

The Potential of Gene Therapy



“The saddest aspect of life today is that science gathers knowledge faster than society gathers wisdom.”

-Isaac Asimov, master of hard science fiction writing

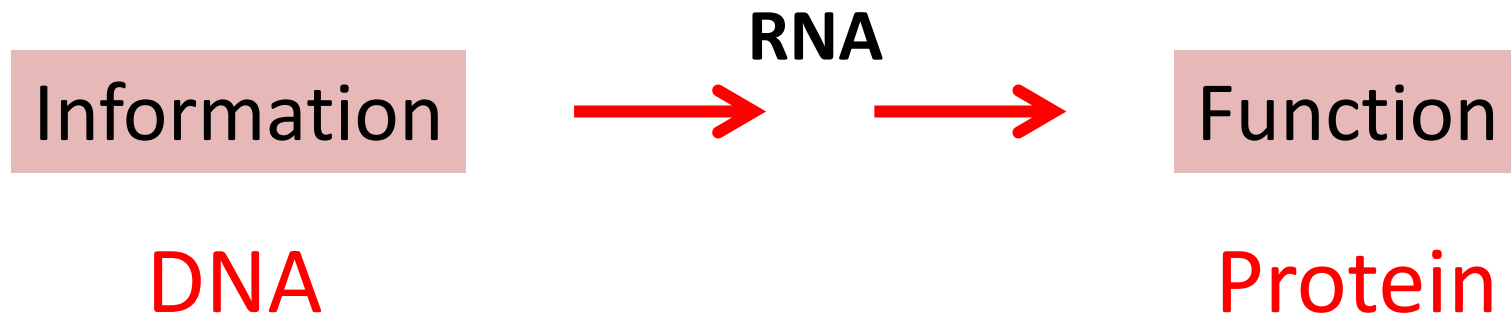


Content

1. Why genes are important in normal and disease biology
2. What is gene therapy?
3. Using silencing techniques to counter hepatitis B virus infection
4. Challenges
5. Relevance of gene therapy research

Genes are fundamental to biology

- Genes are carriers of information
- The information is transformed into function



Conversion of information into
function makes us what we are

The total explanation of all organisms resides within them (genes).... Ultimately, the organism must be explicable in terms of its genes....

- *Sydney Brenner, 1984*



Die Antwoord



Yolandie Vi\$\$er



**n
i
n
j
a**









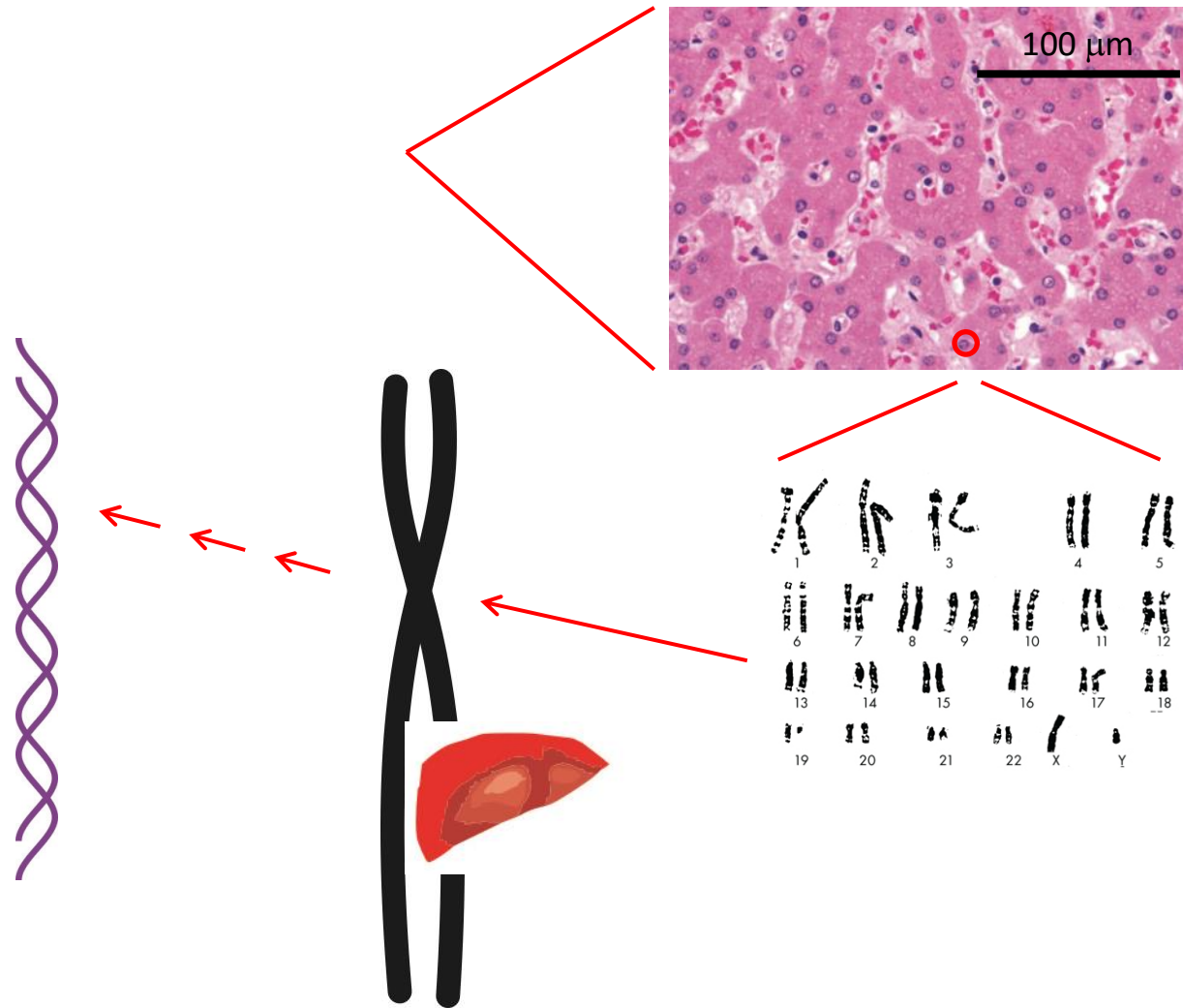








Arrangement of DNA within a cell



Discovery of double helical structure of DNA was crucial



MOLECULAR STRUCTURE OF NUCLEIC ACIDS

A Structure for Deoxyribose Nucleic Acid

WE wish to suggest a structure for the salt of deoxyribose nucleic acid (D.N.A.). This structure has novel features which are of considerable biological interest.

A structure for nucleic acid has already been proposed by Pauling and Corey¹. They kindly made their manuscript available to us in advance of publication. Their model consists of three intertwined chains, with the phosphates near the fibre axis, and the bases on the outside. In our opinion, this structure is unsatisfactory for two reasons:

(1) We believe that the material which gives the X the salt, not the free acid. Without the acidic hydr not clear what forces would hold the structure together as the negatively charged phosphates near the axis; other. (2) Some of the van der Waals distances are small.

Another three-chain structure has also been suggested (in the press). In his model the phosphates are on the bases on the inside, linked together by hydrogen structure as described is rather ill-defined, and for this reason we shall not comment on it.

We wish to put forward a radically different structure for the salt of deoxyribose nucleic acid. This structure has two helical chains each coiled round the same axis (see diagram). We have made the usual chemical assumptions, namely, that each chain consists of phosphate diester groups joining β -D-deoxy-ribofuranose residues with 3',5' linkages. Their bases are related by a dyad perpendicular. Both chains follow righthanded helices, but sequences of the atoms in the two chains run



Each chain follows model No. 1; that inside of the helix the outside. The and the atoms near standard configuration roughly perpendicular base. There is a every 3.4 Å. in it assumed an angle residues in the structure repeats a unit 10 residues on each chain, that is, after 34 Å. The distance of a phosphorus atom from the fibre axis is 10 Å. As the phosphates are on the outside, cations have easy access to them.

The structure is an open one, and its water content is rather high. At lower water contents we would expect the bases to tilt so that the structure could become more compact.

The novel feature of the structure is the manner in which the two chains are held together by the purine and pyrimidine bases. The planes of the bases are perpendicular to the fibre axis. They are joined together in pairs, a single base from one chain being hydrogen-bonded to a single base from the other chain, so

that the two lie side by side with identical z-co-ordinates. One of the pair must be a purine and the other a pyrimidine for bonding to occur. The hydrogen bonds are made as follows: purine position 1 to pyrimidine position 1; purine position 6 to pyrimidine position 6.

If it is assumed that the bases only occur in the structure in the most plausible tautomeric forms (that is, with the keto rather than the enol configurations) it is found that only specific pairs of bases can bond together. These pairs are: adenine (purine) with thymine (pyrimidine), and guanine (purine) with cytosine (pyrimidine).

In other words, if an adenine forms one member of a pair, on either chain, then on these assumptions the other member must be thymine; similarly for guanine and cytosine. The sequence of bases on a single chain, does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on one chain is given, then

guanine and cytosine. The sequence of bases on a single chain does not appear to be restricted in any way. However, if only specific pairs of bases can be formed, it follows that if the sequence of bases on

but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in time following, communications. We were not aware of the details of the results presented there when we devised our structure, which rests mainly though not entirely on published experimental data and stereo-chemical arguments.

It has not escaped our notice that the specific pairing we have

postulated immediately suggests a possible copying mechanism for the genetic material.

Full details of the structure, including the conditions assumed together with a set of co-ordinates for

Medical Research Council Unit for the Study of the Molecular Structure of Biological Systems, Cavendish Laboratory, Cambridge. April 2.

¹Pauling, L., and Corey, R. B. *Nature*, 171, 346 (1953); *Proc. U.S. Nat. Acad. Sci.*, 39, 84 (1953).

²Furberg, S., *Acta Chem. Scand.*, 6, 634 (1952).

³Chargaff, E., for references see Zamenhof, S., Braverman, G., and Chargaff, E., *Biochim. et Biophys. Acta*, 9402 (1952).

⁴Wyatt, G.R., *J. Gen. Physiol.*, 36 201 (1952).

⁵Asbury, W.T., *Symp. Soc. Exp. Biol.*, 1, *Nucleic Acid*, 66 (Camb. Univ. Press, 1947).

⁶Wilkins, M. H. F. and Randall, J. T. *Biochim. et Biophys. Acta*, 10, 102 (1953).

This figure is purely diagrammatic. The two ribbons symbolize the two phosphate-sugar chains, and the horizontal rods the pairs of bases holding the chains together. The vertical line marks the fibre axis.

The sequence of nitrogen bases encodes information in genes



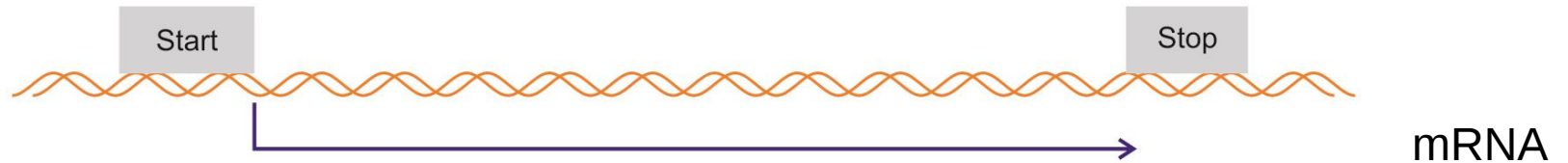
The human genome comprises:

- 46 chromosomes
- Just over 3 billion base pairs (haploid)
 - A adenine
 - G guanine
 - C cytosine
 - T thymine
- Approximately 23,000 protein coding genes

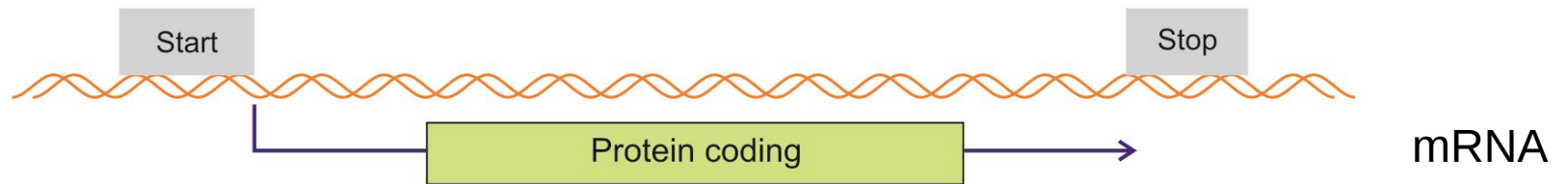
What is a gene?



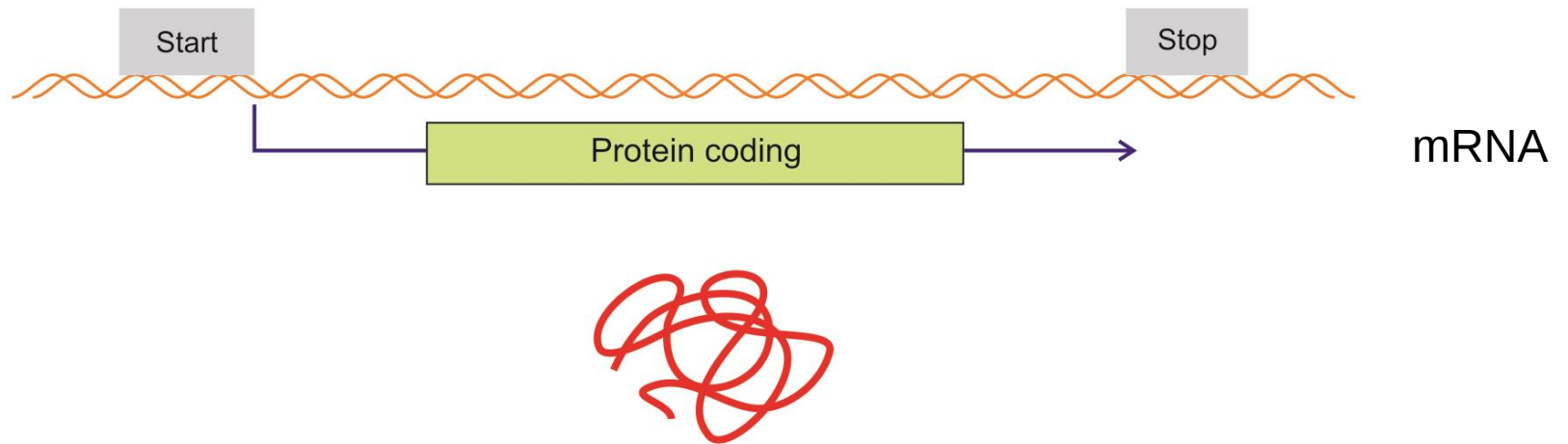
What is a gene?



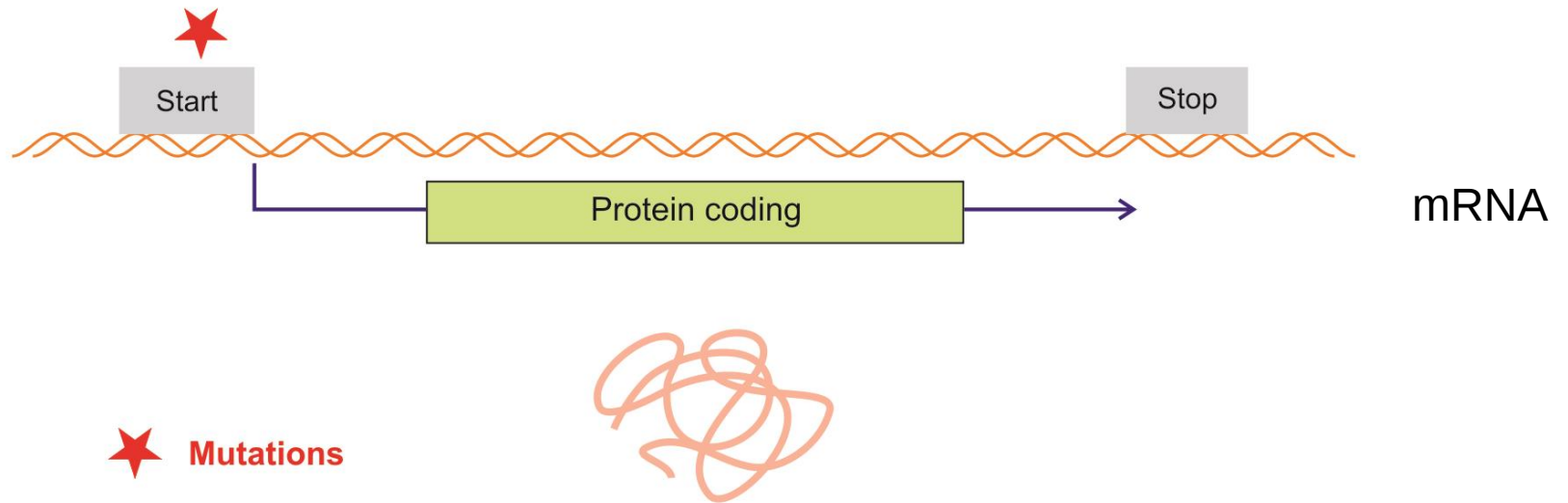
What is a gene?

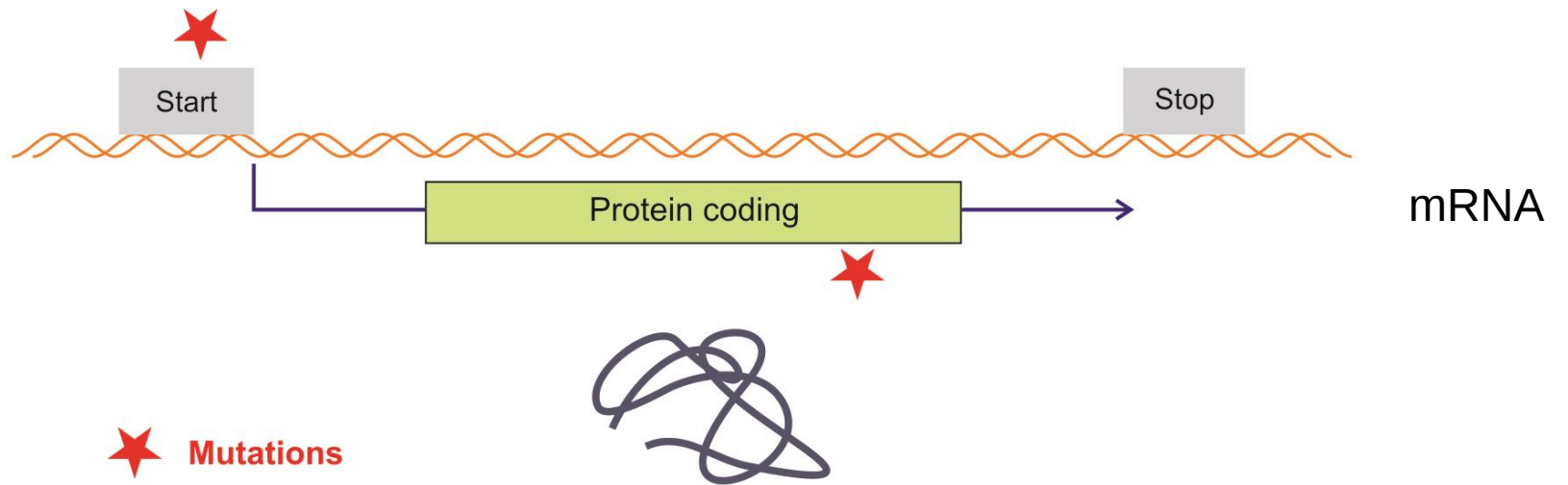


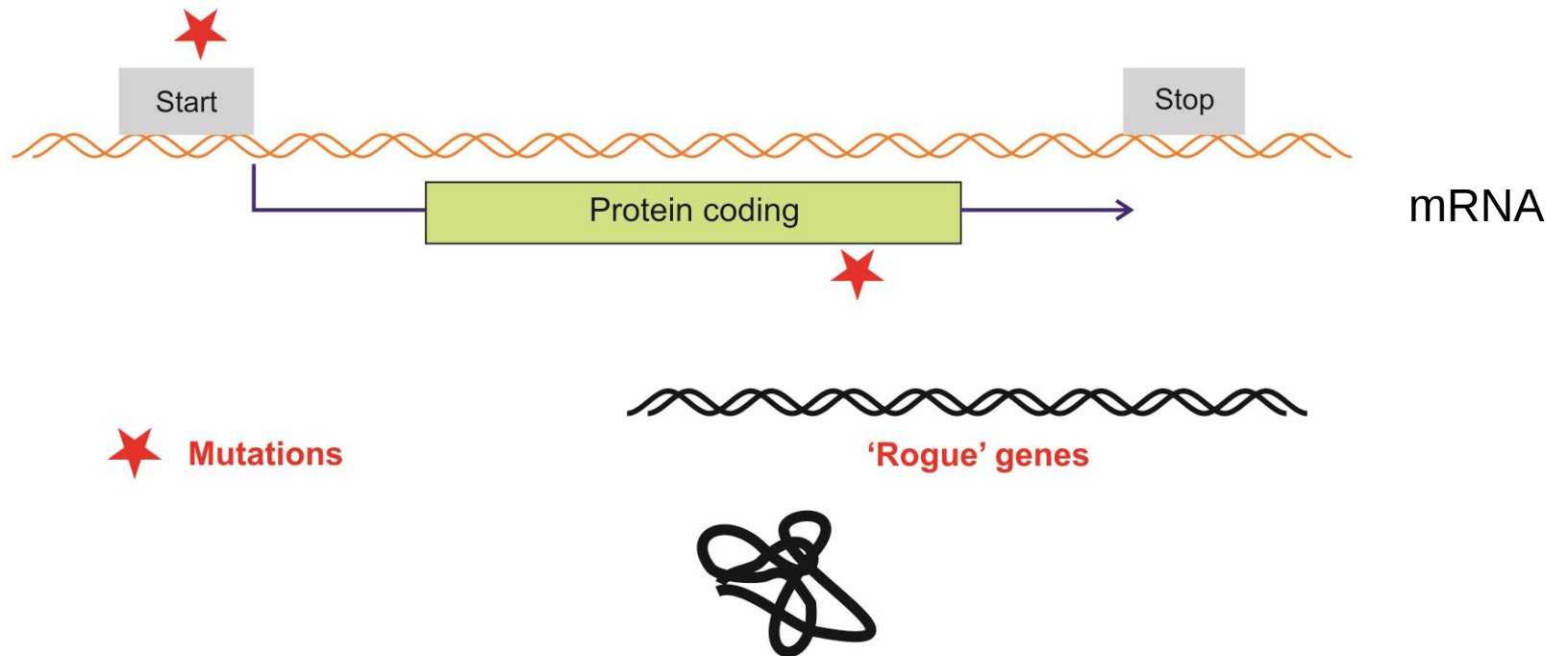
What is a gene?



What is a gene?







What is gene Therapy?

- A therapy that alters gene function?
 - Not really



- Using genes to treat diseases?
 - Now generally accepted that gene therapy may also include use of RNA (not only DNA)

univesitynetwork.edu.kg

Gene Therapy is a procedure that employs nucleic acids to achieve a therapeutic effect

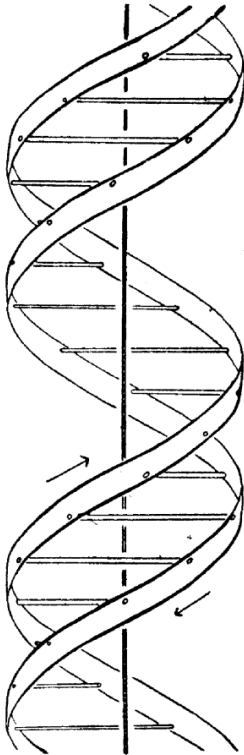
A rational approach to drug design

Gene Therapy Applications

- Used to correct gene expression (e.g. inherited diseases such as haemophilia)
- Induce killing of cells (e.g. cancer treatment)
- Suppress gene expression (e.g. treatment of virus infection)

So far not very useful for bacterial and parasitic infections

DNA is negatively charged



Delivery of nucleic acids remains the greatest challenge



Cell membranes provide a barrier to charged DNA/RNA –
they do not mix
... just like olive oil and balsamic vinegar

Types of carriers (vectors) for gene therapy

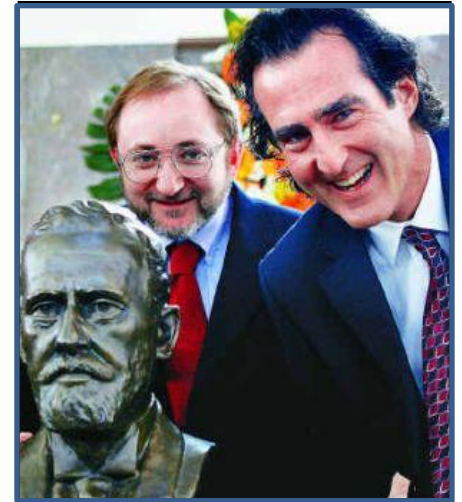
- Engineered viruses
- Chemically synthesised carriers
- Something in between
 - virus-like particles that may be modified chemically

Viruses are considerably more efficient than manmade vectors

Discovery of RNA interference has been important to the field of gene therapy



Nobel prize for Medicine or Physiology in 2006 awarded to Andrew Fire and Craig Mello for discovering the RNA interference pathway



Nobel Prize committee cited the following

RNAi provides

1. Regulation of protein synthesis
2. Protection from viral replication
3. Silencing of mobile genetic elements
4. Transcription modulation
- 5. Potential for therapy**

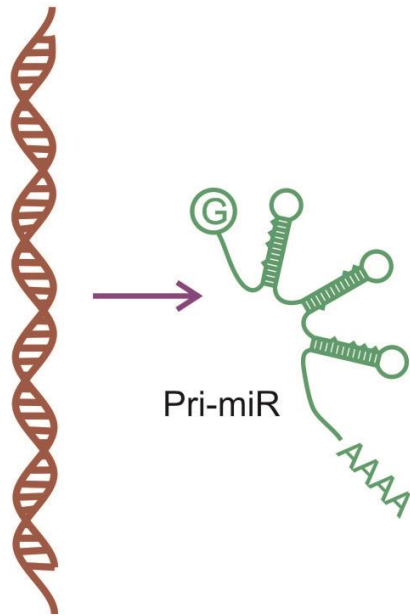
Inhibiting gene expression using RNA interference

- A small fraction of disease-associated genes are suitable targets for small drugs
- RNAi enables rationale drug design
- Powerful & specific gene silencing (antagonism only)
- Rapid and fairly easy to develop lead gene silencers
- Quickly reached a stage of advanced clinical trial

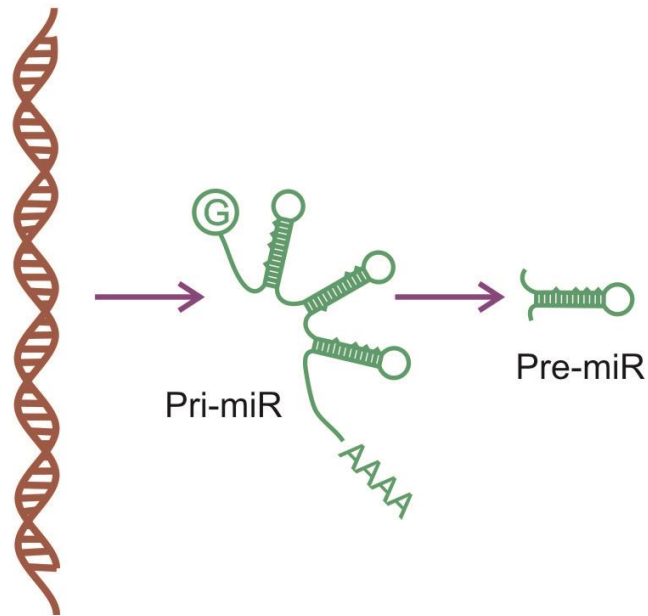
The RNAi pathway and how to design a gene silencer



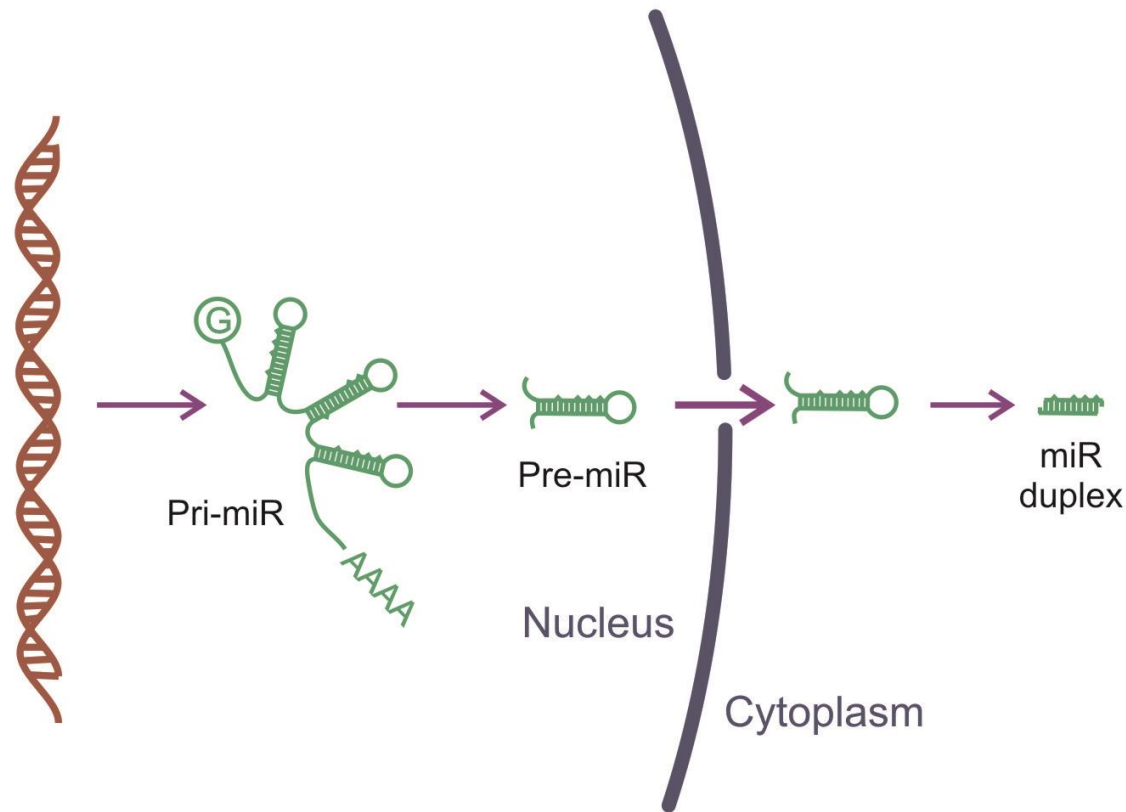
The RNAi pathway and how to design a gene silencer



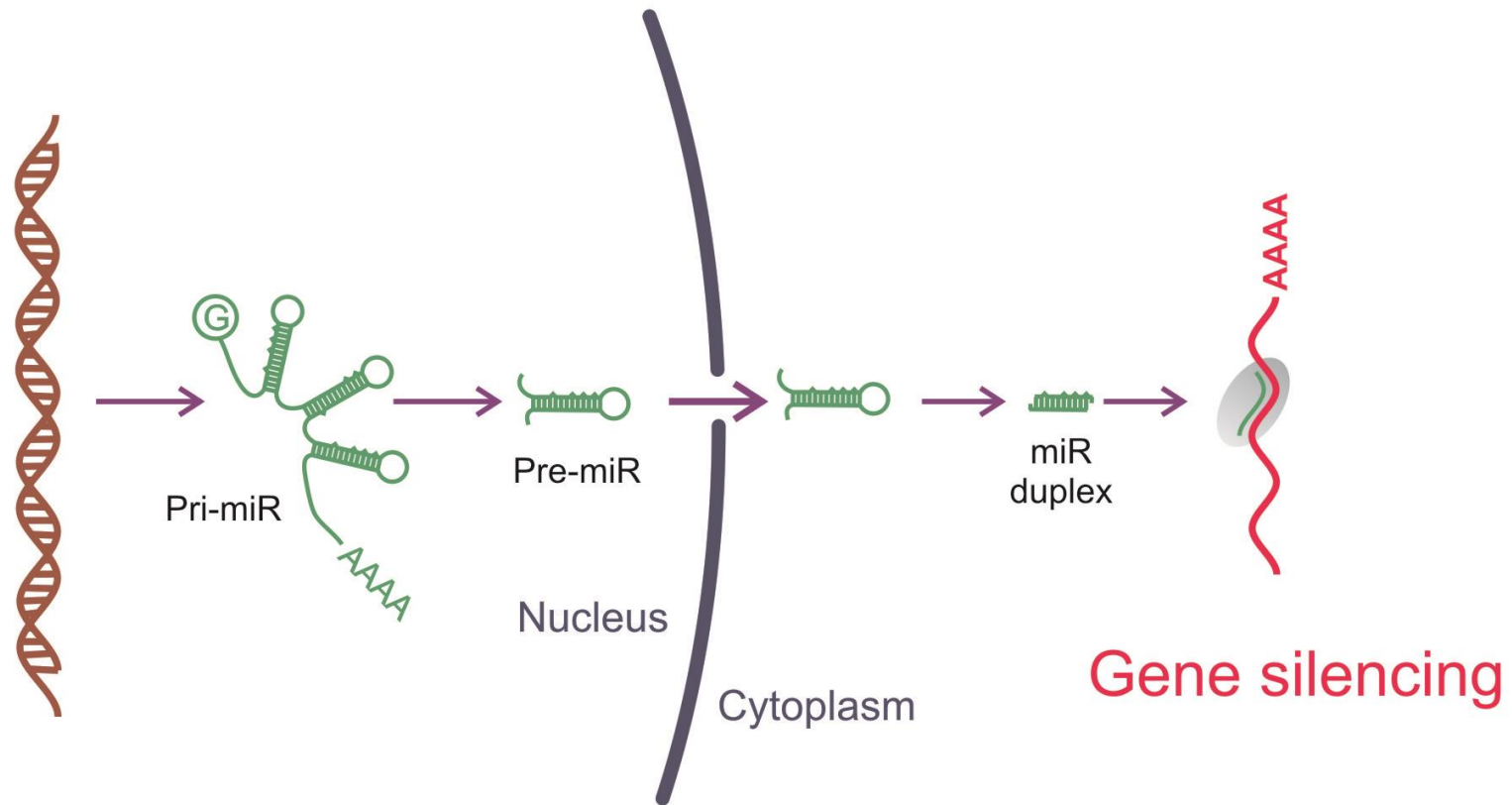
The RNAi pathway and how to design a gene silencer



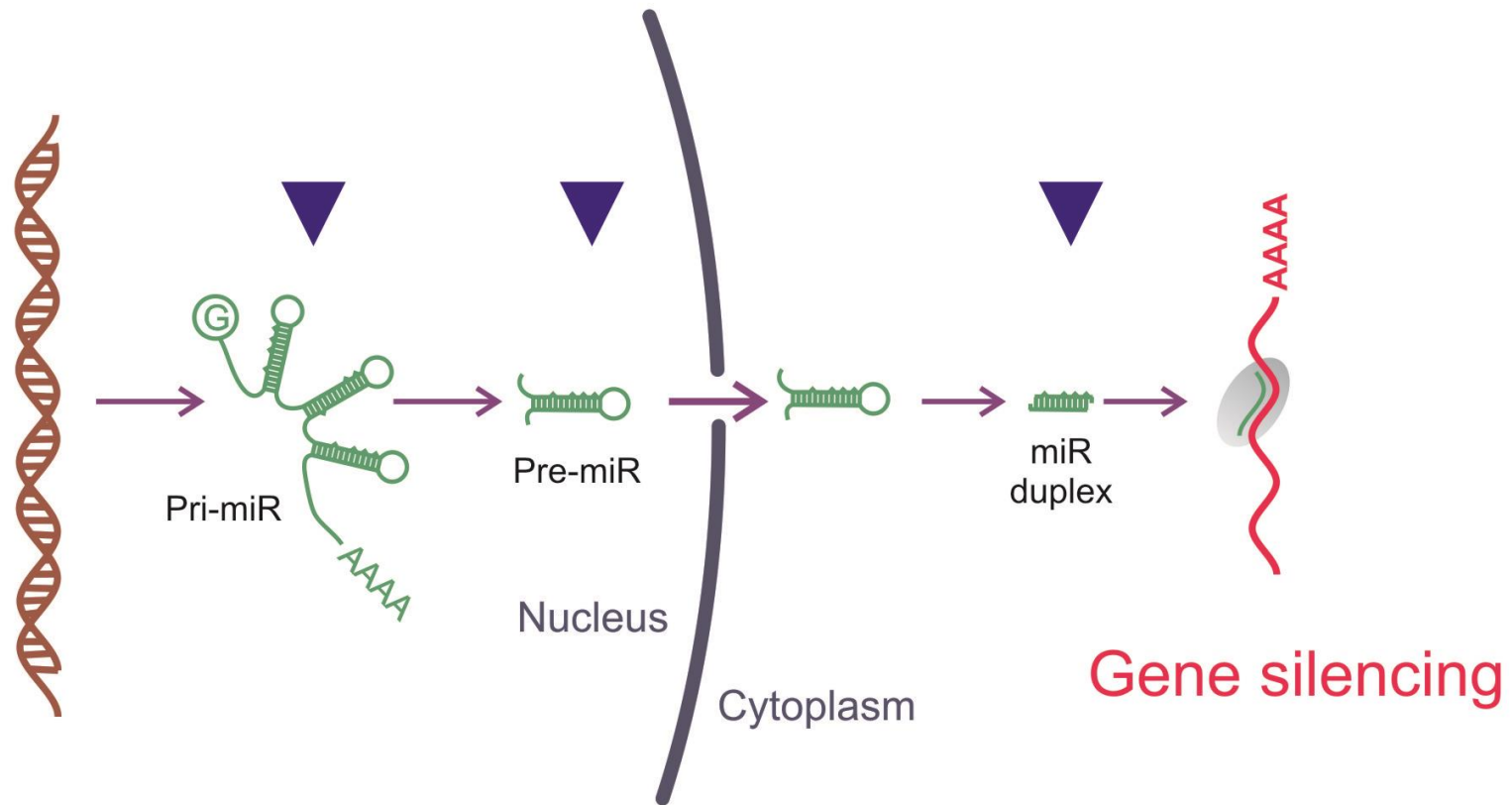
The RNAi pathway and how to design a gene silencer



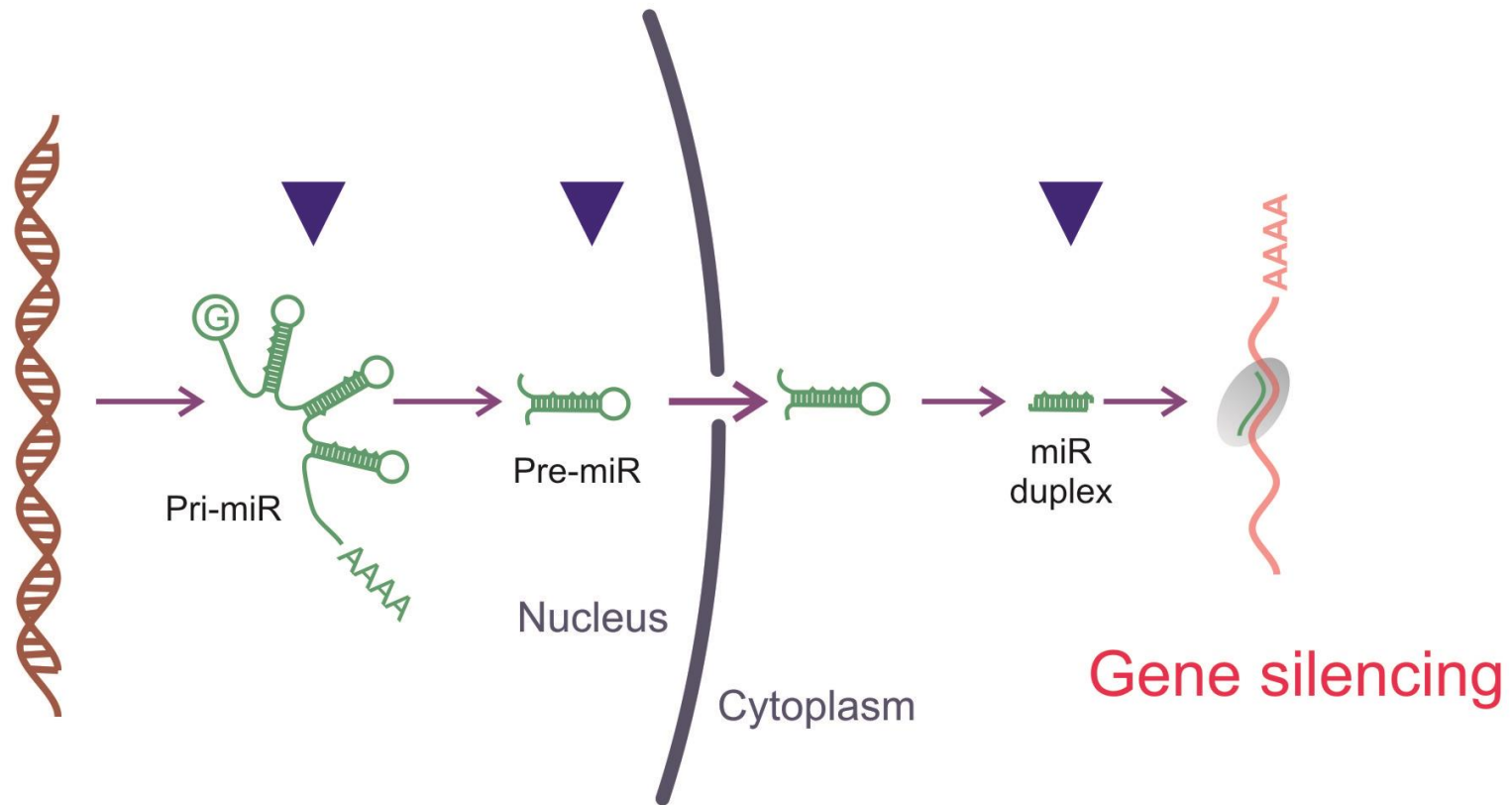
The RNAi pathway and how to design a gene silencer



The RNAi pathway and how to design a gene silencer

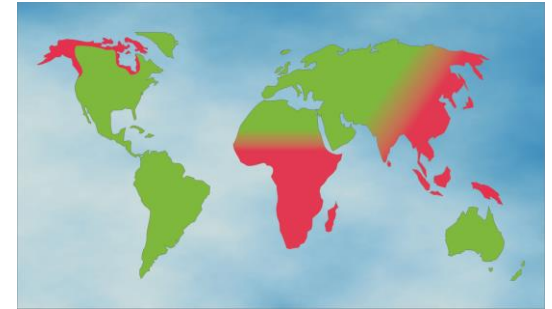


The RNAi pathway and how to design a gene silencer



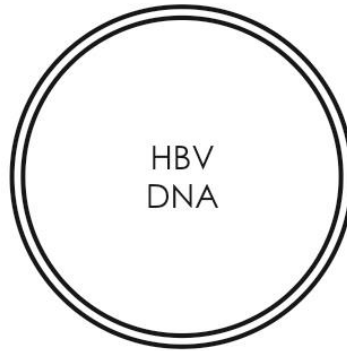
HBV infection

- 387 million chronic carriers in the world
- Childhood infection commonly associated with long term disease
- 25% of HBV carriers will develop liver cancer
- HCC has a very poor prognosis (annual incidence=annual mortality)
- Vaccine prevents HBV infection effectively

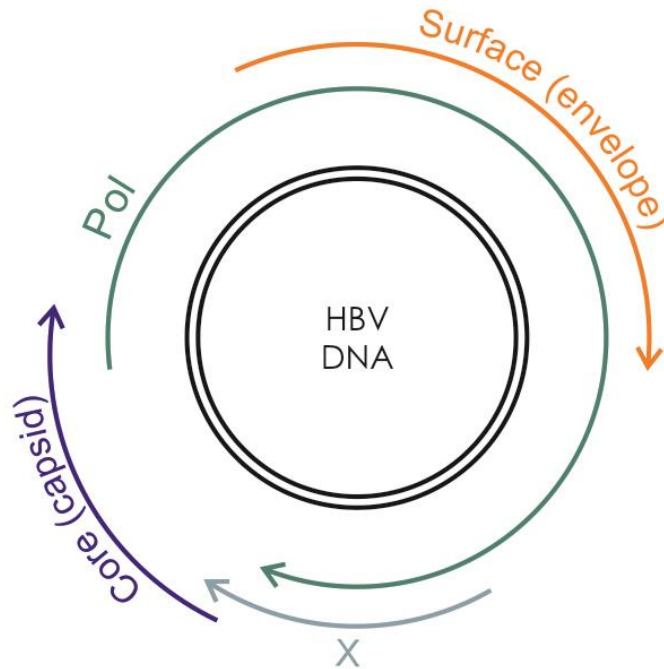


- RNAi-based approaches have shown promise: both expressed and synthetic RNAi-inducers

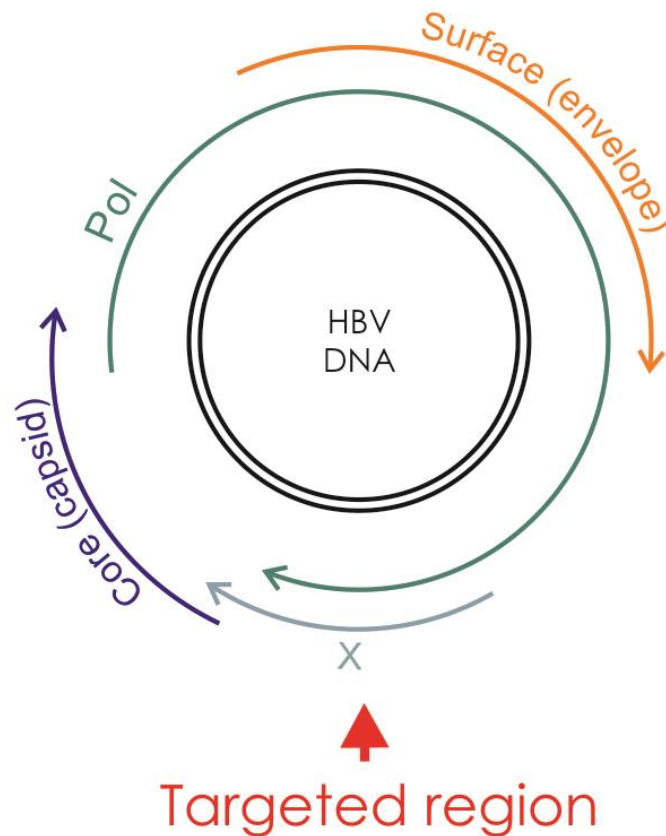
Anti HBV gene silencing strategy



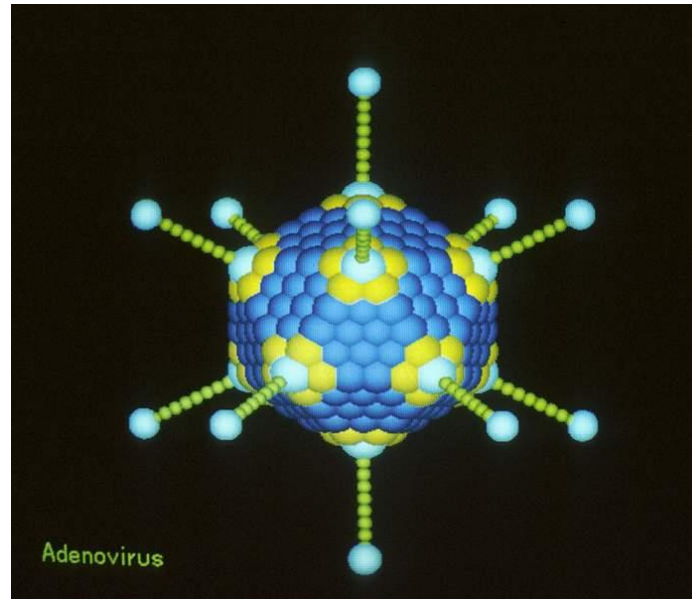
Anti HBV gene silencing strategy



Anti HBV gene silencing strategy



Engineering Adenoviruses to silence HBV



Engineering a virus to silence HBV



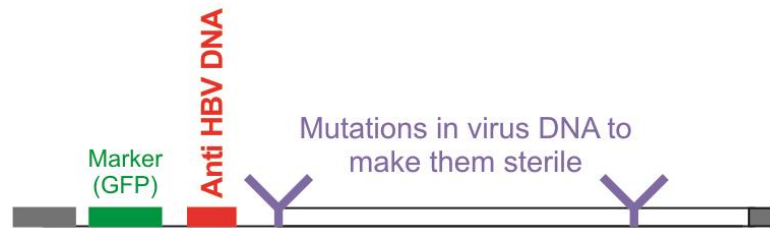
Engineering a virus to silence HBV



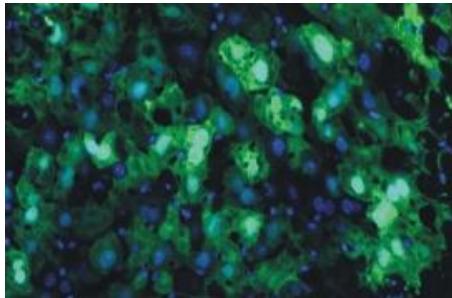
Engineering a virus to silence HBV



Engineering a virus to silence HBV



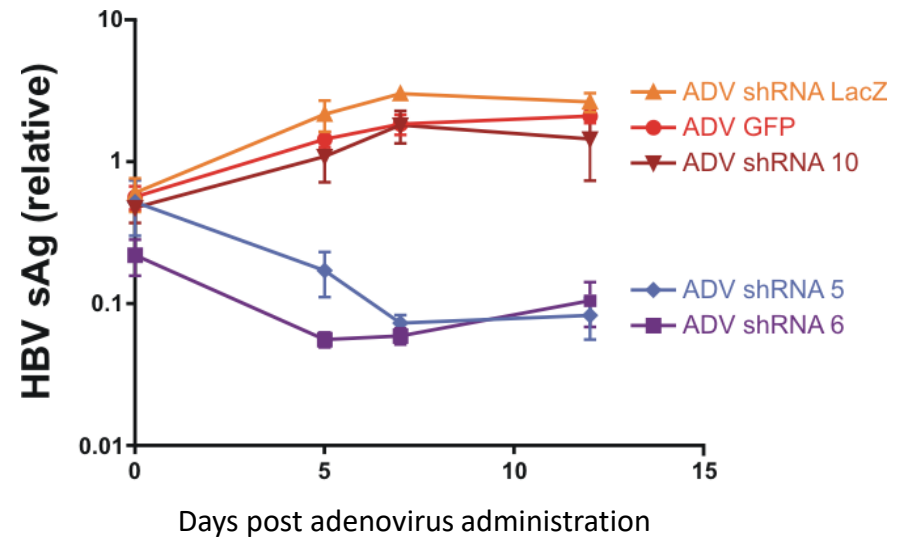
Using engineered adenoviruses to silence HBV



60-80% marker gene
delivery to hepatocytes

Serum HBsAg concentrations

HBV transgenic mice treated with recombinant adenoviruses



Gene Therapy for HBV Infection

- Proof of principle has been established
- Challenge is to convert a complex biological formulations into feasible therapies
- Convenient and safe large scale preparation of efficient vectors remains paramount

Defining the HBV delivery difficulties

- Delivery to enough liver cells
- Targeting the liver
- Sustained and complete 'knocking out' of the virus
- Complex drugs
 - side effects
 - immune responses
 - predictable distribution
 - good dose control
- Expense

Current Focus on Delivery of antiHBV sequences

- [illegible]

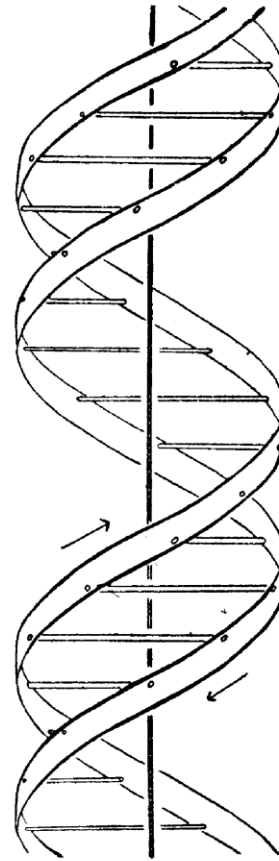
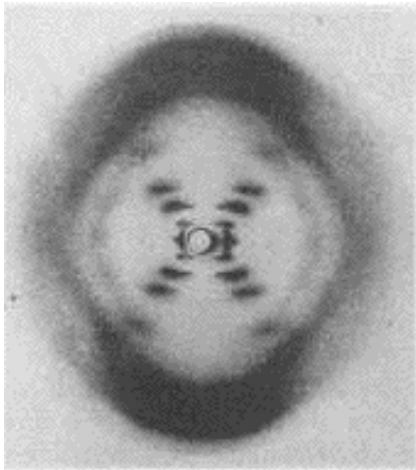
The Appeal of Gene Therapy

.... Science is knowing nature. This implies that there is a fixed set of facts that everyone wants to know. I suspect that artists are not striving for commonality, but rather, that the content as well as the form of their work is unique.

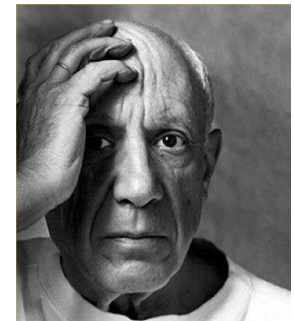
Thomas Cech, Nobel laureate in Chemistry in 1989



Discovery of the double helical nature of DNA



Picasso's Guernica



Pablo
Picasso

Gene Therapy: Prospects and Relevance

- Progress is rapid and the field has considerable momentum
- New technologies continuously being developed
- Successive waves of innovation will come and they will advance gene therapy
- Impressive developments in DNA sequencing technology will have an impact on the future applications of gene therapy

Large scale sequencing

NEWS FEATURE HUMAN GENOME AT TEN

NATURE | Vol 464 | April 2010

NATURE | Vol 464 | April 2010

HUMAN GENOME AT TEN NEWS FEATURE

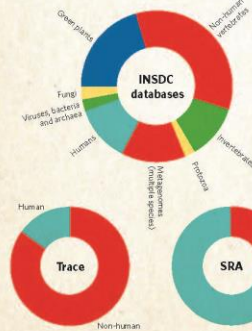


THE SEQUENCE EXPLOSION

At the time of the announcement of the first drafts of the human genome in 2000, there were 8 billion base pairs of sequence in the three main databases for finished sequence: GenBank, run by the US National Center for Biotechnology Information; the DNA Data Bank of Japan; and the European Molecular Biology Laboratory (EMBL) Nucleotide Sequence Database. The databases share their data regularly as part of the International Nucleotide Sequence Database Collaboration (INSDC). In the subsequent first post-genome decade, they have added another 270 billion bases to the collection of finished sequence, doubling the size of the database roughly every 18 months. But this number is dwarfed by the amount of raw sequence that has been created and stored by researchers around the world in the Trace archive and Sequence Read Archive (SRA). See Editorial, page 649, and human genome special at www.nature.com/humangenome

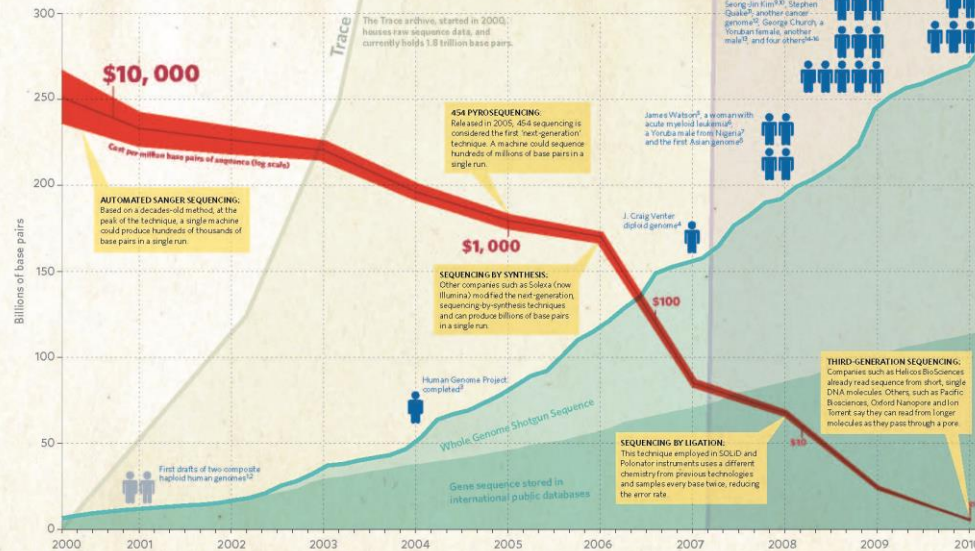
DNA SEQUENCES BY TAXONOMY

International Nucleotide Sequence Database Collaboration: The main repositories of finished sequence span a wide range of organisms, representing the many priorities of scientists worldwide.



Trace Archive: Developed to house the raw output of high-throughput sequencers built in the late 1990s, the trace archive spans a wide range of taxa.

Sequence Read Archive: Houses raw data from next-generation sequencing. Dominated by human sequence, including multiple coverage for more than 170 people.



HOW MANY HUMAN GENOMES?

The graphic shows all published, fully sequenced human genomes since 2000, including nine from the first quarter of 2010. Some are resequencing efforts on the same person and the list does not include unpublished completed genomes.

1. Venter, J. C. *et al.* *Science* **291**, 1304-1309 (2000)
2. International Human Genome Sequencing Consortium *Nature* **409**, 960-991 (2000)
3. International Human Genome Sequencing Consortium *Nature* **431**, 931-945 (2004)
4. Levy, S. *et al.* *PLoS Biol.* **5**, e24 (2007)
5. Wheeler, D. A. *et al.* *Nature* **432**, 872-876 (2006)
6. Lam, T. J. *et al.* *Nature* **456**, 66-72 (2008)
7. Bentley, D. R. *et al.* *Nature* **456**, 53-59 (2008)
8. Wang, J. *et al.* *Nature* **456**, 60-65 (2008)
9. Alts, S.-M. *et al.* *Genome Res.* **19**, 1622-1629 (2009)
10. Kim, J.-I. *et al.* *Nature* **460**, 1011-1015 (2009)
11. Puthi, D., Hoff, N. F., O'Quinn, S. R. *Nature Biotechnol.* **22**, 847-850 (2009)
12. Mardis, E. R. *et al.* *N. Engl. J. Med.* **301**, 1058-1066 (2009)
13. Drenth, R. *et al.* *Science* **322**, 78-81 (2009)
14. McKernan, K. J. *et al.* *Genome Res.* **19**, 1527-1548 (2009)
15. Pearson, E. D. *et al.* *Nature* **463**, 191-194 (2010)
16. Pearson, E. D. *et al.* *Nature* **463**, 184-190 (2010)
17. Clark, M. J. *et al.* *PLoS One* **5**, e100082 (2010)
18. Samuelsen, M. *et al.* *Nature* **463**, 757-762 (2010)
19. Schuster, S. C. *et al.* *Nature* **463**, 943-947 (2010)
20. Lepore, J. R. *et al.* *N. Engl. J. Med.* **362**, 1010-1016 (2010)
21. Road, J. C. *et al.* *Science* **327**, 1010-1016 (2010)

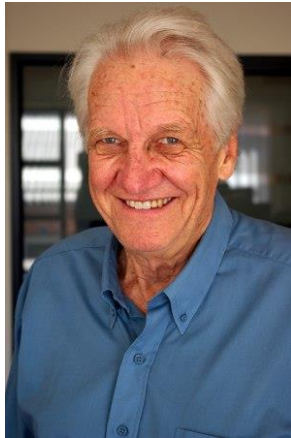
Page size by comparison

Gene Therapy: Prospects and Conclusions 2

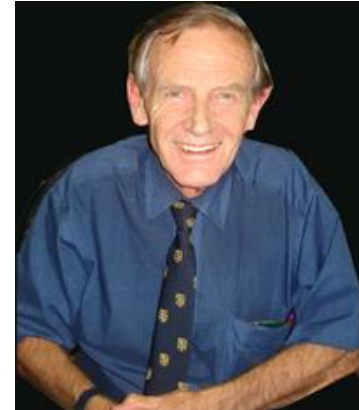
- Blockbuster drugs that will lose their patent exclusivity will be greater than the number of drugs that will be approved
- Gene therapy will enable rapid rationale drug design for many diseases
- Important that scientists in South Africa participate fully in development of these new technologies

Research partners and influential people

**Wyn
Fitschen**



Michael Kew

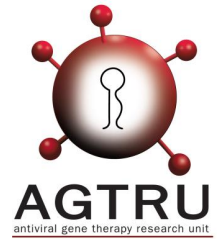


Many international and South African research collaborators

**Nicolas Ferry
Christian Bréchet
Bill Robinson
Pat Marion
Mark Feitelson
Piet Herdewijn
Joachim Engels**



AGTRU Team



**Marc
Weinberg**



**Abdullah
Ely**