PROJECT GENOMED

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Stated problem

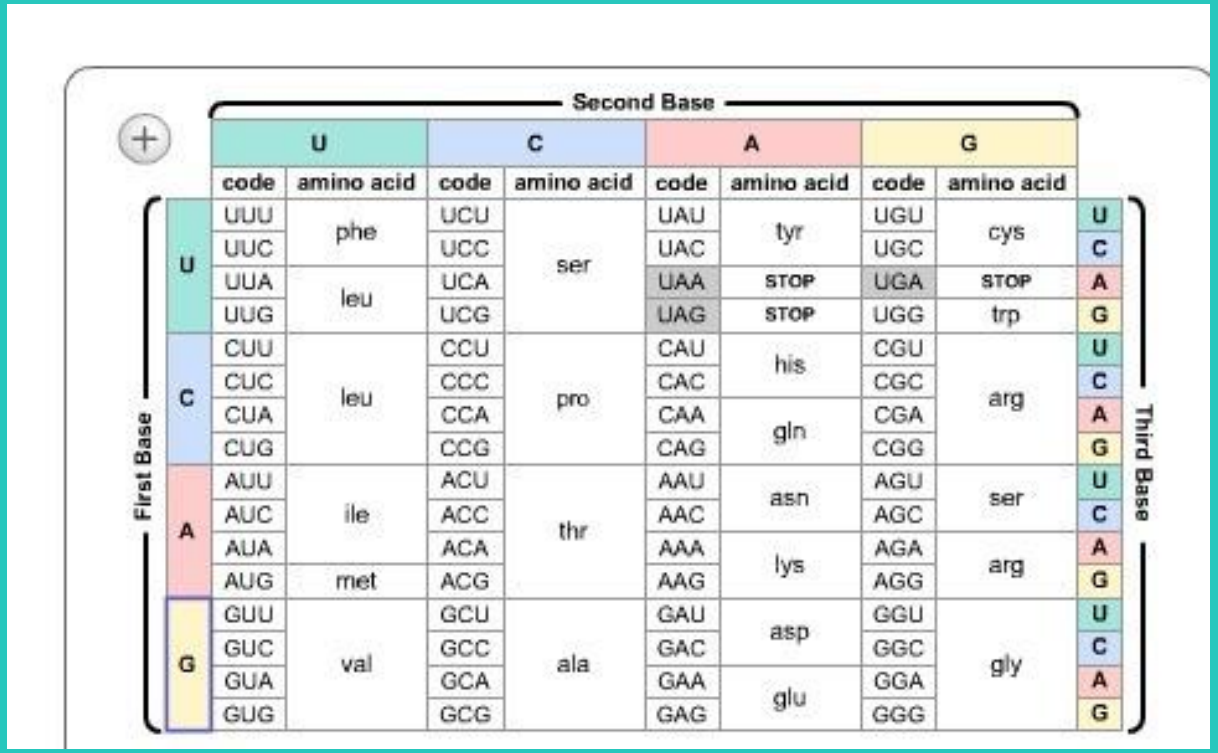
350 million people are affected by a genetic condition and 80% of them are caused by faulty genes.
Plus, in general those disabilities or diseases are diagnosed when we're observing the first symptoms.
In order to solve this problem we wanted to find a way to modify the genetic mistakes that are responsible for such conditions.
Modify the mutated genes was the main point we worked on, also as a system to detect the condition as early as possible.

Background

The DNA molecule is made of nucleotides that are the groupement of a deoxyribose and phosphoric acid with a nitrogenous base.
Nitrogenous bases are responsible of our genetic code, their order, their number are unique for each person and they're responsible of our genetic path and conditions when they're not in the right order on some genes.

The protein that is synthesized by the a certain portion of the DNA gives the role to the cell who's producing it.
For example : Red blood cells are controlled by the Hemoglobin protein.

Amino acids Chart



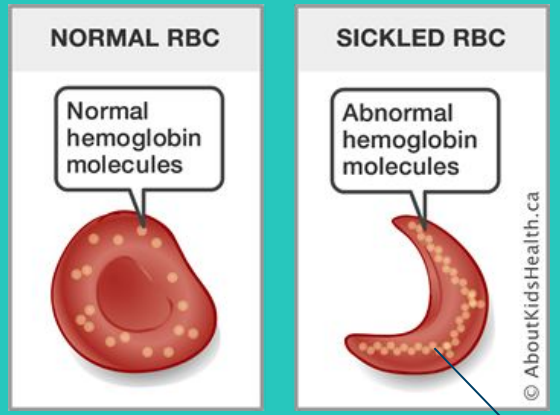
First Base	Second Base: U		Second Base: C		Second Base: A		Second Base: G		Third Base
	code	amino acid	code	amino acid	code	amino acid	code	amino acid	
U	UUU	phe	UCU	ser	UAU	tyr	UGU	cys	U
	UUC		UCC		UAC		UGC		C
	UUA	leu	UCA		UAA	STOP	UGA	STOP	A
	UUG		UCG		UAG	STOP	UGG	trp	G
C	CUU	leu	CCU	pro	CAU	his	CGU	arg	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	gln	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	ile	ACU	thr	AAU	asn	AGU	ser	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	lys	AGA	arg	A
	AUG	met	ACG		AAG		AGG		G
G	GUU	val	GCU	ala	GAU	asp	GGU	gly	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	glu	GGA		A
	GUG		GCG		GAG		GGG		G

We've learned that 3 nitrogenous bases are forming a codon.
And this codon codes an amino acid.
As the DNA degenerates, different codon codes the same amino acids and amino acids are synthesizing a particular protein giving their number and their order.
The synthesis stops when the enzymes are reading the "STOP" codon.

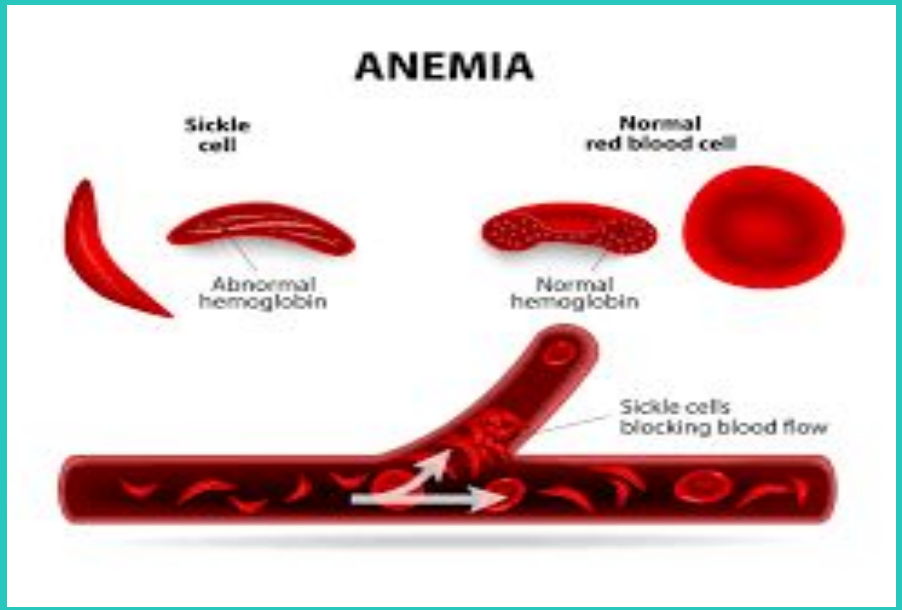
Important : We'll always need to check the amino acids sequence because of some codon that'll stay unchanged even if the order is quite different or if a nitrogenous base had been replaced.

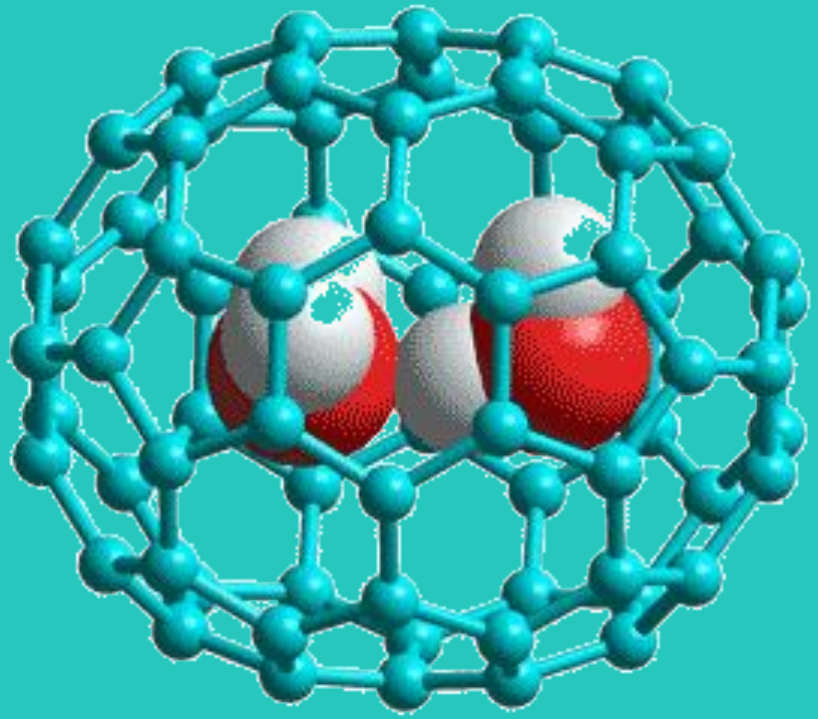
The sickle cell disorder is the most common blood condition in the world and has a huge impact on people.

The protein is mutated, so is the cell functioning and here, especially the form and the flexibility are altered due to fibers caused by the mutated gene.



fibers



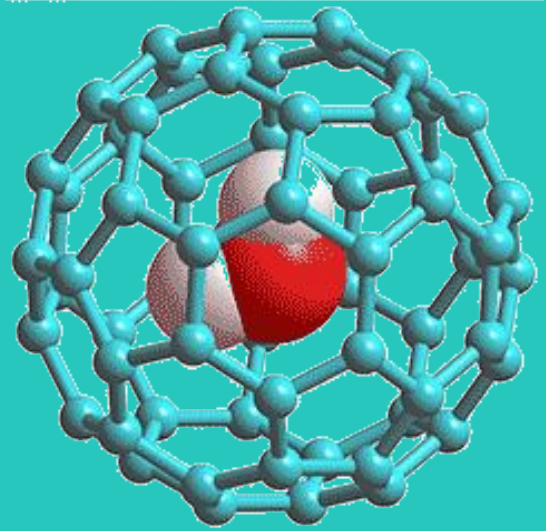


C70

Nanotechnology is a new sector in expansion which provides new uses and applications.

The fullerene C60 or C70 can be used as cage and can contain things as small as an atom !

C60



Hypothesis

“Can we find a way to analyse the patient DNA and find the genetic mutations that are causing genetic conditions by comparing the normal gene sequences with the patient genetic sequences?”

We will aim to imagine a health system and a way to replace the potential mistakes that are occuring in the DNA molecule.
We worked on the Sickle cell disease that is the most common inherited blood disorder in the United States.

Methods

1) Collect data on scientific websites and ask professionals on the sickle cell disease and the functioning of DNA and genes.

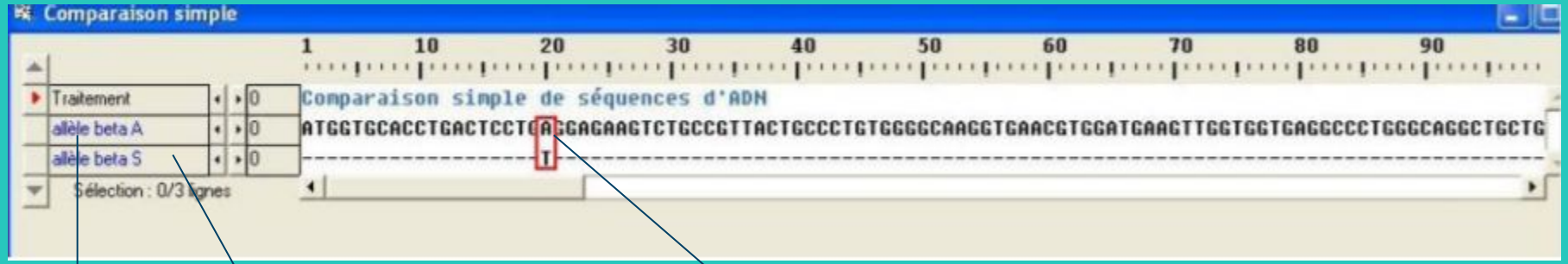
2) Ask professionals' opinion on the feasibility of our project.

3) Find the concerned gene sequences in a database (the normal version of the gene and the mutated one)

4) Compare the 2 sequences with Anagene. (the nitrogenous bases and the amino acids bases)

5) Make links with the results and improve our imaginated system and idea.

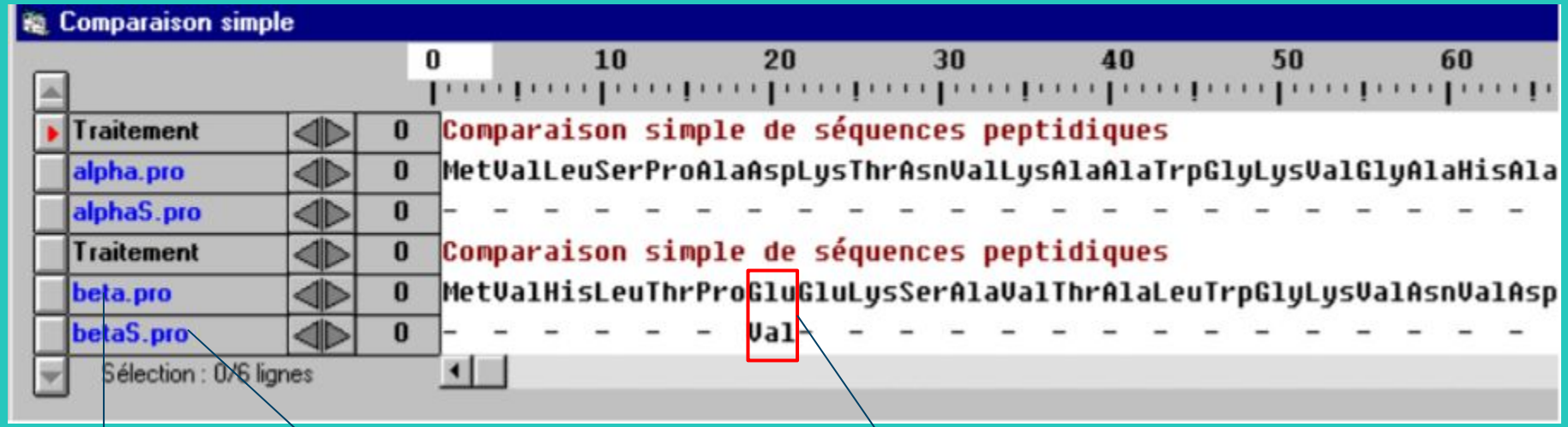
Firstly, we've compared the nitrogenous bases of the normal version of the sequence with its mutated version to seek the differences.
As the Anagene spotted the difference between the hemoglobin beta chains at the 20th position so we looked what impact it had on the amino acids. (which are coding the protein).



Normal hemoglobin gene

Hemoglobin gene version of a sick person

The difference spotted between the 2 nitrogenous sequences of the Hemoglobin gene



Normal hemoglobin gene

Hemoglobin gene version of a sick person

The difference spotted between the 2 amino acids sequences of the Hemoglobin gene

We can clearly see that the 20th amino acid isn't the same, the Glu has been replaced by a Val. A single modification of this amino acids sequence also modifies the protein.

Results

After this test of what our algorithm could do, we've found out that for the sickle cell disorder, there's just one nitrogenous base (at position 20) which has been replaced (Adenine has been replaced by Thymine).

Thymine replacing this Adenine isn't coding the same amino acid. We've also spotted a difference between the amino acid of the right version of the Hemoglobin gene and the patient amino acids sequence. (at position 20)
As it is the only difference between the 2 versions, we know that this nitrogenous base is at the origin of the cell sickle disorder by coding the wrong amino acid and creating a mutated protein.

Solution

- By using big data, we'll be able to track the genetic path of each person by analysing blood sample when they're just new born. This data will be transferred to a worldwide database and it will be treated by a medical algorithm.

- By using this algorithm, which is able to compare sequences like Anagene, identification of anomalies on the molecule will be easier and the program will figure out where the changes have to take place.

Through the algorithm, we can find out the right place(s) where the changes need to occur during the duplication phase. (it could be adding, removing or replacing the incorrect nitrogenous bases)

With the help of the fullerene and his flagella will be controlled by a microchip with the algorithm and we'll inject those with the right nitrogenous bases and they'll reach the selected place.

The integrated flagella will propulse the fullerene who's the cage containing the nitrogenous base inside the body.

After that, the patient will have to wait for a few DNA divisions to have the right genes version on his chromosomes.

Sources

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Nanotechnology conference

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