

المركز العراقي لبحوث السرطان والوراثة الطبية / الجامعة المستنصرية

microRNAs: biogenesis and diagnosis

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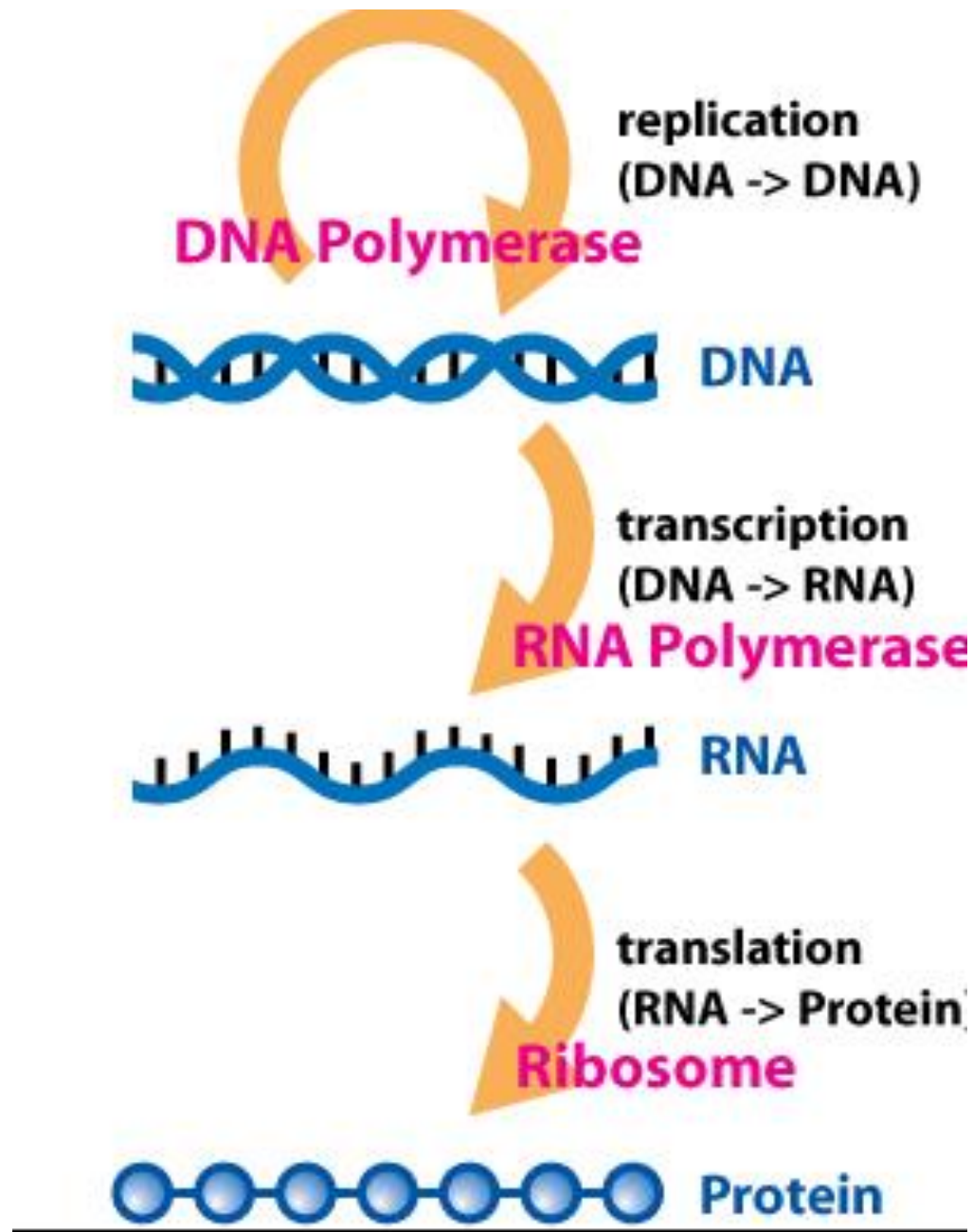
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والدعوة عامة للجميع

- * Introduction : gene silencing
- * Central dogma
- * RNA interference
- * Biomarker and screening
- * Biogenesis
- * Animation
- * miRBase
- * Treatment and trails
- * ICCMGR observation

INTRODUCTION

- **Gene silencing** is a general term describing epigenetic processes of gene regulation.
- The term gene silencing is generally used to describe the "switching off" of a gene by a mechanism other than genetic modification.
- Gene silencing occurs when RNA is unable to make a protein during translation.



- Genes are regulated at either the transcriptional or post-transcriptional level.
- Transcriptional gene silencing is the result of histone modifications, creating an environment of heterochromatin around a gene that makes it inaccessible to transcriptional machinery (RNA polymerase, transcription factors etc.).

- Post-transcriptional gene silencing is the result of mRNA of a particular gene being destroyed or blocked.
- The destruction of the mRNA prevents translation to form an active gene product (in most cases, a protein).
- The blocking of the gene occurs through the activity of silencers, which bind to repressor regions. A common mechanism of post-transcriptional gene silencing is RNAi

Discovery of RNA interference (1998)

- silencing of gene expression with dsRNA



The Nobel Prize in Physiology or
Medicine 2006

"for their discovery of RNA interference - gene silencing by
double-stranded RNA"



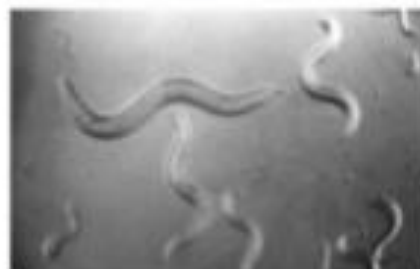
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Andrew Z. Fire



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Craig C. Mello



RNA Interference

- RNA interference (RNAi), is a technique in which exogenous, double-stranded RNAs (dsRNAs) that are complimentary to known mRNAs, are introduced into a cell to specifically destroy that particular mRNA, thereby diminishing or abolishing gene expression .

- RNA interference was known by other names, including post transcriptional gene silencing and quelling .

Different classes of small RNA molecules

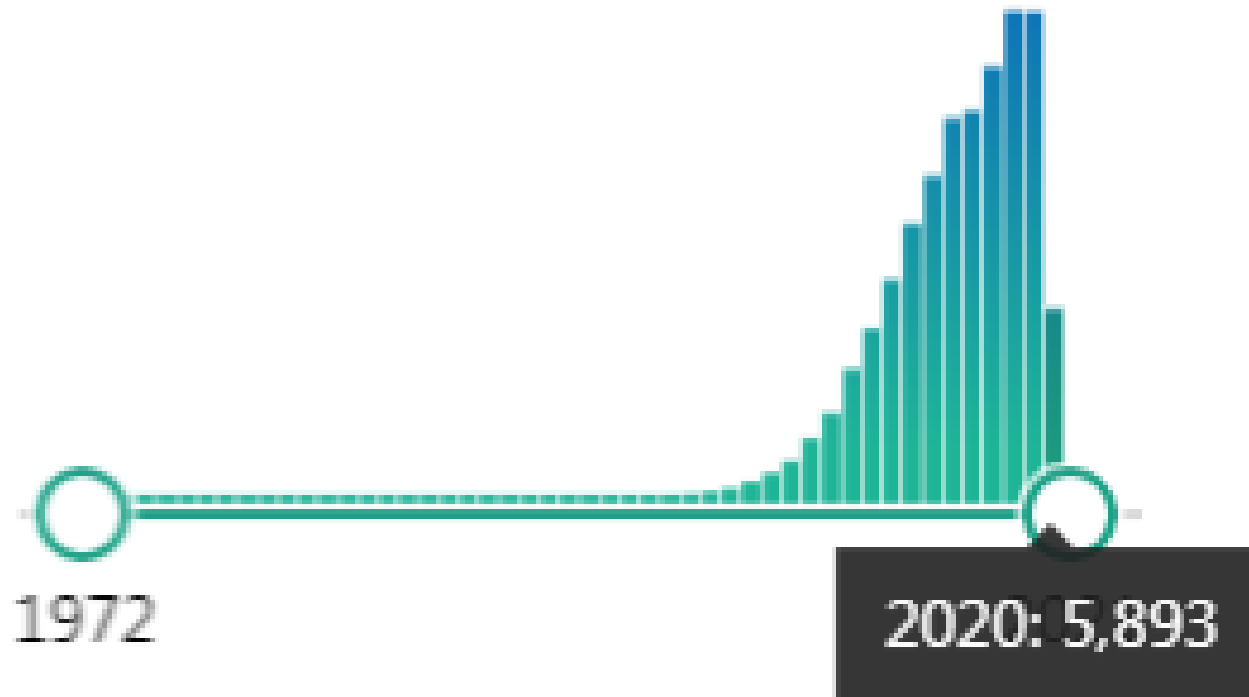
During dsRNA cleavage, different RNA classes are produced:

- siRNA
- miRNA

Small interfering RNA (siRNA):

- Short interfering RNA or silencing RNA
- 21–23 nucleotide-long double-stranded RNA
-
- Can be exogenously (artificially) introduced into cells by transfection

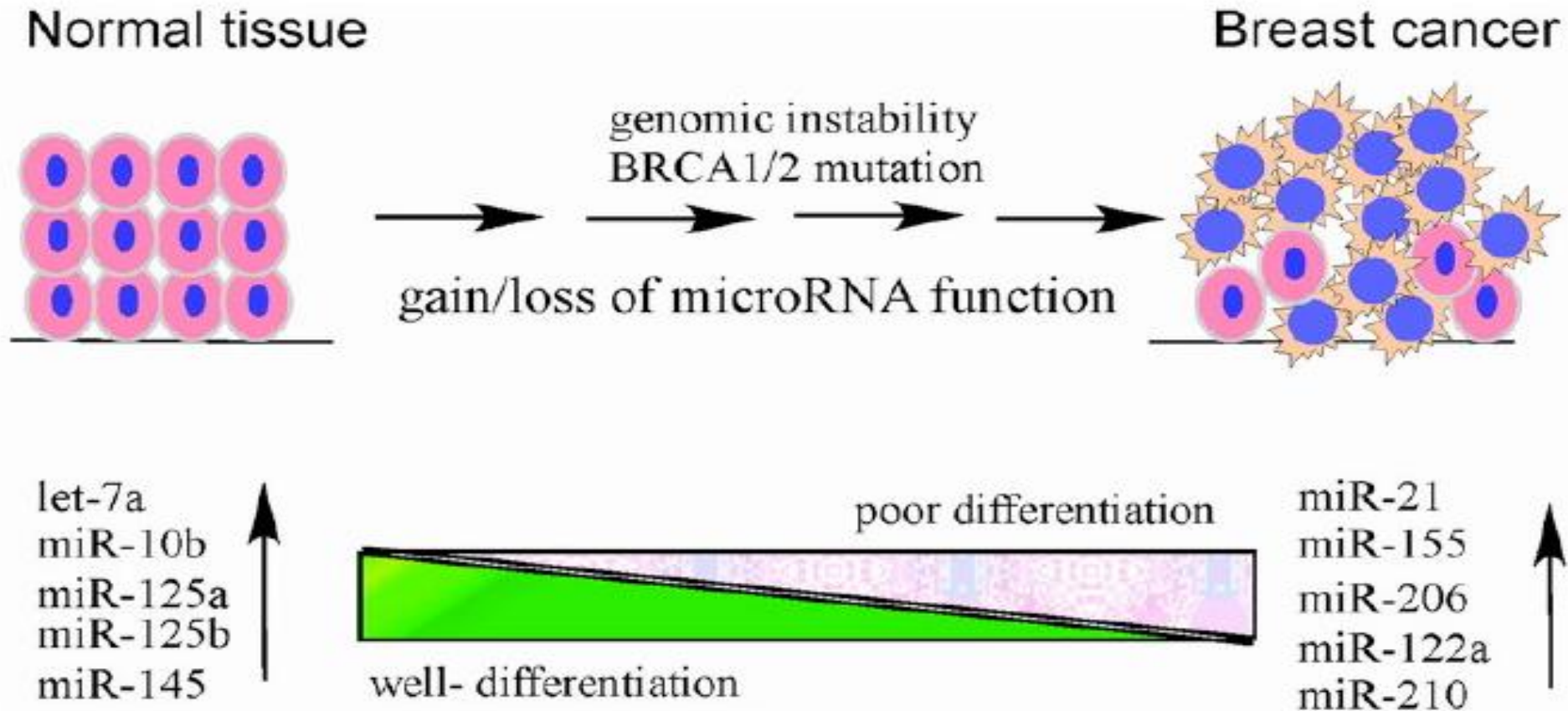
NCBI: microRNA



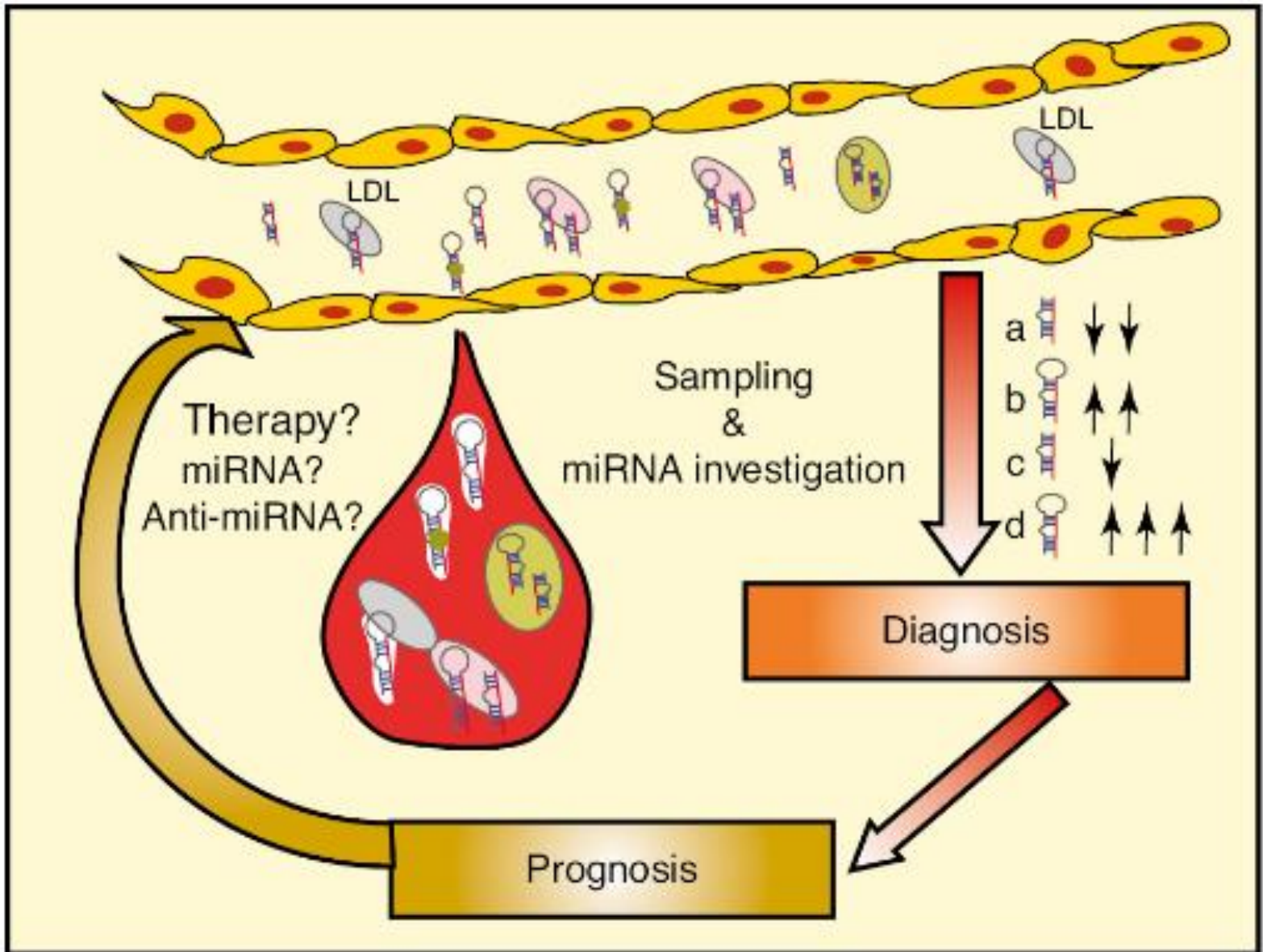
What is a miRNA?

- **Small single stranded RNAs (21-25 nucleotides) but derived from larger precursors (double stranded RNAs)**
- **Non-coding sequences**
- **Form imperfect stem-loop structures (hairpin)**
- **Hybridize by incomplete base-pairing to several sites in the 3'-untranslated regions of target mRNAs**
- **Negative regulators of gene expression (Postranscriptional and Translational regulation)**
- **Role in disease and cancer still in research**

⚡ The increasing number of studies that prove the presence of miRNAs in **circulating (serum/plasma)** increases the chance of using this miRNAs as **a good biomarker for cancer and other diseases.**

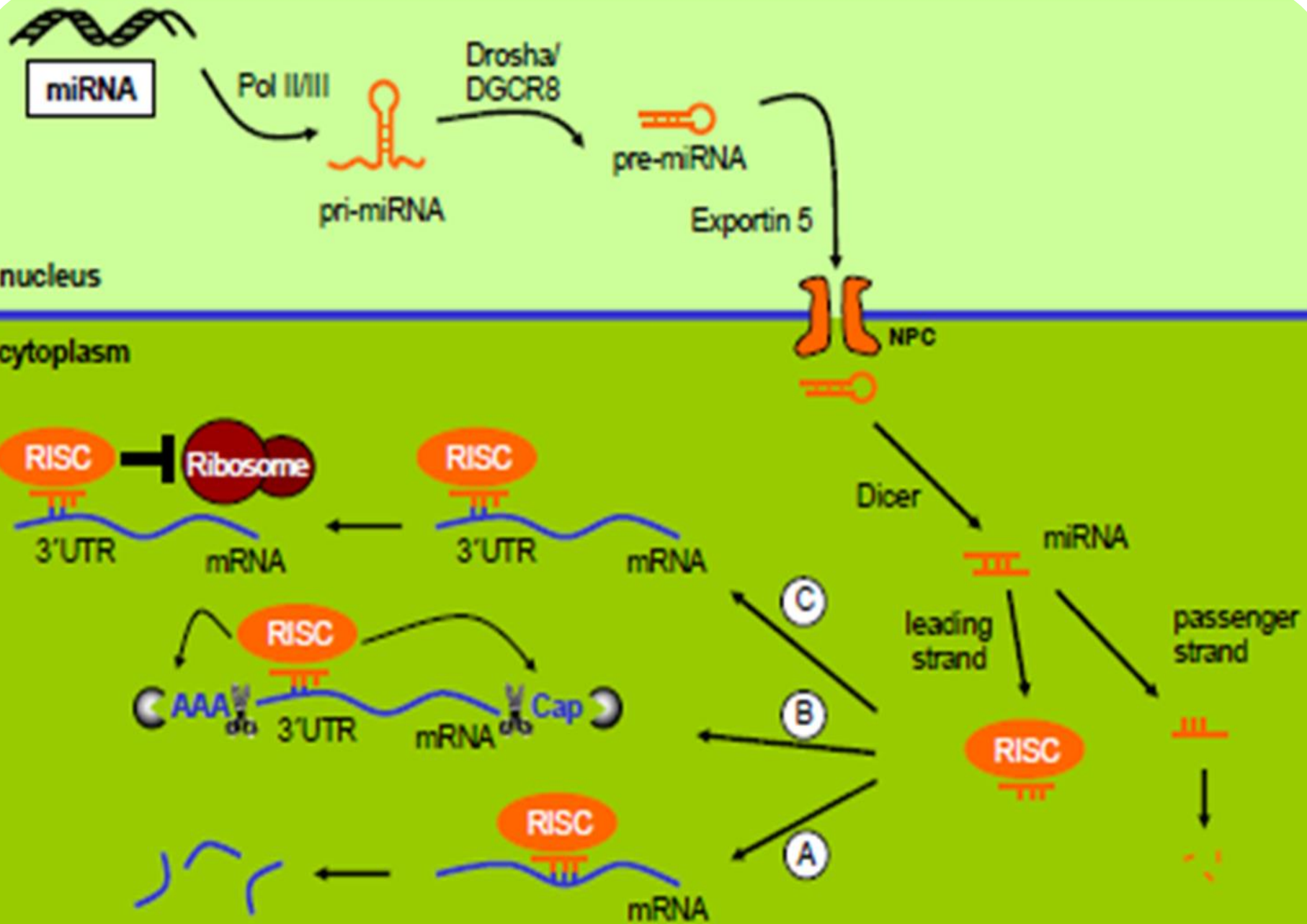


Samples used*	Method(s) used	Key miRNA changes	
		Up-regulated	Down-regulated
MCF-7, T47D breast cancer cell line	Northern blot		miR-143 miR-145 miR-16 let-7a-1
Breast cancer tumor tissues (6) vs. normal tissues (5) MCF-7 cell line	Bead-based flow cytometry Northern blot	miR-21	let-7
Breast cancer tumor tissues (76) vs. normal tissues (30) Breast cancer cell lines	miRNA microarray Northern blot	miR-21 miR-155 miR-206 miR-122a miR-210	let-7 miR-10b miR-125a miR-125b miR-145
Breast cancer tumor tissues (79) vs. normal tissues (6)	miRNA microarray	miR-21 miR-155 miR-206 miR-122a miR-210	let-7 miR-10b miR-125a miR-125b miR-145
Breast cancer tumor tissues (5) vs. normal tissues (5) MCF-7 cell line	TaqMan RT-PCR	miR-21	



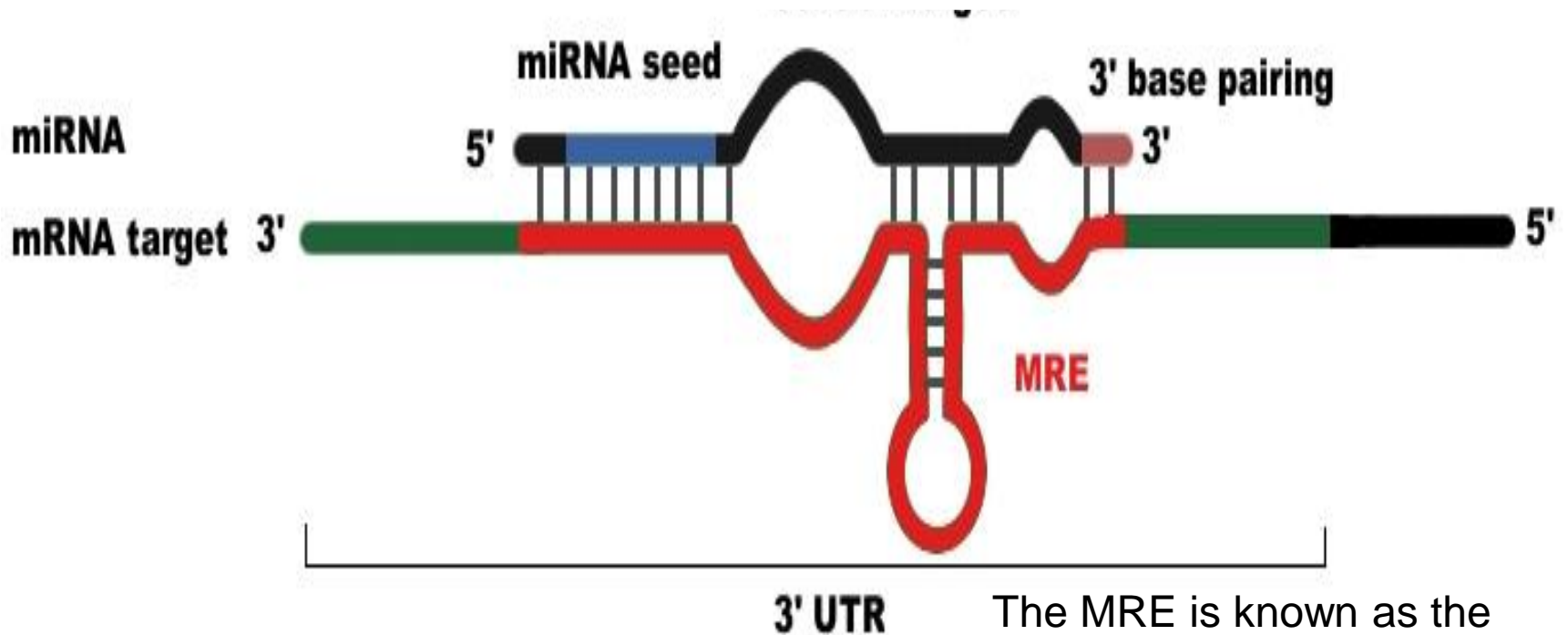
- A select number of miRNAs may serve as **diagnostic markers for different tumor types and diseases.**
- The **ideal properties of biomarker** should be:
 - ❖ disease specific
 - ❖ able to differentiate between pathologies
 - ❖ rapid and significant release during pathology development
 - ❖ long life in sample, rapid, simple, accurate and inexpensive for detection
 - ❖ un affected by environmental conditions
 - ❖ present in accessible body fluid.

Cancer	Tumor marker	Sensitivity
Breast cancer	CEA	29%–53% ^a
	CA15-3	54%–90% ^a
Prostate cancer	PSA (>4 ng/ml)	20%–72%
Lung cancer	None	–
Colon cancer	CEA (>5 ng/ml)	26%
	CA19-9	18%
Uterine cancer	CA125	34.6%
Melanoma	S-100 protein	15%–65%*
Non-Hodgkin's lymphoma	None	–
Ovarian cancer	CA125	71% ^a
Bladder cancer	Urine cytology	71%
Renal cancer	None	–
Pancreas cancer	CA19-9	69%–93%



Symbol	Definition
Prefix: has and mmu	Indicates species
miR-XXX	All microRNA are identified by 3-4 numbers
Pri-miR	Primary miRNA: gene transcript with hairpin loop structure, capped with a specially modified nucleotide at the 5' end, and polyadenylated, may contain 1-6 pre-miR
Pre- miR	Precursor miRNA: hairpin structure obtained from the pri-miRNA and is characterized by two nucleotide overhang at its 3' end
miR-XXX	Mature miRNA that is the guide strand "-3p" anti sense
miR-XXX*	Passenger strand "5-p" sense
miR-XXXa and miR-XXXb	Indicates high homology
miR-XXX-1 and miR-XXX-2	Identical mature miRNAs originating from different regions of the genome
Seed sequence	Nucleotides 2-7 of miRNA complementary to target mRNA

miRNA Binding



The MRE is known as the “miRNA recognition element.” This is simply the sequence in the target that an miRNA binds to mRNA

The major players

- **Dorsha** and **Pasha** are part of the microprocessor protein complex
- **Dorsha** and **Dicer** are RNase III enzymes
- **Pasha** is a ds RNA binding protein
- **Exportin 5** is a member of the nucleocytoplasmic transport factors
- **Argonaute** are RNase enzyme

How to screen for your miRNA



miRBase::Sequences

Home Search Browse Genomics Help Download Submit miRBase Search

miRBase: the home of microRNA data

miRBase (<http://microrna.sanger.ac.uk/>) is the new home of microRNA data on the web, providing data previously accessible from the miRNA Registry. Old miRNA Registry addresses should redirect you to this page.

- The [miRBase Sequence Database](#) is a searchable database of published miRNA sequences and annotation. The data were previously provided by the miRNA Registry.
- The [miRBase Registry](#) continues to provide gene hunters with unique names for novel miRNA genes prior to publication of results.
- The [miRBase Targets](#) database is a new resource of predicted miRNA targets in animals.

Each entry in the miRBase Sequence database represents a predicted hairpin portion of a miRNA transcript (termed mir in the database), with information on the location and sequence of the mature miRNA sequence (termed miR). Both hairpin and mature sequences are available for [searching](#) using BLAST and SSEARCH, and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also [available for download](#).

Please note that the predicted stem-loop sequences in the database are not strictly precursor miRNAs (pre-miRNAs), but include the pre-miRNA and some flanking sequence from the presumed primary transcript.

Please use the tabs along the top of this page to access the different areas of the site, or you can click [here](#) to jump to the help pages.

To receive email notification of data updates and feature changes please subscribe to the [miRNA mailing list](#). Any other queries about the website or naming service should be directed at microrna@sanger.ac.uk.

References

If you make use of the data presented here, please cite the following articles in addition to the primary data sources:

[miRBase: tools for microRNA genomics](#).

Griffiths-Jones S, Saini HK, van Dongen S, Enright AJ.

miRNA count: 9539 entries

Release [13.0](#): March 2009

Search by miRNA name or keyword

Download published miRNA data

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[NetWatch - Science 303:1741 \(2004\)](#)

[Highlights, Web watch - Nature Reviews Genetics 5:244 \(2004\)](#)

Homo sapiens miRNAs (706 sequences)

ID	Accession	Chromosome	Start	End	Strand	Fetch
hsa-let-7a-1	MI0000060	9	95978060	95978139	+	<input type="checkbox"/>
hsa-let-7a-2	MI0000061	11	121522440	121522511	-	<input type="checkbox"/>
hsa-let-7a-3	MI0000062	22	44887293	44887366	+	<input type="checkbox"/>
hsa-let-7b	MI0000063	22	44888230	44888312	+	<input type="checkbox"/>
hsa-let-7c	MI0000064	21	16834019	16834102	+	<input type="checkbox"/>
hsa-let-7d	MI0000065	9	95980937	95981023	+	<input type="checkbox"/>
hsa-let-7e	MI0000066	19	56887851	56887929	+	<input type="checkbox"/>
hsa-let-7f-1	MI0000067	9	95978450	95978536	+	<input type="checkbox"/>
hsa-let-7f-2	MI0000068	X	53600878	53600960	-	<input type="checkbox"/>
hsa-let-7g	MI0000433	3	52277334	52277417	-	<input type="checkbox"/>
hsa-let-7i	MI0000434	12	61283733	61283816	+	<input type="checkbox"/>
hsa-mir-1-1	MI0000651	20	60561958	60562028	+	<input type="checkbox"/>
hsa-mir-1-2	MI0000437	18	17662963	17663047	-	<input type="checkbox"/>
hsa-mir-7-1	MI0000263	9	85774483	85774592	-	<input type="checkbox"/>
hsa-mir-7-2	MI0000264	15	86956060	86956169	+	<input type="checkbox"/>
hsa-mir-7-3	MI0000265	19	4721682	4721791	+	<input type="checkbox"/>
hsa-mir-9-1	MI0000466	1	154656757	154656845	-	<input type="checkbox"/>
hsa-mir-9-2	MI0000467	5	87998427	87998513	-	<input type="checkbox"/>
hsa-mir-9-3	MI0000468	15	87712252	87712341	+	<input type="checkbox"/>
hsa-mir-10a	MI0000266	17	44012199	44012308	-	<input type="checkbox"/>
hsa-mir-10b	MI0000267	2	176723277	176723386	+	<input type="checkbox"/>
hsa-mir-15a	MI0000069	13	49521256	49521338	-	<input type="checkbox"/>
hsa-mir-15b	MI0000438	3	161605070	161605167	+	<input type="checkbox"/>
hsa-mir-16-1	MI0000070	13	49521110	49521198	-	<input type="checkbox"/>

Stem-loop sequence MI0000060

Accession MI0000060

ID hsa-let-7a-1

Symbol [HGNC:MIRLET7A1](#)

Description Homo sapiens let-7a-1 stem-loop

Stem-loop

```
      u  gu                uuagggucacac
uggga gag  aguagguuguauaguu      c
||||| |||  |||||||||||||||||
auccu uuc  ucaucuaacauucaa      a
      -  ug                uagagggucacc
```

[Get sequence](#)

Comments let-7a* cloned in [6] has a 1 nt 3' extension (U), which is incompatible with the genome sequence.

Genome context

<i>Coordinates (NCBI36)</i>	<i>Overlapping transcripts</i>
9: 95978060-95978139 [+]	intergenic

[View flanking features](#)

Clustered miRNAs

< 10kb from hsa-let-7a-1

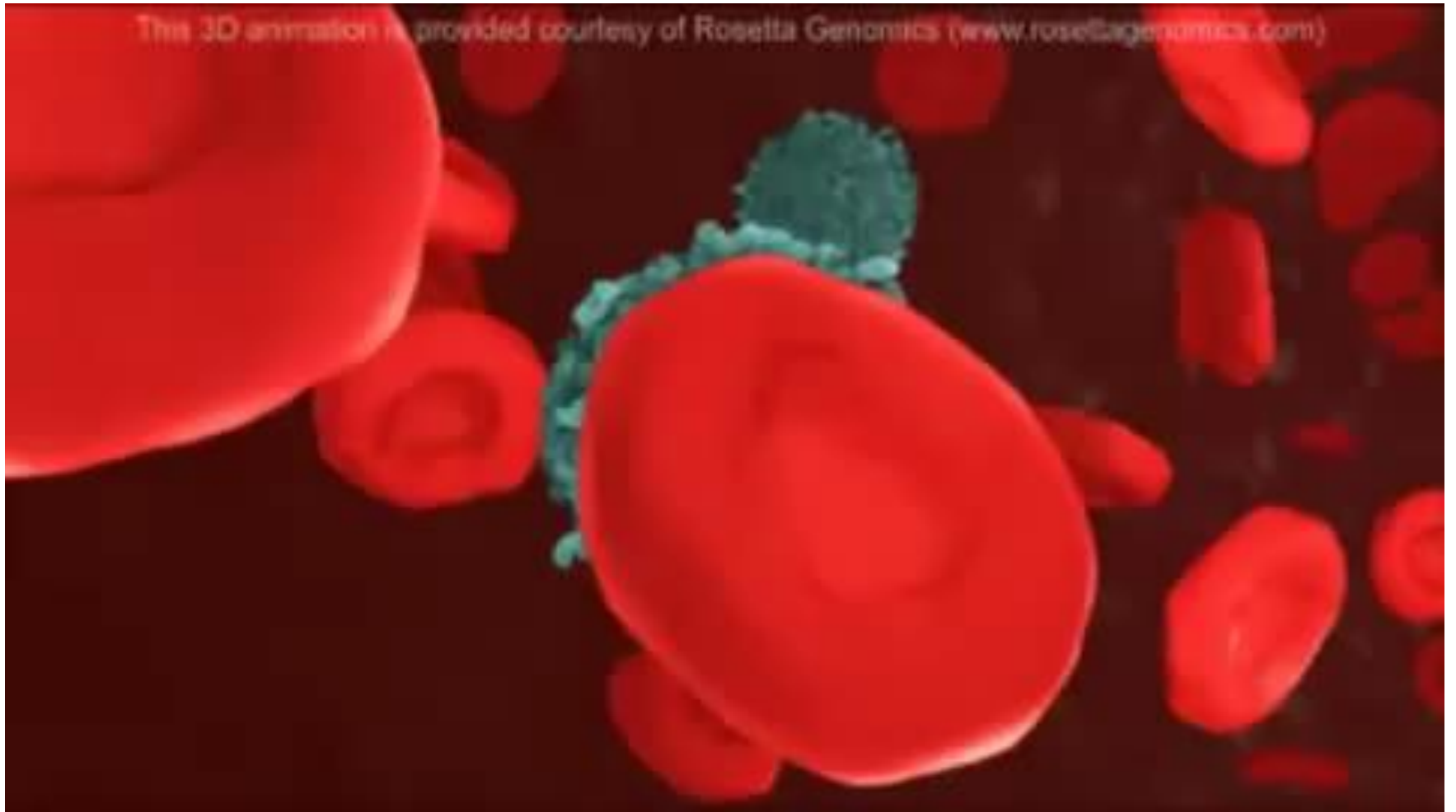
hsa-let-7a-1	9: 95978060-95978139 [+]
hsa-let-7f-1	9: 95978450-95978536 [+]
hsa-let-7d	9: 95980937-95981023 [+]

Database links

EMBL: [AJ421724](#)
RFAM: RF00027; [let-7](#)
HGNC: 31476; [MIRLET7A1](#)
ENTREZGENE: 406881; [MIRLET7A1](#)

Gene family MIPF0000002; [let-7](#)

This 3D animation is provided courtesy of Rosetta Genomics (www.rosellagenomics.com)



miRNAs in Treatment

- Since diseases result from the expression of undesired or mutated genes, or from overexpression of certain normal genes
- The discovery of siRNA and miRNA opens up a new therapeutic approach for the treatment of diseases by targeting genes that are involved in the pathological process

New example about miRNA / blood



NEW BLOOD TEST DEVELOPED TO DIAGNOSE ALZHEIMER'S DISEASE

Submitted by: MEMBS,

🕒 Apr 24, 2016 2:00 pm



University of Otago researchers have discovered a promising new marker that could help diagnose Alzheimer's disease—and all that might be required is a simple blood test.

Before this work began, blood plasma microRNA had been shown to reflect various disease processes, and specific microRNAs were linked to neurological diseases. This led Dr Joanna Williams of Otago's Department of Anatomy to suggest that blood microRNA levels may reflect changes in the brain.

The specific set of blood microRNAs that the Otago researchers have identified can detect Alzheimer's disease correctly 86 per cent of the time.

DIAMIR

DiamiR Receives Award from Alzheimer's Drug Discovery Foundation to Accelerate Development of microRNA Biomarkers for Alzheimer's Disease

Nov 20, 2019

MONMOUTH JUNCTION, N.J., Nov. 20, 2019 /PRNewswire/ — DiamiR, a developer of innovative blood-based diagnostic tests for neurodegenerative and other diseases, announced today a \$492,000 award in support of the project entitled "Circulating brain-enriched microRNAs as peripheral biomarkers of neurodegeneration." The award will accelerate the development of DiamiR's targeted diagnostic technology for detection and prediction of Alzheimer's disease (AD) progression. The award is provided by the Alzheimer's Drug Discovery Foundation (ADDF) Diagnostics Accelerator, a fund set up in collaboration with Bill Gates and other philanthropic partners.



DiamiR Announces Additional \$345,000 Funding from the NIH for Development of CogniMIR™

Sep 17, 2019

MONMOUTH JUNCTION, N.J., Sept. 16, 2019 /PRNewswire/ — DiamiR, a developer of innovative blood-based diagnostic tests for neurodegenerative and other diseases, announced today that the National Institute on Aging (NIA) of the National Institutes of Health (NIH) has awarded DiamiR \$345,000 in supplemental funding under the ongoing Small Business

PROGRAM	INDICATION	IND				
		PRECLINICAL	ENABLING	PHASE 1	PHASE 2	PHASE 3
COBOMARSEN (MRG-106) BLOOD CANCERS	CUTANEOUS T-CELL LYMPHOMA (CTCL)					
	ADULT T-CELL LYMPHOMA/LEUKEMIA					
REMLARSEN (MRG-201) PATHOLOGIC FIBROSIS	CUTANEOUS FIBROSIS					
	OCULAR FIBROSIS					
MRG-229 PATHOLOGIC FIBROSIS	IDIOPATHIC PULMONARY FIBROSIS					
MRG-110 TISSUE REPAIR	HEART FAILURE					
	WOUND HEALING					

REVIEW

siRNA Versus miRNA as Therapeutics for Gene Silencing

Jenny KW Lam^{1,2}, Michael Y T Chow¹, Yu Zhang¹ and Susan W S Leung^{1,2}

Table 5 A summary of siRNA therapeutics in clinical trials (registered with *clinicaltrials.gov*, last accessed 13 June 2015)

Name	Indications	siRNA target	Phase	Delivery system	Route of administration	Trial ID (reference)
Cancer						
ALN-VSP02	Advanced solid tumors with liver involvement	KSP and VEGF	1, completed	Lipid nanoparticles	Intravenous	NCT01158079; NCT00882180 ²
Atu027	Advanced solid tumor Pancreatic ductal carcinoma	PKN3	1, ongoing 1/2, ongoing	Liposomal particles (AtuPLEX®)	Intravenous	NCT00938574 ³ NCT01808638
CALAA-01	Solid tumor	RRM2	1, terminated	Polymer-based targeted nanoparticles	Intravenous	NCT00689065 ¹⁸⁵
DCR-MYC (Dicer-substrate siRNA)	Solid tumor, multiple myeloma, non-Hodgkin's lymphomas Hepatocellular carcinoma	MYC oncogene	1, ongoing 1/2, ongoing	Lipid nanoparticles (EnCore)	Intravenous	NCT02110563 NCT02314052
siG12D LODER	Advanced pancreatic cancer	mutated KRAS oncogene	1, completed; 2, ongoing	Biodegradable polymer-based scaffold	Local implantation	NCT01188785; NCT01676259
siRNA-EphA2-DOPC	Advanced cancers	EphA2	1, ongoing	Neutral liposomes	Intravenous	NCT01591356
TKM-080301 (TKM-PLK1)	Primary or secondary liver cancer Neuroendocrine tumors and adrenocortical carcinoma	PLK1	1, completed 1/2 ongoing	Lipid nanoparticles	Intravenous	NCT01437007 NCT01262235

Table 6 A summary of miRNA therapeutics in clinical trials (registered with *clinicaltrials.gov*, last accessed 13 June 2015)

Name	Indications	miRNA	Phase	Delivery system	Route of administration	Trial ID
MRX34	Primary liver cancer or liver metastasis from other cancers	miRNA-34a	1, ongoing	Liposomes (SMARTICLES)	Intravenous	NCT01829971
TargomiRs	Malignant pleural mesothelioma; non-small-cell lung cancer	miRNA-16	1, ongoing	Nanoparticles (nonliving bacterial minicells)	Intravenous	NCT02369198

The Potential for microRNA Therapeutics and Clinical Research

[Johora Hanna](#), ¹ [Gazi S. Hossain](#), ¹ and [Jannet Kocerha](#) ^{2, *}

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Abstract

Go to:

As FDA-approved small RNA drugs start to enter clinical medicine, ongoing studies for the microRNA (miRNA) class of small RNAs expand its preclinical and clinical research applications. A growing number of reports suggest a significant utility of miRNAs as biomarkers for pathogenic conditions, modulators of drug resistance, and/or as drugs for medical intervention in almost all human health conditions. The pleiotropic nature of this class of nonprotein-coding RNAs makes them particularly attractive drug targets for diseases with a multifactorial origin and no current effective treatments. As candidate miRNAs begin to proceed toward initiation and completion of potential phase 3 and 4 trials in the future, the landscape of both diagnostic and interventional medicine will arguably continue to evolve. In this mini-review, we discuss miRNA drug discovery development and their current status in clinical trials.

Table 1

Interventional clinical trials for miRNAs.

miRNA gene; drug name	Clinical trial number; phase status	Disease/disorder investigated
miR-34; MRX34	NCT01829971 ; phase 1 (terminated) NCT02862145 ; phase 1 (withdrawn)	Liver cancer, lymphoma melanoma
miR-92; MRG 110	NCT03603431 ; phase 1 (recruiting)	wound healing, heart failure
miR-16; MesomiR-1	NCT02369198 ; phase 1 (completed)	Mesothelioma, lung cancer
miR-122; Miravirsen	NCT02508090 ; phase 2 (completed) NCT02452814 ; phase 2 (completed) NCT01200420 ; phase 2 (completed) NCT01872936 ; phase 2 (unknown status) NCT01727934 ; phase 2 (unknown status) NCT01646489 ; phase 1 (completed)	Hepatitis C virus
miR-29; MRG-201	NCT03601052 ; phase 1 (recruiting)	Keloid, fibrous scar tissue formation
miR-21; RG-012	NCT02855268 ; phase 2 (suspended, sponsor decision) NCT03373786 ; phase 1 (active, not recruiting)	Alport syndrome
miR-155; Cobomarsen (MRG- 106)	NCT03713320 /phase 2 (recruiting) NCT03837457 /phase 2 (new/not yet recruiting)	T-cell lymphoma/mycosis fungoides

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Showing: 1-25 of 103 studies 25 ▾ studies per page

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1	<input type="checkbox"/>	Completed	Study on the Difference of Plasma microRNA Expression in Patients With Genetic Susceptibility to Mental Disorders	<ul style="list-style-type: none"> Plasma microRNA in Patients With Genetic Susceptibility to Mental Disorders 		

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Status	Study Title	Conditions	Interventions	Locations
		Diseases		
Completed	microRNA Profile in Early-stage Cervical Cancer	<ul style="list-style-type: none"> Cervical Cancer 		
Completed	Blood microRNA Depression Change After DHCA	<ul style="list-style-type: none"> Aortic Aneurysm 	<ul style="list-style-type: none"> Other: collect blood 	<ul style="list-style-type: none"> Xuanwu Hospital Beijing, Beijing, China
Completed	The Potential Role Of MicroRNA-155 And Telomerase Reverse Transcriptase In Diagnosis Of Non-Muscle Invasive Bladder Cancer And Their Pathological Correlation	<ul style="list-style-type: none"> Bladder Cancer Bladder Disease Bladder Neoplasm Micro-RNA 	<ul style="list-style-type: none"> Diagnostic Test: MicroRNAs-155 Diagnostic Test: Human telomerase reverse transcriptase 	<ul style="list-style-type: none"> Urology and Nephrology Center Mansourah, Aldakahlia, Egypt
Completed	Establishment of a Signature of Circulating microRNA as a Tool to Aid Diagnosis of Primary Brain Tumors in Adults	<ul style="list-style-type: none"> Brain Tumors 		<ul style="list-style-type: none"> Groupe Hospitalier Pitié-Salpêtrière Paris, France
Completed	Expression Profiling of microRNA Following Administration of Dexmedetomidine	<ul style="list-style-type: none"> Coronary Disease 	<ul style="list-style-type: none"> Drug: Dexmedetomidine Injection 	<ul style="list-style-type: none"> Jinqiao Qian Kunming, Yunnan, China
Completed	Microarray Analysis of microRNA Expression in Basal Cell Carcinoma	<ul style="list-style-type: none"> Basal Cell Carcinoma 		<ul style="list-style-type: none"> Department of Dermatology, Venereology and Allergology, Ruhr-University Bochum Bochum, NRW, Germany
Completed	Tocilizumab Effect on microRNA Expression and Adipokine Levels in Rheumatoid Arthritis Patients	<ul style="list-style-type: none"> Rheumatoid Arthritis 	<ul style="list-style-type: none"> Other: laboratory blood tests 	
Completed	MicroRNA Diagnostics in Subarachnoid Hemorrhage 2	<ul style="list-style-type: none"> Subarachnoid Hemorrhage Delayed Cerebral Ischemia Acute Lung Injury 		<ul style="list-style-type: none"> Rigshospitalet Copenhagen, Denmark

Future observation of ICCMGR

- Develop
- Understand
- Target



Novel expression of microRNAs in serum samples of Iraqi breast cancer women

Saad, Zaynab, Arif, Muhammad, Yassen, Nahi, Jasim, Hameed, Jelawe, Majed and [Brown, James](#) (2014). Novel expression of microRNAs in serum samples of Iraqi breast cancer women. *American Journal of Biomedicine*, 2 (5), pp. 567-574.

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Abstract

Although a lot of hard work against cancer to reduces its spread but it still continues to kill with abandon. The need for a biomarker for cancer early detection becomes the most mind concentrated scientists. MicroRNAs the tiny non coding RNA molecules opened new path for the scientists to determine the cancer in its early stages. Expression of microRNAs profiles has been investigated to be involved in cancer development. Here we determined the expression of microRNAs in serum of Iraqi healthy volunteers and other women diagnosed with breast cancer. MicroRNAs expression has been determined by using real time qPCR and delta method has been

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ABSTRACT ONLY | VOLUME 42, ISSUE 5, PS20, MAY 01, 2016



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A differential expression of miRNA in plasma and breast tissue: A potential biomarker

M.Arif Nasir • Zaynab Abdul-Ghany • Zartasht Carmichael • James E.P. Brown • Amtul R. Carmichael

DOI: <https://doi.org/10.1016/j.ejso.2016.02.083>

Introduction: Breast cancer is a complex disease and is the leading cause of cancer mortality in women after lung cancer. A non-coding class of RNA called micro RNA (miRNA) is implicated in many diseases including breast cancer where it has been suggested as a potential biomarker.

Article Info

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