding birds, clear diagnosis of the presence of pathogenic adenoviruses (and hence their appropriate control) has been difficult historically due to a reliance on serological typing methods. In a similar vein, determination of the relationship (or lack of) between source flock adenoviruses and those isolated in progeny flocks and the resultant causal relationship between any observed pathologies has been extremely problematic.

To facilitate a clarification of these possible relationships, x-OvO Limited has developed a centralised diagnostic service able to screen and classify different types of Fowl Adenovirus A based on hexon loop (L1) genotyping.

The hexon protein is the major capsid protein of the non-enveloped virion on which type, group and subgroup specific determinants are located. The hexon consists of conserved regions (pedestals), which are located inside the virion, and variable loops which protrude from the surface containing the type-specific neutralizing epitopes. Due to this interaction with the immune system, the sequence identity between loop regions of different serotypes is low.

Using these properties of the virus, it is possible to group together different Fowl Adenovirus strains in 5 (A-E) Genogroups based on their hexon L1 sequences. Inside each Genogroup it is possible to distinguish different clades that may be associated with individual serotypes. Pyrosequencing analysis of key variable regions allows the rapid determination of lack of association of any two analysed samples. Should samples display characteristics that indicate possible association with each other, the use of boot strapping analysis on extended genetic sequences allows the investigator to arrive at statistically significant conclusions regarding the genotype of a strain and its association with another strain. Thus the technology is ideally suited to determine if an adenovirus isolated from one flock is genetically the same (and hence a candidate for vertical transmission) as a virus isolated from its source supply flock.

Further details of this novel diagnostic technology are available directly from x-OvO Limited. www.x-ovo.com



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