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Room: Seminar Room

Avian ecological epigenetics: what do we know about DNA methylation in hole-breeding passerines

Presenting author: **Kees van Oers**

Authors: **Kees van Oers¹**

Affiliations: ¹Department of Animal Ecology, Netherlands Institute of Ecology, Wageningen, The Netherlands

The past decade has seen an increasing interest in studying epigenetic mechanisms such as DNA methylation. This attention is present in both geneticists and non-geneticists interested in the mechanisms explaining variation in gene expression. For geneticists, the search for the hereditary mechanisms underlying quantitative traits traditionally focussed on the identification of underlying genomic polymorphisms such as SNPs, but this has not been very fruitful. It has now become clear that epigenetic mechanisms, such as DNA methylation, can consistently alter gene expression over multiple generations. Non-geneticists found out that these methylation patterns are prone to changes and such changes may be transmitted over generations. DNA methylation may therefore be an explanation for non-genetic inheritance such as maternal effects.

Much of what we know however, is based on studies on plants and mammals, mainly humans and laboratory strains. This raises the question whether the knowledge we have from these model systems can be generalized over species or classes and urges for a better understanding of the function of the methylome in passerine birds. In this talk I will first give a background on the current status of epigenetic research in passerines. I will follow this up by using the great tit (*Parus major*) as a case study to show i) the structure and function of the methylome ii) the relative role of induced versus inherited variation in methylation and iii) some methodological considerations for analysing DNA methylation.

Identification of variation in DNA methylation and changes in variation over time offer a great opportunity to combine genetic and non-genetic studies. Hole-breeding passerines could be ideal ecological model species for studying epigenetic mechanisms in natural populations.