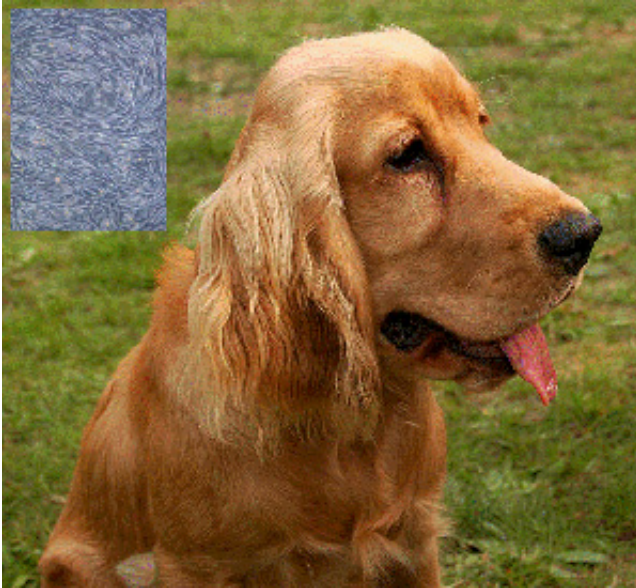


Dog's epigenome gives clues to human cancer

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A cocker spaniel. Credit: PEBC

The bond between humans and dogs is strong and ancient. From being the protector of the first herds in a faithful pet, dogs and people share many aspects of life. The relationship between the two species has been studied by psychologists, anthropologists, ethnologists and also by genetic and molecular biologists. In this sense, dogs are a great model for understanding the causes of human diseases, especially cancer.

Unlike other mammals used in research, [dogs](#) develop cancer spontaneously as humans do and cancer is the most common cause of death in this species. The dog genome has been obtained in recent years,

but we still don't know how is controlled and regulated, what we call the epigenome.

This week the team led by Manel Esteller, director of the Program for Epigenetics and Cancer Biology (PEBC) at Bellvitge Biomedical Research Institute (IDIBELL), Professor of Genetics at the University of Barcelona and ICREA researcher, has characterized the dog's epigenome and transferred the results to [human cancer](#) to understand the changes in appearance of tumors. The finding is published this week in the journal *Cancer Research*.

"We have characterized the epigenome level of each nucleotide of DNA of cells from the cocker species spaniel. In these canine cells we induced a morphological change similar to what happens in [cancer progression](#) and we have seen displayed significant alterations in the modulation of genes, called epigenetic lesions "says Manel Esteller.

"The interesting thing is that when we looked the same dog genes in human breast cancer, epigenetic aberrations occur in the same regions of DNA. Data suggests the existence of common epigenetic mechanisms in both species that have been evolutionarily conserved to change the shape and consistency of our cells and tissues, "concludes the researcher.

Study results suggest that act pharmacological action on these epigenetic alterations may be helpful in slowing disease progression.

More information: A Comprehensive DNA Methylation Profile of Epithelial-to-Mesenchymal Transition. armona FJ, Davalos V, Vidal I, Gomez A, Heyn H, Hashimoto Y, Vizoso M, Martinez-Cardus A, Sayols S, Ferreira H, J Sanchez-Mut, Moran S, Margeli M, Castilla Y, Berdasco M, Stefansson OA, Eyfjord JE, Gonzalez-Suarez Y, Dopazo J, Orozco M, Gut Y, Esteller M. *Cancer Research*, 2014

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