



HAL
open science

Functional analysis of candidate interactions between miRNAs encoded by the pseudorabies virus (PrV) and pig genes.

Nada Mahjoub, Sophie Pollet, Gail Sherba, Thomas Mettenleiter, Elisabetta Giuffra

► To cite this version:

Nada Mahjoub, Sophie Pollet, Gail Sherba, Thomas Mettenleiter, Elisabetta Giuffra. Functional analysis of candidate interactions between miRNAs encoded by the pseudorabies virus (PrV) and pig genes.. 34. International Society for Animal Genetics Conference (ISAG), Jul 2014, Xi'An, China. hal-01606096

HAL Id: hal-01606096

<https://hal.science/hal-01606096>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - ShareAlike 4.0 International License

Assay (I), nuclear extracts of muscle tissue from Guanling cattle and recycled and purified the purpose segments of Myod I gene Promoter to screen out transcription factor binding sites of Myod I gene promoter in Guanling cattle. At the same time, synthesizing the predicting result of transcription factor binding sites of Myod I gene promoter with online software to eventually screen out the transcription factor binding sites of Myod I gene promoter in Guanling cattle.

【Results】 I preliminary screen out transcription factor binding sites of Myod I gene promoter in Guanling cattle. They are SRF, YY1, CDP, FAST - 1, NF - 1, MEF2.

P3063 Functional analysis of candidate interactions between miRNAs encoded by the pseudorabies virus (PrV) and pig genes. Nada Mahjoub and Sophie Dhorne-Pollet (Institut National de la Recherche Agronomique, AgroParisTech, UMR1313 Animal Genetics and Integrative Biology.), Gail Scherba (Department of Pathobiology, College of Veterinary Medicine, University of Illinois), Thomas Mettenleiter (Friedrich Loeffler Institut, Institute of Molecular Biology) and Elisabetta Giuffra (Institut National de la Recherche Agronomique, AgroParisTech, UMR1313 Animal Genetics and Integrative Biology.)

MicroRNAs (miRNAs) post-transcriptionally repress gene expression and are active against a large proportion of the transcriptome. Herpesviruses produce latent infections and are completely dependent upon latency as mode of persistence. Most herpesviruses encode miRNAs with targets in their own genomes and that of their host. Among alpha-herpesviruses, the Pseudorabies (PrV) genome contains 11 miRNA genes clustered in the Large Latency Transcript (LLT) region.

We use the pig-PrV system as a model to study and validate the biological role of viral miRNAs. Previously, a PrV BAC clone was depleted of a cluster (2.5 Kb) of nine miRNA genes. An in

vivo experimental infection was carried out to compare the ability of a mutant clone to establish latency in porcine trigeminal ganglia. The Pence of miRNAs did not hamper the establishment of latency. However, animals infected by the mutant virus carried an increased number of viral particles in ganglia compared to those infected with the wild type virus, and the ganglia displayed an altered expression pattern of host cell mediated immune response. Some differentially expressed genes carried multiple targets for most PrV's miRNAs, suggesting that they could be modulated by these miRNAs during the dynamics of PrV's latency (N. Mahjoub, S. Dhorne-Pollet, W. Fuchs, M-L. Endale Ahanda, A. Arya, J. Loveland, F. Lefevre, T. Mettenleiter, E. Giuffra. To be submitted).

The OBG400 (porcine neuroblast) and PK15 (porcine epithelial) cell lines allow exploring miRNA-mRNA interactions in two distinct transcriptomic backgrounds. We are using RISC-IP (Immunoprecipitation of the RNA-Induced Silencing Complex) to figure out the functionality of PrV's miRNAs and the co-enrichment in RISC of previously identified candidate host gene targets. Preliminary results indicated that LCT4 (leukotriene C4 synthase) is enriched 3.7 time in the RISC of OBG400 cells upon PrV-mit-LLT1 mimics. Luciferase assays are being performed to support the most relevant results

P3064 MicroRNA-128 promotes myoblast differentiation in myogenesis. Lei Shi, Pinghua Li, Han Wang, Huizhi Li, Lingling Fu, Lichun He, Lei Tang, Ruihua Huang and Bo Zhou (Institute of Swine Science, Nanjing Agricultural University)

MicroRNAs play critical roles in skeletal muscle development. In order to elucidate the biology function and potential molecular mechanism of miR-128 in myogenesis, we constructed a plasmid which contains the target region of *Myostatin* (*MSTN*) bound by miR-128,