



RumimiR: a detailed microRNA database focused on ruminant species

*C. Bourdon, P. Bardou, E. Aujean, S. Le Guillou, G. Tosser-Klopp,
F. Le Provost*

Mammary Gland and Lactation (GaLac) team
Animal Genetics and Integrative Biology (GABI) unit
INRA
Jouy-en-Josas, France



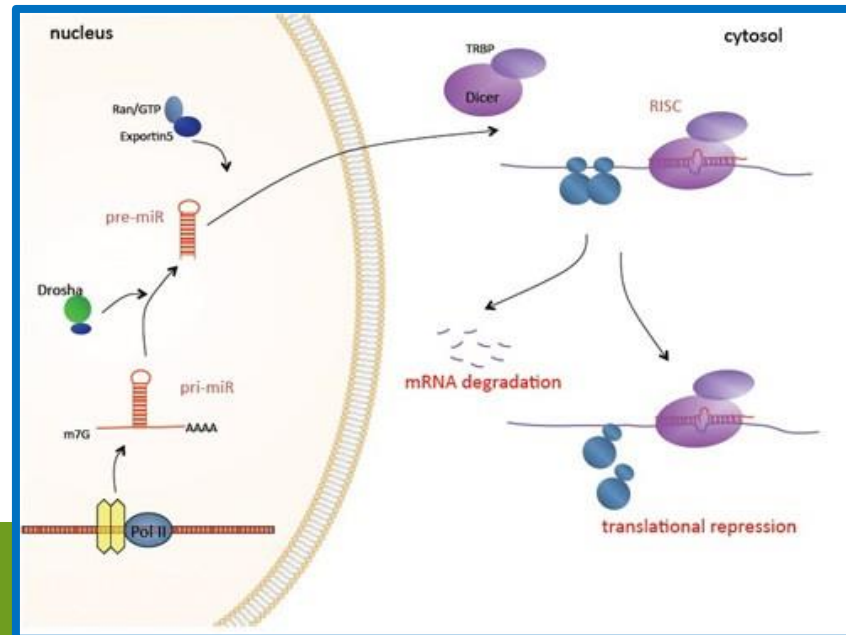


microRNAs

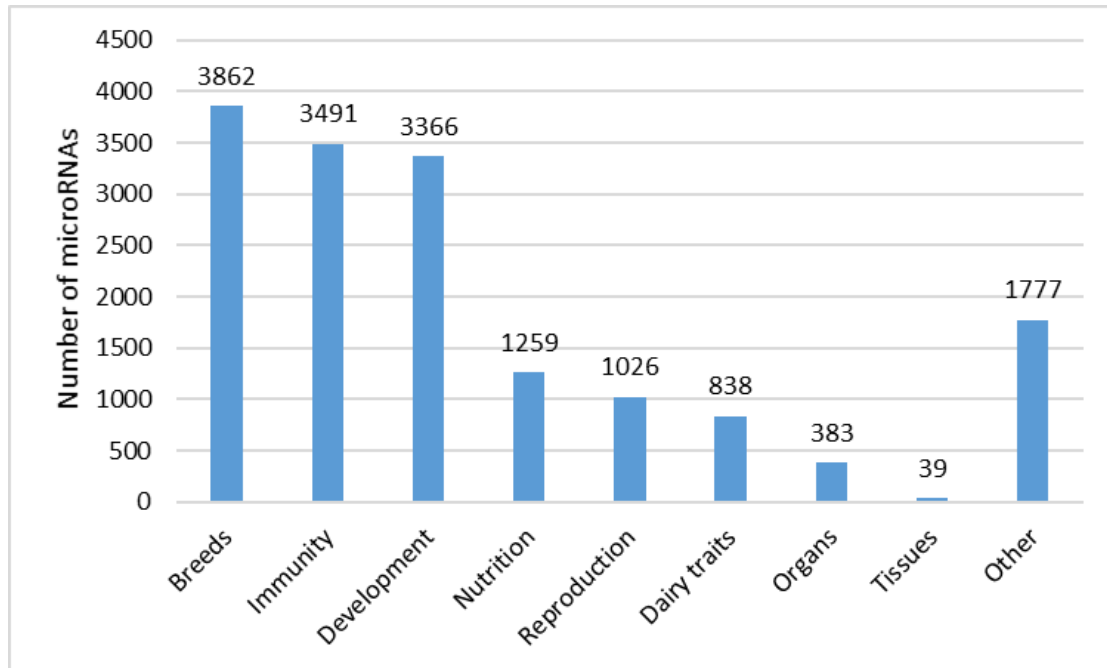
Small non-coding
endogenous RNAs
17-22 nt in length

Post-transcriptional
regulators of genes

Highly conserved
among species



78 papers describing ruminant microRNAs



Bovine and caprine mammary gland miRNomes

(Le Guillou et al., 2014; Mobuchon et al., 2015a)

Nutritional regulation of microRNA expression in lactation cattle and goat mammary gland

(Mobuchon et al., 2015b; Mobuchon et al., 2017)

miRNome differences in mammary tissue of lactating Holstein and Montbéliarde COWS (Billa et al., 2019)

miRNome differences in Holstein and Normande whole milk (Le Guillou et al., 2019, EAAP)

The searchable
database of published
microRNA sequences
and annotations

Last release
miRBase 22
(october 2018)

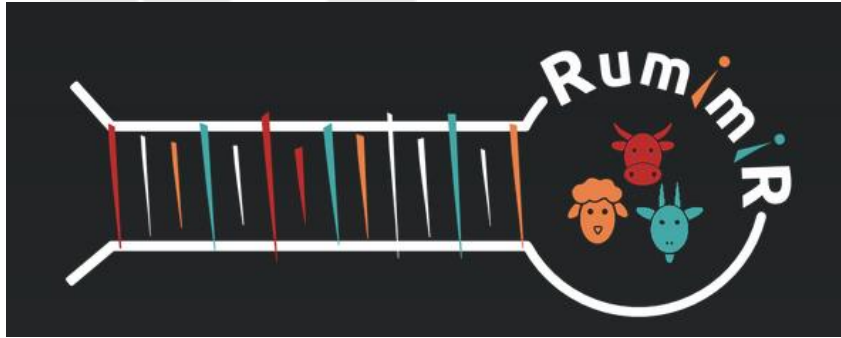
Created in 2006
by Griffiths-
Jones
University of
Manchester, UK



Does not contain all
published microRNAs:
Only 5% of small RNA deep
sequencing data are collected
(Kazomara et al, 2019)

Listing
microRNAs for
271 species
38 589 entries

Bovine: 1 025
Caprine: 436
Ovine: 153



A detailed microRNA database focused on ruminant species



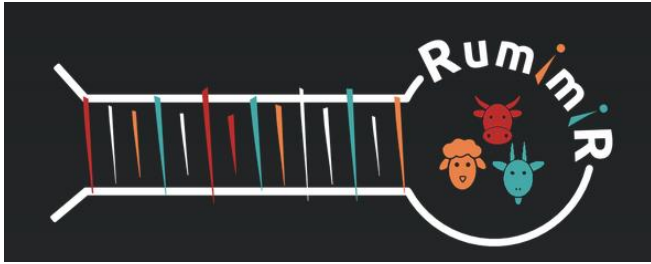
An exhaustive microRNA database containing all published microRNAs

An adapted microRNA database for ruminant research

Freely available online:

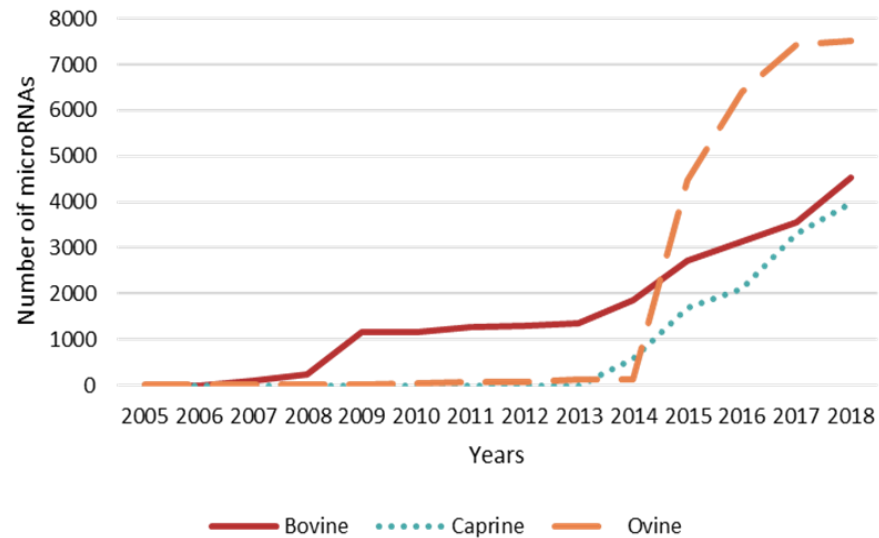
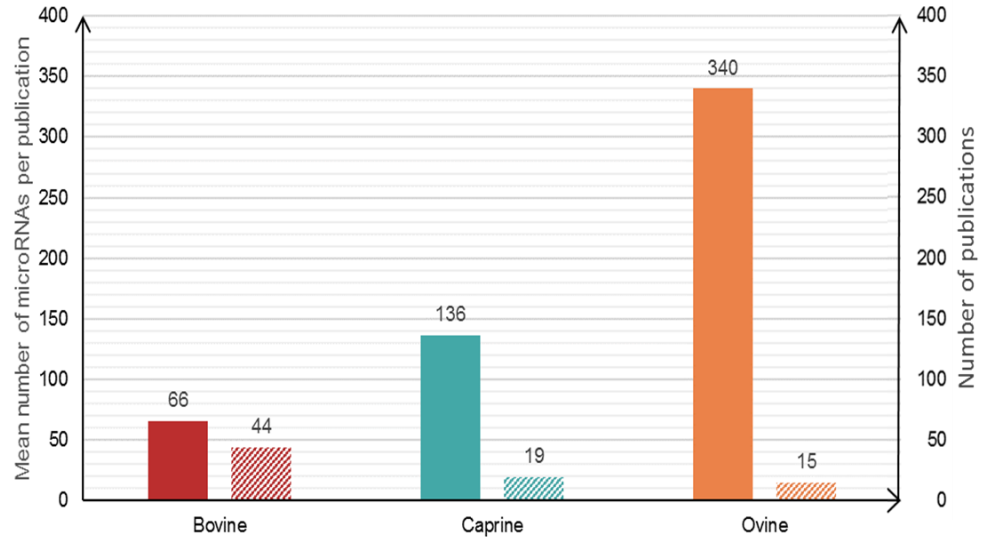
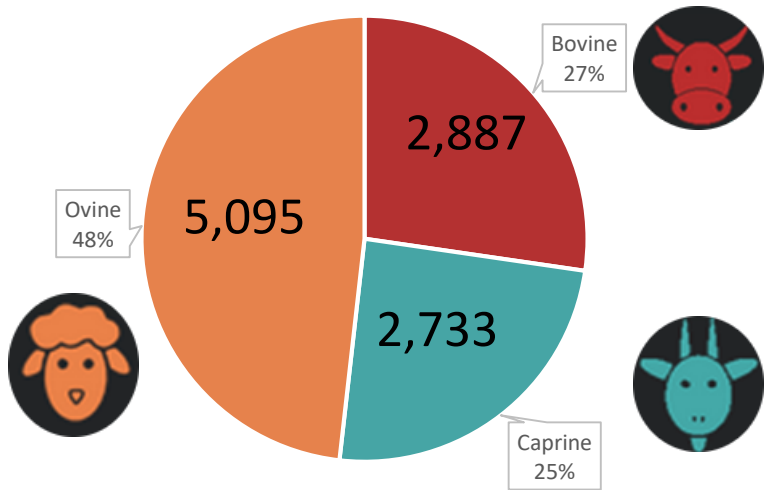
<http://rumimir.sigenae.org/>

rumimir@inra.fr



Data collected from 78 publications

10,715 microRNAs
(miRBase V22: 1,634)



User interface

EXPLORE

Available boxes below allow you to explore miRNA
Show/hide columns, filter by position and/or by source and/or by feature and export...

SHOW/HIDE COLUMNS

Configure the table below by selecting column name(s)

5 items selected

- Multi-mapping
- Sequence
- Publication
- Name
- IsomiRs
- RumimiR id
- Family
- Tissue
- Breed
- Study condition
- Lactation stages
- Age
- Species
- Number
- Cut-off
- Method

SEARCH

By position | By source | By feature | By blast

Species: Bovine
Select one or more species.

Breed: Holstein
Select one or more breed(s).

Tissue: Blood
Select one or more tissue(s).

Specific
Select tissue-specific.

EXPORT

For the filtered row(s) export...

Copy Excel CSV

The data.

Fasta
A fasta file of the miRNA sequence(s).

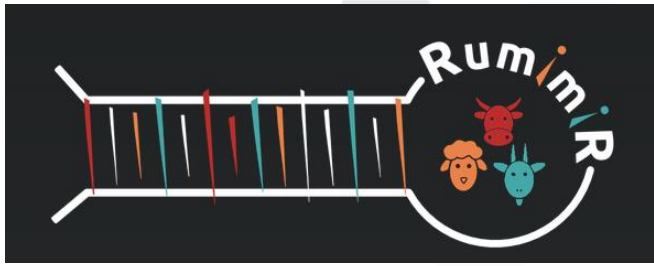
GFF
A GFF file of the miRNA.

Search:

Sequence	Name	Tissue	Breed	Species
AGCAGCAGUGUACAGGGCUCUG	Novel:14_7917	Blood [®]	Holstein	Bovine

(16,041 total entries)

Previous 1 Next



Alignement to unique reference genome:

Bovine: UMD3.1.1

Caprine: ARS1

Ovine: Oar v4.0



For each microRNA:
29 items are collected when available in the publication

Column name	Description
Chr (Start, End)	Genomic position of the microRNA
Multi-mapping	Number of localisations in case of multi-mapping (with 100% query cover and 100% identity)
Sequence	Sequence of the mature microRNA
Publication	Publication in which the microRNA is described
Name	Name assigned to the microRNA
IsomiRs	Name of isomiRs of the microRNA (sequence and genomic position almost identical)
RumimiR ID	Name of the microRNA with the RumimiR nomenclature
Family	microRNA family to which the microRNA is affiliated
Tissue	Tissue in which the microRNA was discovered
Breed	Breed used during the study
Study conditions	Conditions prevailing during the study
Lactation stages	Lactation stages of the animals studied
Age	Age of the animals studied
Species	Species of the animals studied (bovine, caprine or ovine)
Number	Number of novel microRNAs described in the publication
Cut-off	Cut-off point used in the publication to detect novel microRNAs
Method	Method used to detect novel microRNAs
Number and breed	Number of animals studied in each breed
Reference genome	UMD3.1.1, ARS1 or Oar v4.0
Bioinformatics tools used	Software used in the study for the microRNA detection
Condition details	Details of study conditions (i.e. number of animals per condition)
5p/3p	If the microRNA is 5p or 3p
Strand (+/-)	Strand in which the microRNA is situated
Star sequence	Sequence of the star microRNA
Matching seed	Known microRNA with the same seed
small RNAs	If the microRNA described is in fact part of an snoRNA, tRNA, snRNA or rRNA
hsa homology	Similarity with a human microRNA
mmu homology	Similarity with a mouse microRNA
False-positive code	Four-digit false positive code



For each microRNA:
29 items are collected when available in the publication

12 items not available in miRBase

Column name	Description
Chr (Start, End)	Genomic position of the microRNA
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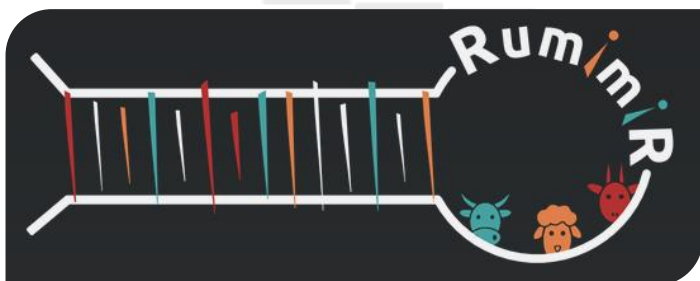


A false-positive code is proposed

Based on 4 criteria:

- ✓ Single or multiple genomic positions
- ✓ Presence or not in the RumimiR database
- ✓ Homology or not with other small RNAs
- ✓ Identity or not with human or mouse microRNAs

Column name	Description
Chr (Start, End)	Genomic position of the microRNA
Multi-mapping	Number of localisations in case of multi-mapping (with 100% query cover and 100% identity)
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Tissue	Tissue in which the microRNA was discovered
Breed	Breed used during the study
tools used	
Condition details	Details of study conditions (i.e. number of animals per condition)
5p/3p	If the microRNA is 5p or 3p
Strand (+/-)	Strand in which the microRNA is situated
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False-positive code	Four-digit false positive code



Chr. ↑↓	Start ↑↓	End ↑↓	Sequence ↑↓	Name ↑↓	Tissue ↑↓	Breed ↑↓	Species ↑↓	small RNAs ↑↓	hsa homology ↑↓	mmu homology ↑↓
1	132669822	132669838	AAUUUUUUGAGGCCUUG	chr1_1453	Mammary tissue	Alpine	Caprine	snRNA	null	null

In the future

Integration of new data at
least twice a year

Integration of genetic
variants: miRSNPs

May be extended to other
livestock species



"RumimiR: a detailed microRNA database focused on ruminant species"
Bourdon et al. 2019 Database (Oxford) in press

<http://rumimir.sigenae.org/>

rumimir@inra.fr

PARTNERS

See below the partners involved in the RumimiR project



INRA

*French National Institute for
Agricultural Research*



GABI

*Animal Genetics and Integrative
Biology Unit - @INRA*



GenPhySE

*Genetics Physiology and Breeding
Systems Unit - @INRA*



SIGENAE

*Information System for Livestock
Genomes - @INRA*

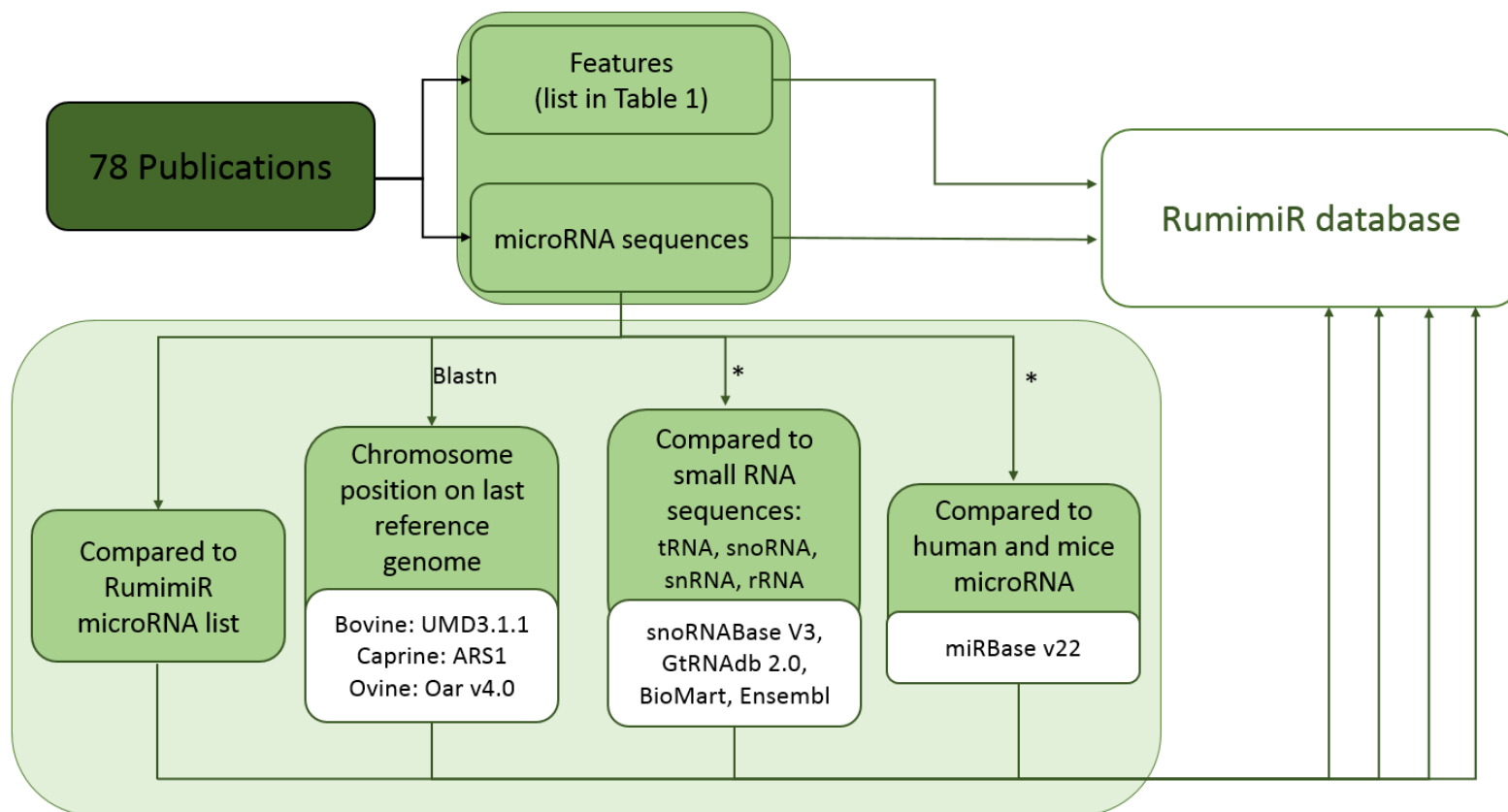


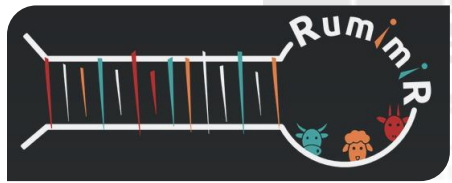
APIS-GENE

*Investing Innovating Adding value
to Ruminant Genomics Research*









Example: small RNAs

Chr. ↑↓	Start ↑↓	End ↑↓	Sequence ↑↓	Name ↑↓	Tissue ↑↓	Breed ↑↓	Species ↑↓	small RNAs ↑↓	hsa homology ↑↓	mmu homology ↑↓
1	132669822	132669838	AAUUUUUUGAGGCCUUG	chr1_1453	Mammary tissue	Alpine	Caprine	snRNA	null	null

Example: identity *hsa- mmu-*

Chr. ↑↓	Start ↑↓	End ↑↓	Sequence ↑↓	Name ↑↓	Tissue ↑↓	Breed ↑↓	Species ↑↓	small RNAs ↑↓	hsa homology ↑↓	mmu homology ↑↓
22	48724047	48724068	UGAGGUAGUAGUUUGUACAGUU	novel-miR-45	Ovaries	Jintang black and Tibetan	Caprine	null	hsa-let-7g-5p	mmu-let-7g-5p

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