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Abstracts (in order of presentations)

Epigenetics and phenotypic variability: insights from birds and long-term effects of embryonic environment in avian species

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The chicken genome was one of the first genome of agronomic interest to be sequenced and annotated (although incompletely), and is characterized by a relatively small size, the existence of micro- and macro-chromosomes with contrasting epigenetic properties, and a different sex determinism as compared to mammals. Although epigenetic mechanisms such as DNA methylation, histone modifications and chromatin regulators appear to be conserved in chicken, some mechanisms may be differing compared to mammal species. For instance, the absence of imprinted genes in birds was suggested by several studies.

The avian embryo is a unique model for developmental studies given its potential for *in ovo* manipulation. The embryo is sensitive to environmental influences that can be of maternal (yolk hormones and egg nutrients...) or external origin (incubation conditions including temperature, relative humidity, light colour, gas concentrations...) that have long been known to affect the liveability, development and metabolism of embryos and later chicks. Breeder nutrition and environmental temperature may alter the offspring feeding behaviour, growth or body composition. However, information is scarce about the molecular mechanisms involved in the interaction between environment and the developing embryo. While global and local epigenetic changes have been shown to be involved in the setting of thermoregulation in the chick, the role of such mechanisms in embryo metabolic plasticity and phenotypic variability, and their long term or transgenerational effects remain to be explored.