Feline microRNA transcriptome in whole blood in 6 healthy cats and in 6 cats with preclinical hypertrophic cardiomyopathy

SND-ID: 2021-334-1. **Version**: 1. **DOI**: https://doi.org/10.5878/ex7j-1q61

Download data

miR_Counts.csv *(109.85 KB)*
miR_DE_Breed_HCM.csv *(19.94 KB)*
miR_DE_Interaction_HCM_breed.csv *(19.96 KB)*
miR_DE_Overall_HCM_healthy.csv *(19.99 KB)*
miR_DE_Sign_breed.csv *(19.97 KB)*
miR_DE_Sign_HCM_NF.csv *(19.96 KB)*
miR_Deep2_counts_DEsignmiRNAcontrasts_compiled.xlsx *(364.96 KB)*
miR_miRDeep2_report.csv *(186.51 KB)*
miR_miRNAs_in_other_feline_paper.csv *(1.68 KB)*
Target_feline_miRNA_target_genes.csv *(20.73 KB)*
Target_feline_novel_miRNA-targets.csv *(196.06 KB)*
Target_GO-fca-let-7f-5p.csv *(4.05 KB)*
Target_GO-fca-miR-151a-3p.csv *(2.75 KB)*
Target_GO-fca-miR-204-5p.csv *(3.23 KB)*
Target_GO-fca-miR-26b-5p.csv *(5.27 KB)*
Target_GO-fca-miR-330-5p.csv *(477 bytes)*
Target_GO-fca-miR-3613-5p.csv *(479 bytes)*
Target_GO-fca-miR-98-5p.csv *(767 bytes)*
Target_GO-hsa-let-7f-5p.csv *(24.14 KB)*
Target_GO-hsa-miR-151a-3p.csv *(3.01 KB)*
Target_GO-hsa-miR-204-5p.csv *(35.86 KB)*
Target_GO-hsa-miR-26b-5p.csv *(54.52 KB)*
Target_GO-hsa-miR-330-5p.csv *(12.72 KB)*
Target_GO-hsa-miR-3613-5p.csv *(3.62 KB)*
Target_GO-hsa-miR-98-5p.csv *(26.71 KB)*
Target_human_miRNA_targets.csv *(14.5 KB)*
Target_HumanGOmiRNA_Feline_GOmiRNA_compiled.xlsx *(590.6 KB)*

Associated documentation

ReadMeDescription.txt *(3.96 KB)*

Download all files

2021-334-1-1.zip *(~1.72 MB)*

Citation

Hanås, S., Lorent, J., & Ohlsson, Åsa. (2022) Feline microRNA transcriptome in whole blood in 6 healthy cats and in 6 cats with preclinical hypertrophic cardiomyopathy (Version 1) [Data set]. Swedish University of Agricultural Sciences. Available at: https://doi.org/10.5878/ex7j-1q61

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Principal's reference number

SLU.kv.2021.4.4-197

Description

Aim to characterize differentially expressed miRNAS between healthy Norwegian Forest cats and healthy Domestic Shorthair cats, and to compare with cats with hypertropic cardiomyopathy (HCM)
Six neutered healthy cats, three male domestic cats (DOM) and one male and two female Norwegian Forest (NF) cats were included. Each healthy cat was matched (breed, sex, age, body-weight and body condition score) with a cat with HCM.
The dataset includes the miRDeep2 report, rawcounts miRNAs, differentially expressed miRNAs for contrasts compared using DESeq2, human and feline target genes producing messenger RNA (mRNA) and gene ontology analysis (GO) for these 12 cats.

Whole blood was collected in PAXgene blood RNA System frozen and stored in -20 °C until date of RNA-extraction for a median storage time of 177 days. Total RNA was extracted. Samples with an RNA integrity number (RIN)-value of 7.7 or higher were included in the study. Libraries were prepared and quantified and normalized prior sequencing. Paired-end sequencing data was generated. Bioformatic data processing and count genertion of known and novel miRNAs in cats were identified using miRDeep2. Mature miRNA and hairpin sequences were downloaded from miRBase with human as main reference, an mouse and dog assigned as close relatives. Main reference miRNAs identified in the dataset were classified as predicted known miRNAs, and miRNAs previously not described in the main reference were classified as novel miRNAs by miRDeep2. Only novel miRNAs with a miRDeep2 score of >5.0 was included in the count-file generated for subsequent differently expressed (DE)-analyses. Identification of DE miRNAs were performed in DESeq2.
Number of variables 6: breed, age, sex, body-weight, body condition score, healthy or hypertrophic cardiomyopathy.
The compiled files gives an overview of the data set.
Compiled Excel file “miRDeep2_counts_DEsignmiRNAcontrasts_compiled” is a compiled file with the miRDeep2 report, raw counts of miRNAs and the differentially expressed miRNAs found in the dataset. The following nine csv-files are named miR_ and the name of the file in the compiled Excel file.
Compiled Excel file “Target_HumanGOmiRNA_Feline_GOmiRNA_compiled” is a compiled file with the human and feline target genes producing messenger RNA for the differentially expressed miRNAs found in the dataset, gene ontology analysis of these miRNAS both for human and feline genes. The following nineteen csv-files are named Target_ and the name of the file in the compiled Excel file.

Data contains personal data

No

Language

English

Unit of analysis

Individual/Patient

Population

12 cats, 2 breeds 6 cat of each breed (Norwegian Forest cats and Domestic cats), within each breed 3 healthy and three cats with hypertrophic cardiomyopathy (HCM)

Study design

Observational study

Description of study design

Six neutered healthy cats, three male domestic shorthair (DSH) and one male and two female NF cats were selected and matched with respect to breed, sex, age, and bodyweight with a cat with hypertrophic cardiomyopathy (HCM). One of the healthy DSH cats was matched with a Domestic Longhair cat (DLH), thus the DSH and DLH are hence called domestic (DOM) for the cats with preclinical HCM. Inclusion criteria were apparently healthy NF, and DSH cats, 1–14 years, with normal echocardiograms were included, as were cats of these two breed-groups with preclinical HCM. Diagnosis of HCM was based on characteristic findings on an echocardiogram. No cats receiving medical treatment were allowed into the study.

Sampling procedure

Other

Total RNA was extracted from WB, filtered for small RNA, and sequenced. Identification and prediction of miRNAs were performed with miRDeep2. Differential expression analysis of miRNAs was performed with DESeq2. The effect of breed was evaluated for healthy cats. The effect of preclinical HCM was evaluated for all cats and within breed. IntaRNA and miRDB was used for target-prediction, and DAVID for evaluation of gene ontology and gene enrichment.

Variables

6

Number of individuals/objects

12

Data format / data structure

Numeric

Text

Other

Data collection 1

- Mode of collection: Measurements and tests
- Time period(s) for data collection: 2014-12-04 – 2016-06-13
- Source of the data: Research data

Responsible department/unit

Department of Clinical Sciences

Funding 1

- Funding agency: Agria and the Swedish Kennel Club’s research fund
- Funding agency's reference number: Projektnummer N2013-0025, P2014-0014, P2015-0004 och P2016-0003.
- Project name on the application: Felina cirkulerande biomarkörer för hjärtsjukdom hos katt

Funding 2

- Funding agency: SLU Companion Animals Research Fund
- Project name on the application: Cirkulerande biomarkörer hos katter med och utan hjärtsjukdom

Funding 3

- Funding agency: Sveland Research Fund
- Project name on the application: Cirkulerande biomarkörer hos katter med hjärtsjukdom

Funding 4

- Funding agency: Foundation Strömsholms Djursjukvård
- Project name on the application: Cirkulerande biomarkörer hos katter med och utan hjärtsjukdom

Ethics Review

Uppsala - Ref. C137/13

Research area

Bioinformatics (computational biology) (Standard för svensk indelning av forskningsämnen 2011)

Genetics (Standard för svensk indelning av forskningsämnen 2011)

Basic medicine (Standard för svensk indelning av forskningsämnen 2011)

Medical genetics (Standard för svensk indelning av forskningsämnen 2011)

Veterinary science (Standard för svensk indelning av forskningsämnen 2011)

Keywords

Norwegian forest cat, Breed, Microrna, Hypertrophic cardiomyopathy, Domestic cat

Accessibility level

Access to data through SND
Data are freely accessible

Use of data

Things to consider when using data shared through SND

Versions

Version 1. 2022-01-07

Download metadata

DataCite

DDI 2.5

DDI 3.3

DCAT-AP-SE 2.0

JSON-LD

PDF

Citation (CLS)

File overview (CSV)

Published: 2022-01-07