

POSSIBLE ROLE OF microRNAs IN CKD PROGRESSION

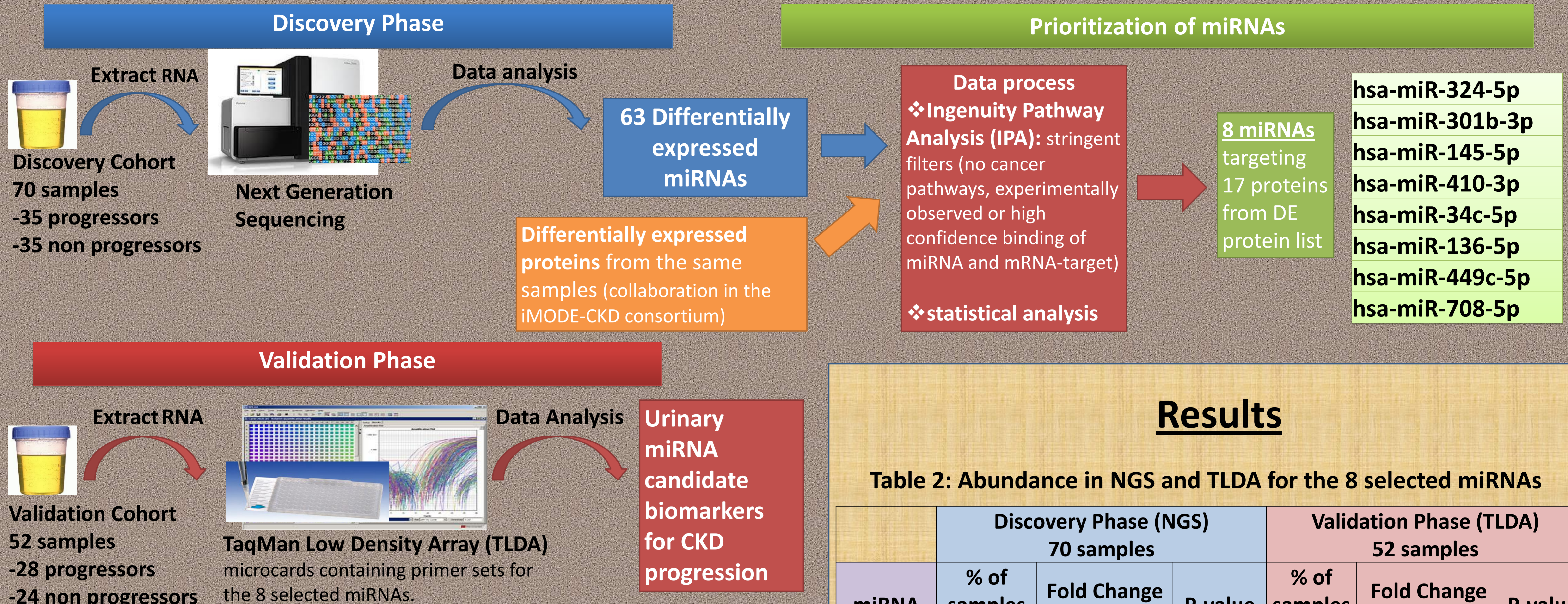
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Introduction – Objectives

miRNAs are short non coding RNAs that regulate mRNA expression. Similar to other diseases, miRNAs have been found to be modified in renal tissue and urine during kidney disease and therefore could serve as markers or provide information on the pathophysiology of disease. In this study, in the context of the European project iMODE-CKD, we aimed to correlate changes in urinary miRNA abundance to progression of chronic kidney disease (CKD).

Workflow – Clinical Data



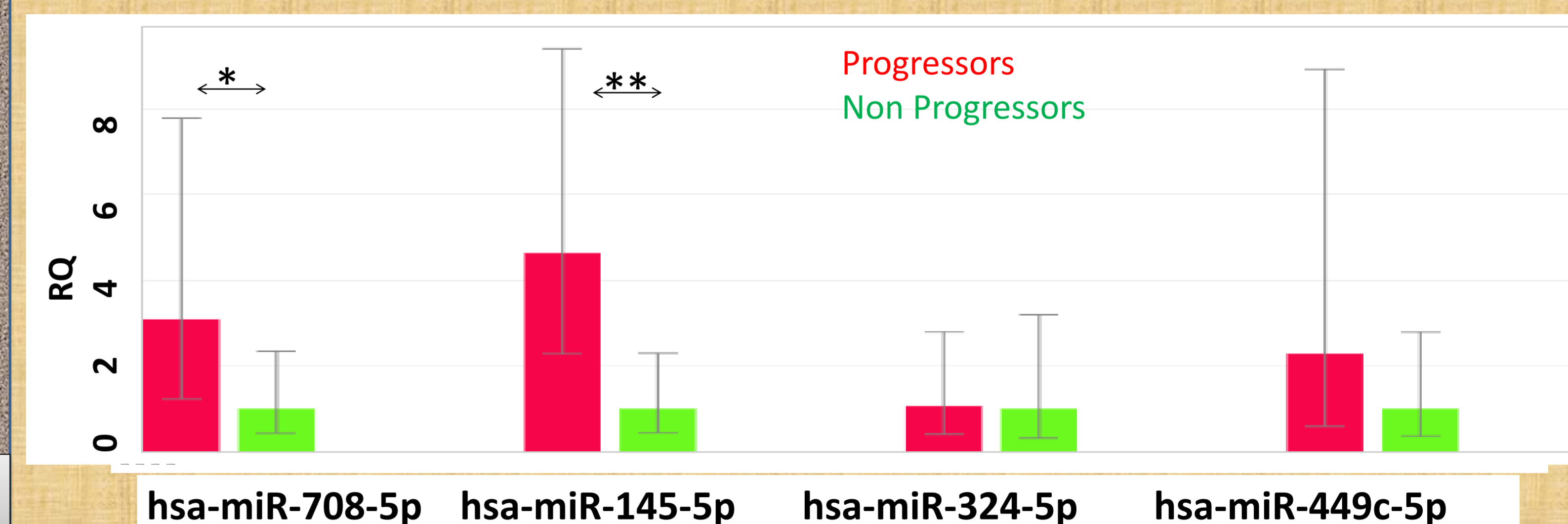
Results

Table 2: Abundance in NGS and TLDA for the 8 selected miRNAs

miRNA	Discovery Phase (NGS) 70 samples			Validation Phase (TLDA) 52 samples		
	% of samples detected	Fold Change (Prog vs Non)	P-value	% of samples detected	Fold Change (Prog vs Non)	P-value
hsa-miR-34c-5p	37,1 (26)	8,743	4,56E-21	15,4 (8)	4,508	0,332
hsa-miR-410-3p	37,1 (26)	1,734	4,64E-06	11,5 (6)	3,955	0,174
hsa-miR-324-5p	41,4 (29)	0,301	3,93E-05	21,2 (11)	1,062	0,517
hsa-miR-301b-3p	32,9 (23)	3,377	3,81E-04	3,8 (2)	0,698	-
hsa-miR-708-5p	22,9 (16)	0,809	7,32E-04	25,0 (13)	3,941	0,040
hsa-miR-145-5p	14,3	4,850	1,39E-03	40,4 (21)	5,055	0,016
hsa-miR-136-5p	37,1 (26)	0,973	1,84E-03	1,9 (1)	-	-
hsa-miR-449c-5p	34,3 (24)	4,108	3,93E-03	21,2 (11)	2,461	0,145

Table 1: Clinical data of the samples used in the study

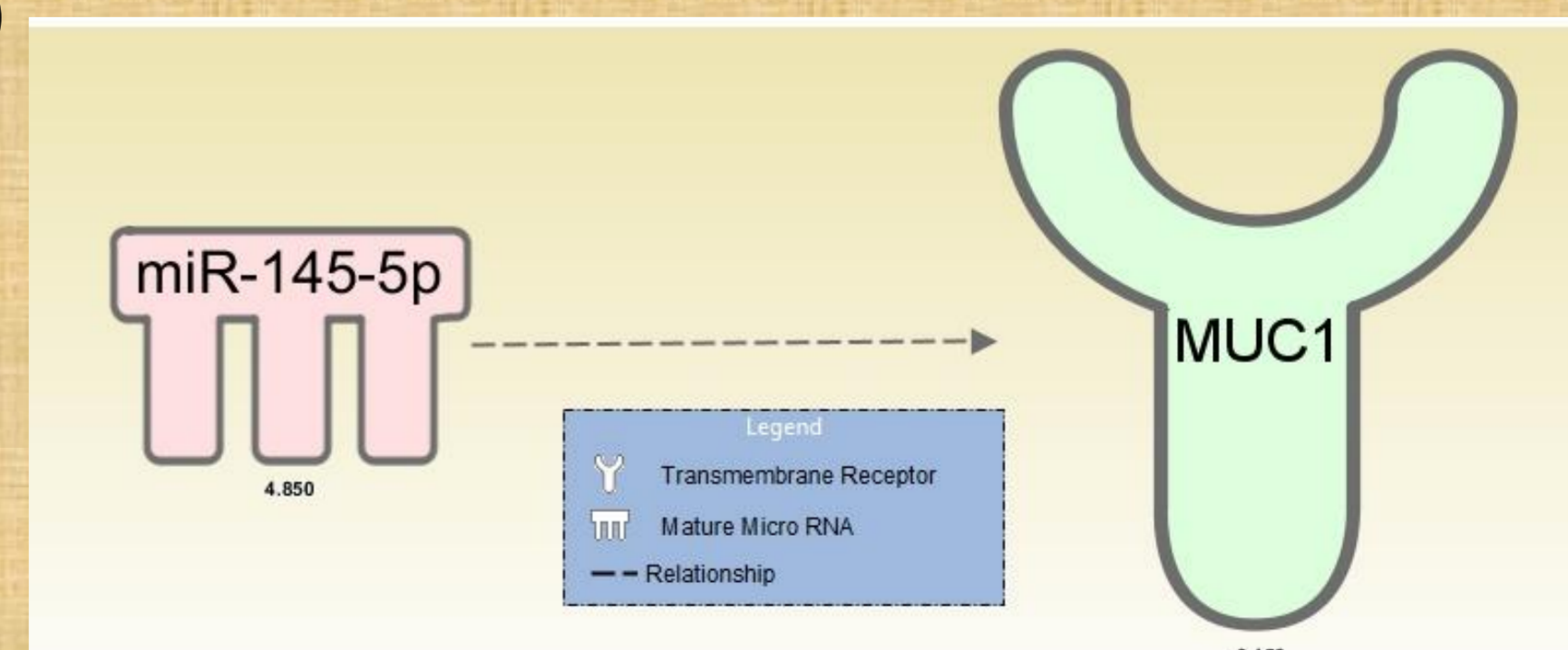
Discovery Cohort	All n=70	Non progressors n=35	Progressors n=35	Significance
Gender (F/M)	23/47	11/24	12/23	P = 1.0000
Age (years)	65±15	63±15	67±15	P = 0.0964
Diabetes (Y/N)	25/45	11/24	14/21	P = 0.6179
baseline eGFR (ml/min/1.72)	44±16	47±16	41±16	P = 0.1154
Proteinuria (µg/µl)	0.471±0.866	0.158±0.260	0.784±1.120	P = 0.0285
Follow up duration (years)	2.6±0.4	2.6±0.4	2.6±0.4	P = 0.5213
%slope/year	-6±9	0.7±1.4	-13±8	P = 0.00001
Validation Cohort	All n=52	Non progressors n=24	Progressors n=28	Significance
Gender (F/M)	16/36	7/17	9/19	P = 0.8274
Age (years)	58±16	60±16	57±17	P = 0.5324
Diabetes (Y/N)	42/10	6/18	4/24	P = 0.3399
baseline eGFR (ml/min/1.72)	49±21	51±18	47±23	P = 0.4627
Proteinuria (µg/µl)	1.378±2.166	0.691±1.255	1.967±2.596	P = 0.0099
Follow up duration (years)	2,0±0,7	2.4±0,4	1.6±0,7	P = 0.0010
%slope/year	-13,4±21,8	0.8±1,9	-26.1±23,7	P = 0.0001



Boxplots of the Relative Quantity (RQ) of the targets per biological group in the validation study.

Reference group : Non Progressor (green)
Normalization : hsa-miR-30a

Strongest possible connection revealed in this study in relation to CKD



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Conclusions

✓ hsa-miR-145-5p and hsa-miR-708-5p were validated to be modified in urine of CKD patients with progressive disease.

✓ Limited number of miRNAs were validated →

- Variability in the samples?
- Change in technology?
- Change in normalization?
- Change in cohort?

Future Plans

➢ Treat renal cells with miRNA antagonists for miR-708 and miR-145 and investigate the possible changes in their targets with LC-MS/MS → possibly reveal the direct regulation of the miRNAs to the proteins and enlighten prospects of the CKD progression.