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Understanding the complex interaction between pseudorabies virus (PrV) and its natural host using RIP-Chip enrichment analysis

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► To cite this version:

Sophie Pollet, Jérôme Lecardonnell, Florence Jaffrezic, Marco Moroldo, Elisabetta Giuffra. Understanding the complex interaction between pseudorabies virus (PrV) and its natural host using RIP-Chip enrichment analysis. 34. International Society for Animal Genetics Conference (ISAG), Jul 2014, Xi'An, China. 2014, Proceedings of the 34th International Society for Animal Genetics Conference. hal-01603396

HAL Id: hal-01603396

<https://hal.science/hal-01603396>

Submitted on 2 Jun 2020

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Ovulation rate is the first restrictive factor of litter size in pig. The difference in ovulation rate between breeds with high and low ovulation rate originate from the differences during mid- to later follicular phase in dynamics of follicular growth. In high ovulation rate sows, the follicle selection phase is prolonged and more preovulatory follicles emerge. The dynamic process involving selection and maturation of follicles is regulated and controled by a highly synchronized and exquisitely timed cascade of gene expression. Since miRNAs regulate gene expression extensively, and play an important role in the development of ovarian and female reproductive cells, the difference in ovulation rate between Chinese Meishan and Duroc sows maybe affected by the different expression of miRNAs in their ovarian follicles. Ovarian tissues of Meishan and Duroc at day 4 of follicular phase were collected, miRNA libraries were constructed and next-generation sequencing was conducted. In ovaries of Duroc and Meishan, a total of 272 and 275 pig miRNAs were detected, 125 and 155 predicted miRNAs sharing high homologies with known miRNA of other species were found, 49 and 57 novel miRNAs were detected, respectively. And some of the new miRNAs were verified. miRNA chips were used to screen the miRNAs differentially expressed in medium Follicles (with a diameter of diameter 5.0mm-6.9mm) between Meishan and Duroc sows. A total of 158 pig miRNAs were detected, and ssc-miR-30a, ssc-miR-708, ssc-miR-187, ssc-miR-486 shown significant difference in expression level between Meishan and Duroc, and 31 mammalian miRNAs unreported in pig shown significant difference as well. And the expression difference of some miRNAs were conformed. The expression profiles of several differentially expressed miRNAs in various tissues and follicles at different stages were investigated. The research provide an insight for better understanding the genetic basis and

molecular mechanism of follicle development and high prolificacy affected by miRNAs in pigs.

P3090 Understanding the complex interaction between pseudorabies virus (PrV) and its natural host using RIP-Chip enrichment analysis. Sophie Dhome-Pollet, Jérôme Lecardonnell, Florence Jaffrézic, Marco Moroldo and Elisabetta Giuffra (Institut National de la Recherche Agronomique, AgroParisTech, UMR1313 Animal Genetics and Integrative Biology.)

MicroRNAs modulate cellular pathways by acting at the post-transcriptional level, through molecular interactions with target mRNAs via the RNA-induced silencing complex (RISC). During a viral infection, complex interactions take place between the virus and its host which involve, among other factors, microRNAs. Some host microRNAs are crucial for immune responses, and a few of them target viral mRNAs and inhibit viral replication. Moreover, microRNAs encoded by some viruses (mostly herpesviruses) can modulate the transition from latent to lytic replication and attenuate the host antiviral immune responses.

An interesting model to study these complex interactions is the pseudorabies virus (an alpha-herpesvirus, PrV) responsible for Aujeszky's disease in pigs, its natural host. The intron of the large latency transcript of the PrV genome has been shown to encode a cluster of 11 microRNAs. To understand the biological role of viral microRNA during PrV infection, we previously compared a mutant PrV clone depleted of a cluster of microRNAs and a parental clone for their ability to establish latency *in vivo* in trigeminal ganglia.

Here we present a functional genomics approach based on the RIP-Chip assay to better understand the intricate interactions between the miRNAs found expressed by PrV during latency and the host mRNAs. We first optimized the experimental procedures in terms of cell lines,