





Small RNAs are modified with N-glycans and displayed on the surface of living cells

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Outline

Introduction

- I. Are RNAs modified with glycan structures?
- II. What type of RNA are glycoRNAs?
- III. What kind of glycan structures modify RNAs?
- IV. Does the canonical glycan biosynthetic machineries contribute to glycoRNA production?
- V. Where are localized glycoRNAs in the cell?
- VI. Can Siglec receptors and anti-RNA antibodies recognize cell surface glycoRNAs?

Conclusion & perspectives

Introduction - Cell surface membrane biomolecules





- The fluid mosaic model of membranes
- Phospholipids
- Proteins
- Carbohydrates (Glycoconjugates)

✤ Different functions

- Internal / external compartmentalization
- Cell identity and integrity
- Cell interactions and communications
- Cell morphology
- Cell exchanges
- Endocytosis
- Exocytosis
- ...



Fig.2. The glycoconjugate categories ^[2]



- Glycolipids = carbohydrates + lipids
- 2 types of glycolipids:
 - Glycoglycerolipids (glycerol backbones)
 - Glyocosphingolipids (sphingosine backbones)
- Functions: Cell interactions (immune response, pathogene interactions), blood group determination





Fig.3. The ABO blood group glycolipid determinants [3]



- Proteoglycans = <u>glycosaminoglycans (carbohydrates)</u> + proteins
- One of the major components of extracellular matrix
- Functions: Cell adhesion, water osmosis, molecules sequestration (growth factors)
- Example: Fibroglycans (heparan sulfate proteoglycans) interact with adhesion molecules and growth factors and support the cell shape



- Glycoproteins = carbohydrates + proteins
- Functions: cell-cell recognition, cell interaction and communication, ligand binding, cell signaling, cell transport
 - Carbohydrates

Fig.4. Secondary structure of the P-glycoprotein ^[4]

 Example: P-glycoproteins (exportation transmembrane transporter) cause a phenomenon of multi-drug resistance

Introduction – Two major types of glycosylation

Glycosylation is the controlled enzymatic modification of an organic molecule (lipid or protein) by addition of a sugar molecule.

	N-linked Glycosylation [2, 5, 6]	O-linked Glycosylation [2, 5, 6]			
	Complex Hybrid High mannose				
	O-linked glycosylation	Oxygen atom Oxygen atom Oxygen atom			
	Ser/Thr Ser/Thr Ser/Thr Ser/Thr Nitrogen atom Nitrogen atom	Core 1 Core 2 Core 3 Core 4			
	Core I Core Z Core 3 Core 4				
Glycosylation chemical linker	Nitrogen atom	Oxygen atom			
Glycosylation localization	Endoplasmic reticulum and Golgi (maturation)	Golgi (only)			
Glycosylation target	Lipids and proteins				
Proteins target site	Asparagine on consensus sequence Asn-X-Ser/Thr (X, every AA except Pro)	Serine or Threonine no known consensus sequence			
Lipids target site	Amine group directly linked to C1 of lipids	Hydroxyl group directly linked to C1 of lipids			
Glycosylation relevance	Folding and trafficking of proteins and lipids for secretion or membrane presentation				
Cell functions involving glycosylation	Cell interaction, Cell communication, Host-pathogen recognition, Immune system activation,				
Occurence	Occurs mainly in Eucaryotes and Archae Occurs in Eucaryotes, Archae and Bacteria				

Introduction - Reminder on RNA classification



Fig.5. Classification of RNAs ^[7, 8]

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Introduction – RNA modifications

- RNA is the substrate for post-transcriptional modifications (PTMs)
- PTMs include the 5' cap and polyA tail







- PTMs can also occur in the internal part of the transcripts
- Over 100 PTMs have been identified
- These RNA modifications are likely reversible and regulated

Introduction – RNA modifications

	N ⁶ - methyladenosine	Pseudouridine	5-methylcytosine	N ¹ - methyladenosine	2'-O-methylation
Structure					2'OMe RNA RNA CH ₃
Main functions	 Degradation of transcripts Promotion of translation initiation 	 Response to stress conditions Readthrough of stop codon 	 Function remains unclear Involvement in nuclear export? 	- Upregulation of translation	- Roles remain to be identified

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Small RNAs are modified with N-glycans and displayed on the surface of living cells

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https://doi.org/10.1016/j.cell.2021.04.023

Graphical abstract



Authors' hypothesis: Possible existence of RNA modified with sialoglycans

• Method: Glycoconjugates metabolic labeling and high purity RNA extraction





Authors' hypothesis: Possible existence of RNA modified with sialoglycans

Results by RNA blotting



Fig.9. RNA blotting of RNA from HeLa cells treated with $Ac_4ManNAz$ for the indicated amount of time ^[11]

◆ Glycans are revealed thanks to Ac₄ManZAz/DBCObiotin conjugaison and Streptadivin visualization

Total RNA is stained by Sybr Gold

 \rightarrow In an Ac₄ManNAz and time-dependent manner, biotinylated species are identified in a high molecular weight region

Are these biotinylated species really RNA transcripts?

- Same labeling and purification methods as previously
- Treatment with Turbo DNase, RNases and SUPERaseIn (Rnases inhibitor)
- Results by RNA blotting
- Treatment of RNA with DNase did not affect the glycoRNA signal
- Treatment of RNA with RNase cocktail digested the total RNA
- SUPERaseIn rescued the biotinylated glycoRNA signal

 \rightarrow Cells treated with Ac₄ManNAz incorporated the azide label into cellular RNA, which migrates on an agarose gel as a high MW species



Fig.10. RNA blotting of $Ac_4ManNAz$ labeled HeLa RNA treated *in vivo* with turbo DNase or RNase cocktail ^[11]

Are these glycoRNAs present in other cells types?

Results by RNA blotting



Fig.11. Blotting of RNA from various cell types labeled with $Ac_4ManNAz$ ^[11]

Different cell types tested:

HeLa: Human epithelial adenocarcinoma cell line
GM78 (GM12878): Human lymphoblastoid cell line
K562: Human myelogenous leukemia cell line
4188 (MYCT-ALL4188): Mouse lymphoblastic leukemia cell line
CHO: Chinese hamster ovary cell line

✤ H9 and 4188 cells showed significantly more labeling with Ac₄ManNAz per mass of total RNA than other cell types

→ Evidence of the presence of glycoRNAs in different amount, in other cell types and also in another mammalian species (mouse)

Does this labeling occur in vivo?



- Ac₄ManNAz Intraperitoneal injection in mice
- Same labeling and purification methods as previously

→ Dose-dependent and RNase-sensitive AC₄ManNAz labeling of RNAs in the same MW region as glycoRNAs from cultured cells Results by RNA blotting



Fig.12. RNA blot of murine RNA after in vivo $Ac_4ManNAz$ delivery via intraperitoneal injection (RNA from liver and spleen) ^[11]

Take-home message

This data suggests that glycoRNAs are not an artifact of tissue culture and that this modification occurs broadly: in cultured cells, *in vivo*, across multiple cell and tissue types of different mammals and at different abundances.

<u>Authors' hypothesis:</u> If glycoRNAs migrate as a high molecular weight species, they are expected to be long length poly-adenylated RNAs

Method: PolyA enrichment of RNA



Fig.13. Blotting of total or poly-adenylated enriched RNA from HeLa cells treated with Ac_4ManNAz $^{\rm [11]}$

→ Unable to purify glycoRNAs from extracted RNA with this method

Method: Fractionation method according to length



Fig.14. Blotting of total RNA from HeLa cells treated with $Ac_4ManNAz$ after differential precipitation fractionation using silica-based columns ^[11]

→ GlycoRNAs fractionated only with the small RNA population of total RNA

Are glycoRNAs small RNAs?



Method: RNA labeling and extraction, sucrose gradient fractionation, RNA blotting

Fig.15. Blotting of total RNA from H9 human embryonic stem cells treated with Ac₄ManNAz after sucrose density gradient fractionation ^[11]

\rightarrow GlycoRNAs fractionated with small RNAs

 \rightarrow Very slow migration of glycoRNAs can be due to their association with glycans

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Take-home message

This data shows that glycoRNAs are small non-coding RNAs (ncRNA) and tRNAs, even if they migrate slowly. This abnormal migration behavior is thought to be due to their association with glycans.

What RNAs are selectively labeled by Ac₄ManNAz treatment?

• Method:



Fig.16. Ac₄ManNAz-labeled glycoRNAs identification protocol [11]

HeLa vs H9 small RNA 10-(no tRNAs) SNORD36 SNORD30 SNORD35A SNORD32/ 5-HeLa, log₂(Ac₄ManNAz/Input) ○ -log₁₀(p-adjusted) 75 50 25 -5-H9 HeLa 10 5 _5 H9, log (Ac, ManNAz/Input)

Fig.17. Scatterplot analysis of $Ac_4ManNAz$ enriched RNAs purified from the small RNA fraction ^[11]

What RNAs are selectively labeled by Ac₄ManNAz treatment?

- Enrichment values are calculated as the RNA quantity after streptavidin pulldown divided by the input RNA quantity
- Y RNA, snRNA, rRNA, snoRNAs are enriched in both H9 and HeLa cells
- The enrichment values of HeLa and H9 cell glycoRNAs show a strong positive correlation

 \rightarrow Some small non-coding RNAs (Y RNA, snRNA, rRNA, snoRNAs) seem to be selectively glycosylated in both H9 and HeLa cells, despite the different lineage of these cell types

Is Y5 really a glycoRNA? How to prove if a given RNA is a glycoRNA?

- Y RNA family transcripts are able to bind proteins and ribonucleoproteins
- Y RNAs are highly conserved in vertebrates
- Y RNAs are known to be antigens associated with autoimmune diseases



Fig.18. Systemic Lupus Erythematosus (SLE)^[12]

Is Y5 really a glycoRNA? How to prove if a given RNA is a glycoRNA?

• Method: Gene knock-out (KO) using CRISPR-Cas9, Northern Blot, Growth analysis



Fig.19. Northern blot of total RNA from WT and Y5 KO 293T cells. The KO resulted in a complete loss of the Y5 RNA, with the 5S rRNA serving as a loading control ^[11]

 \rightarrow Validation of the KO efficiency: absence of Y5 transcripts



Fig.20. Growth rate analysis of the WT and KO clones across four days of culture. Three independent wells of cells were counted each day $^{[11]}$

→ Validation of the KO efficiency: absence of growth defects, consistent with previous reports of Y RNA silencing

Is Y5 really a glycoRNA? How to prove if a given RNA is a glycoRNA?

■ Method: gene knock-out (KO) using CRISPR-Cas9, Ac₄ManNAz labeling



Fig.21. Representative blot and quantification of total RNA from WT or Y5 KO 293T cells treated with Ac_4ManNAz $^{[11]}$

- Reduction of biotin signal compared to wild-type cells, without MW changes
- Consistent with the sequencing data, which identified Y5 as a strongly enriched RNA among a pool of other candidate glycoRNAs

 \rightarrow Y5 is one of the glycoRNAs found in Hela, H9 and HEK293T cell lines

Take-home message

This data shows that among the glycoRNAs, we can find Y RNAs, snRNAs, rRNAs, snoRNAs, expressed in different cell types. Some of these glycoRNAs are involved in diseases, such as the Y5 RNA and SLE, an auto-immune disease. This proves the relevance of glycoRNAs studies.



Fig.22. Pathway of $Ac_4ManNAz$ metabolism, conversion to sialic acid and sialic acid conversion into CMP ^[13]

The pathway for Ac₄ManNAz metabolism in human cells requires the conversion to sialic acid, then to CMP sialic acid and finally the addition to the termini of glycans

<u>Key:</u>

UDP-GlcNAc: Uridine diphosphate N-acetylglucosamine ManNAc: N-Acetylmannosamine ManNAc-6-P: N-acetyl-mannosamine 6-phosphate NeuAc-9-P: N-acetylneuraminic acid 9-phosphate Neu5Ac: N-acetylneuraminic acid (sialic acid) CTP: Cytidine triphosphate CMP: Cytidine-5'-monophosphate OGS: Oligosaccharide

Is Ac₄ManNAz shunted into unexpected metabolic pathways, thus creating artifacts?



Fig.23.Blotting of RNA from HeLa cells treated with 9-azido sialic acid for the indicated times ^[11]

- Method: use of 9-Azido sialic acid that directly converts into CMP-sialic acid, instead of Ac₄ManNAz
- As previously, 9Az-sialic acid produces time-dependent labeling of slowly migrating cellular glycoRNAs

 \rightarrow This comparative labeling approach suggests that Ac₄ManNAz follows the canonical pathway of ManNAc, and thus, the labeling is not due of artifacts

Is Ac₄ManNAz shunted into unexpected metabolic pathways, thus creating artifacts?

Method: Vibrio cholerae sialidase assay



Fig.24. Blotting of $Ac_4ManNAz$ -labeled HeLa cell RNA treated with *Vibrio cholerae* sialidase (VC-Sia) or heat-inactivated sialidase (VC-Sia-HI) ^[11]

- Vibrio cholerae sialidase (VC-Sia) is known to abolish the labeling signal obtained by the same method for glycoprotein labeling
- VC-Sia abolishes biotin signal
- Heat-inactivated (HI) VC-Sia unable to reduce the signal

 \rightarrow Ac₄ManNaz-dependent glycoRNA labeling signal depends on the presence of the azide-sialic group at the extremity of the glycan

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What is the extent of the contribution of sialic acid biosynthesis enzymes?



Fig.25.Blotting of RNA from HeLa cells treated with $Ac_4ManNAz$ and the indicated concentrations of P-3F_{AX} - Neu5Ac ^[11]

- Method: use of P-3 F_{AX} Neu5Ac, a cell permeable metabolic inhibitor of sialoside biosynthesis
- Treatment with P-3F_{AX} Neu5Ac resulted in a dose-dependent reduction of the total glycoRNA signal
- Shift to higher MW

 \rightarrow The dose-dependent reduction in total glycoRNA signal proves the involvement of canonical sialic acid biosynthesis enzymes in glycoRNA synthesis

 \rightarrow The reduced mobility is due to the reduced amount of sialic acid and therefore the reduced negative charges per glycoRNA molecule

Are glycoRNAs really sialylated?



Fig.26. Schematic of experimental steps of the DM B assay with associated structures of the two major types of sialic acid (Neu5Ac and Neu5Gc) ^[11]

- Method: use of DMB (4,5-Meth- ylenedioxy-1,2phenylenediamine dihydrochloride) probe to derivatize free sialic acids, then detect and quantify by high performance liquid chromatography (HPLC)
- Two forms of sialic acids in animals:
 - Neu5Ac: N-acetylneuraminic acid
 - Neu5Gc: N-glycolylneuraminic acid

Are glycoRNAs really sialylated?

3 ı. RNA Sybr 2. Neu5Gc 3. Neu5Ac Other sialic acid forms Sialic acid reference panel H9 total RNA + no enzymes H9 total RNA + VC sialidase H9 total RNA + RNase cocktail 10 15 20 25 Elution time (min) 0 5

Fig.27. HPLC analysis of the presence and the abundance of specific sialic acid in H9 cells $^{\rm [11]}$

- Method: use of DMB (4,5-Meth- ylenedioxy-1,2phenylenediamine dihydrochloride) probe to derivatize free sialic acids, then detect and quantify by high performance liquid chromatography (HPLC)
- Two forms of sialic acids in animals:
 - Neu5Ac: N-acetylneuraminic acid
 - Neu5Gc: N-glycolylneuraminic acid
- The peaks are reduced or gone with VC-Sia or RNase cocktail

 \rightarrow GlycoRNAs are modified with sialic acid containing glycans

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Are other glycoforms associated with RNAs?

• Method: mass spectrometry is used to define the composition of glycans on RNA



Fig.28. Schematic of the method used to release glycans from RNA samples and purify free glycans for mass spectrometry analysis [11]

Are other glycoforms associated with RNAs?

293 H9 HeLa Р Ρ P R Ρ R R P R R R 1.0 (+) Fucose Fucose +) Sialic Acid Fraction of glycans ID'ed 0.8 Sialic Acid 0.6 0.2 0.0 55 14 62 10 40 29 32 40 # of glycans 56 13 63 9 D'ed with mod

Fig.29. Bar plots of the fraction of glycans containing fucose (red) or sialic acid (purple) modifications that were released from proteins/peptides (P) or RNA samples (R) $^{[11]}$

- Fucosylation and sialylation are the two main components of glycan structures modifying RNAs
- GlycoRNAs from 293T and H9 cells have higher fucosylation
- GlycoRNAs from HeLa cells have higher sialylation

→ Thanks to this MS-based approach, it was revealed that the glycoforms are mainly fucosylated and sialylated

Take-home message

This data further confirms that glycoRNAs are modified with sialic acid containing structures, but also with fucose.

<u>IV. Does the canonical glycan biosynthetic machineries contribute to</u> <u>glycoRNA production?</u>

Authors' hypothesis: similarly to glycoproteins, glycoRNAs may be related to O- and/or N-glycan biosynthetic machinery

1) <u>Genetic approach</u>



Fig.30. Blotting of RNA from IdID CHO cells labeled with Ac4ManNAz, Galactose, N-acetylgalactosamine, or all $^{\left[11\right] }$

- Method: use of IdID CHO cell line, lacking GALE enzyme necessary for Nglycan elongation and initiation of O-glycosylation
- Culture of cells in minimal media enabled very low glycoRNA labeling
- Supplementation with Gal, but not with GalNac, partially restored glycoRNA labeling
- Supplementation with both Gal and GalNac fully restored glycoRNA labeling

 \rightarrow In CHO cells, the glycoRNA biosynthesis seems to depend on GALE activity, a N-/O- glycosylation enzyme

IV. Does the canonical glycan biosynthetic machineries contribute to glycoRNA production?

Authors' hypothesis: similarly to glycoproteins, glycoRNAs may be related to O- and/or N-glycan biosynthetic machinery

2) Pharmacological approach



Fig.31. Blotting of RNA from HeLa cells treated with $Ac_4ManNAz$ and indicated concentrations of NGI-1, an inhibitor of OST ^[11]

- Method: use of NGI-1, an OST (Oligosaccharyltransferase) inhibitor, an enzyme of the N-glycosylation pathway
- Treatment with NGI-1 induced a loss of glycoRNA labeling, with a dose-dependent effect

→ N-glycosylation pathway seems to be required for glycoRNA biosynthesis

<u>IV. Does the canonical glycan biosynthetic machineries contribute to glycoRNA production?</u>

Authors' hypothesis: similarly to glycoproteins, glycoRNAs may be related to O- and/or N-glycan biosynthetic machinery

3) Enzymatic approach



• Method: use of a panel of endoglycosidases to cleave off the glycoforms

- Positive control: VC-sia induces a complete loss of glycoRNA labeling
- Treatment with PNGaseF causes an almost complete loss of glycoRNA labeling
- Treatment with endo F2, F3 and Hf causes a partial loss of glycoRNA labeling
- Treatment with O-glycosidase has no effect

→ GlycoRNA are likely composed of N-glycans, degraded only by N-glycan endoglycosidases

Fig.32. Quantification of $Ac_4ManNAz$ signal after treatment of $Ac_4ManNAz$ -labeled He La cell RNA with the indicated enzymes *in vitro* ^[11]

IV. Does the canonical glycan biosynthetic machineries contribute to glycoRNA production?

Take-home message

This data shows that the canonical N-glycan biosynthetic machinery used in glycoprotein formation also contributes to glycoRNA production.

Method: separation of subcellular compartments and detection of glycoRNAs 5 3 2 \rightarrow GlycoRNAs are not found in \rightarrow GlycoRNAs are found exclusively the nuclei fraction in the membrane fraction 0.5 0.5 Sybr Sybr glycoRNA glycoRNA 2' 0.5 0.5 kb kb Strep Strep 50 90 70 αGAPDH αRPN1 Fig.34. Blotting of RNA and proteins after Fig.33. Blotting of RNA and proteins after nuclei 70 separatation of cytosol from membranous purification. Non-nuclear proteins GAPDH and 90 organelles. Membrane proteins RPN1, Sec63, and α β-**Tubulin** αSec63 tubulin and nuclear marker H3K4me3 are visualized soluble tubulin are visualized by western blot ^[11] 25 by western blot [11] aH3K4me3 15 $\alpha \beta$ -Tubulin kDa kDa

In which cellular comparment are glycoRNAs present?

<u>Authors' hypothesis:</u> considering the canonical trafficking and localization of glycoconjugates, glycoRNAs may be present on the extracellular surface of the plasma membrane of living cells

 Method: VC-Sia has a specific ability to cleave sialic acids off the surface of living cells



Fig.35. Blotting of RNA from HeLa cells labeled with $Ac_4ManNAz$ and exposed or not to VC-Sia ^[11]

 \rightarrow VC-Sia is able to cleave glycoRNAs at the surface of living cells

 Method: validation with an Ac₄ManNAzindependent labeling technique



Fig.36. Schematic of the lectin-based proximity labeling of RNA on cell surfaces $^{\left[11\right] }$

→ This technique is able to label glycoconjugate structures on the surface of living cells

- Method: validation with an Ac₄ManNAz-independent labeling technique
- Assay on live HeLa cells



Fig.37. Blotting of total RNA samples after labeling. Lanes 5 and 6 were processed *in vitro* with RNase cocktail or VC-Sia ^[11]

- GlycoRNAs are labeled when cells are stained with MAAII and WGA but not with ConA
- Treatment of glycoRNAs with RNase strongly abrogates glycoRNA signal
- Treatment with VC-Sia induces a shift in molecular weight but does not reduce signal

 \rightarrow GlycoRNAs are found at the surface of living cells and contain sialic acid structures

- Method: validation with an Ac₄ManNAz-independent labeling technique
- Assay on HeLa cell lysate



Fig.38. Blotting of total RNA samples from lysed cells. Lanes 5 and 6 were processed with RNase cocktail or VC-Sia $^{\left[11\right] }$

- GlycoRNAs are still labeled when using MAAII and WGA even though there is no plasma membrane
- Weak but consistent labeling of internal rRNAs
- Treatment with VC-Sia induces a shift in molecular weight but does not reduce signal

→ Most glycoRNAs are found on the cell surface

Take-home message

This data suggests that the majority of glycoRNAs are exposed on the surface of living cells, on the extracellular surface of plasma membrane.

VI. Can anti-RNA antibodies recognize cell surface glycoRNAs?

Method: FACS using J2 antibody recognizing dsRNA on HeLa cells





- 20% cells are J2-positive
- Treatment with RNase A strongly abrogates staining with J2 antibody
- Staining is rescued when a RNase inhibitor is added
- \rightarrow RNA is indeed present on the surface of live cells

VI. Can anti-RNA antibodies recognize cell surface glycoRNAs?



Fig.40. FACS analysis of single HeLa cells pre-treated with the OST inhibitor NGI-1 at the indicated concentrations. Dashed vertical line denotes a J2-high population ^[11]

- Method:
- FACS using J2 antibody recognizing dsRNA on HeLa cells
- Cell treatment by NGI-1, an inhibitor of the canonical glycoprotein pathway

Treatment with NGI-1 induces a dose-dependent reduction of J2-positive cells

→ The RNAs present on the cell surface revealed by J2 staining are glycoRNAs

VI. Can Siglec receptors recognize cell surface glycoRNAs?

Can glycan-binding receptors interact with the glycoRNAs displayed at the cell surface?



Fig.41. FACS analysis of single HeLa cells pre-treated or not with RNase then stained with the indicated Siglec-Fc reagents $^{\left[11\right] }$

- Siglec receptors bind sialic acid structures
- 9 out of 12 Siglec-Fc reagents tested showed staining
- 2 out of the 9 (Siglec-11 and Siglec-14) were sensitive to RNase A treatment
- → GlycoRNAs could be ligands of Siglec receptors

VI. Can Siglec receptors and anti-RNA antibodies recognize cell surface glycoRNAs?

Take-home message

This data suggests that glycoRNAs found at the surface of live cells may play a role in molecular interactions at cell junctions, notably with receptors of the Siglec family, which have a role in immune modulation.

Conclusion and perspectives

- In mammals, proteins and lipids are not the only biomolecules to be glycosylated in cells
- In mammalian species, RNA was found to be modified with glycan structures rich in sialic acid and fucose
- These glycoRNAs are small non-coding RNAs and are conserved across species and cell types
- GlycoRNAs are present on the surface of living cells and are ligands for Siglec receptors
- \rightarrow Perspectives
 - Defining in more details all glycoforms that can possibly modify RNAs
 - Defining the chemical linkage between the RNA transcript and the glycoform
 - Pathology implication (auto-immune diseases)









Thank you for your attention! Any questions?



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