V.I.S SYSTEM (2)

DNA Sequencing and reading from eye photo

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Abstract – The V.I.S. system is an important discovery. it allows us in addition to the visualization of pathological organs, which we outlined in our subsequent publication Worlds Comp 2011, to view the chromosomes in a remarkable way and therefore to see the composition of DNA with an accuracy defying any method known today. We can get from the photo of the eye, the reading and the sequencing of the DNA.

1. Introduction

It's a discovery which allows us to visualize chromosomes and DNA from the photo of the eye, classically to see the DNA, it is necessary to use a whole log and complex process, namely several stages, to take a sample of the person with its consent, obtain chemically the insulation of chromosomes, and radiologically, to bombard them with X rays in order to get a print of nucleotides, all this in a time exceeding several days. Our method is unique, from the photo of the eye of a person we can have the image of its chromosomes and its specific DNA in a time not exceeding one hour.

I put kindly to your attention the images obtained by the V.I.S system and the progress, you can judge for yourself the quality of these images which are unique in the world.

2. Equipements and Methods

2.1 Equipment

Equipment is very simple; it consists of a camera and computer,

2.1Methods

- Photo of the eye.
- Front view photo of the eye
- Camera without flash
- Environment slightly enlightened without important source of light
- The "*vitreous imagery system*" makes it possible to visualize the images of the patient's organs in the vitreous humor , these images are laid out in bulk, with sometimes the repetition more than one organ,same organ with different view.
- We resize each image of organs obtained in the humor vitreous in order to isolate it. we isolate an organ visualized by the technique of V.I.S system and we use use the second technique wich involves the display the chromosomes in the organ.

2.2 Theory & explanation

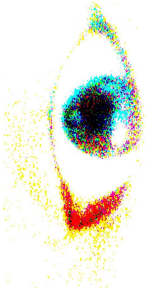
The cell is the Small functional unit alive , the human being amounts to approximally 100 billons of cells, they are grouped indifferrent tissues and organs , these cells are grouped into differenttissues and organs and are different from one tissue to another and from one organ to another, the cells consists of a cytoplasm and anucleus chromosomes that composed of a long molecules called DNA or desoxyribonucleic acid.
The DNA is in the form of strands twisted arond each other forming a double helix, two srands are formed of nucleotides consisting of a sugar, a phosphorus and nitrogen bases , these nitrogenous bases are four : A : adenine T : thymine C : cytosine G : guanine , these two strands of DNA are linked to each other through these base pairs , adenine binds to thymine and cytosine with guanine , the order of the arrangement of these bases determines séquences and a change in sequences can entail diseases.

In practice, to have the DNA of an individual, we make a sample of blood of saliva or other; after a sample of blood, we proceed to several stages to have the DNA, the blood is spin-dried, we collect white blood cells or leucocytes which contain the DNA. The second phase consists in releasing the DNA by adding reagent and by proceeding to a wash; then comes the purification and so we realize a precipitation. The images obtained by the V.I.S. system are images < < data bank > >, as we explained it in our previous publication: it means that they contain all information appropriate for this organ; these images contain those of the chromosomes. For

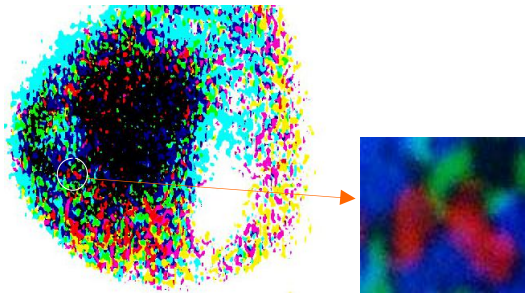
that purpose, we use a second technique which consists of the display of chromosomes. The DNA or the deoxyribonucleic acid containing all the information, thus all the previously explained stages by the current techniques are not acceptable for the V.I.S. system because it gives directly the image of the chromosome and by increase the double helix DNA.

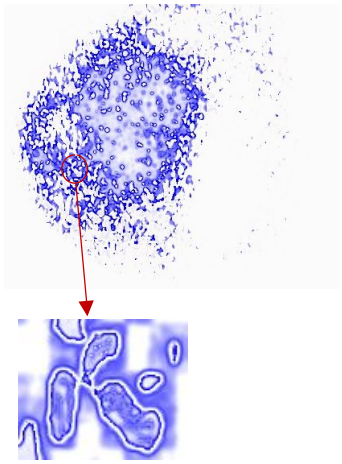
2.3 Processus et technique: V.I.S. system serves to display organs at the level of the vitreous humor.S. Système pour visualiser les organes au niveau de l'humeur vitrée

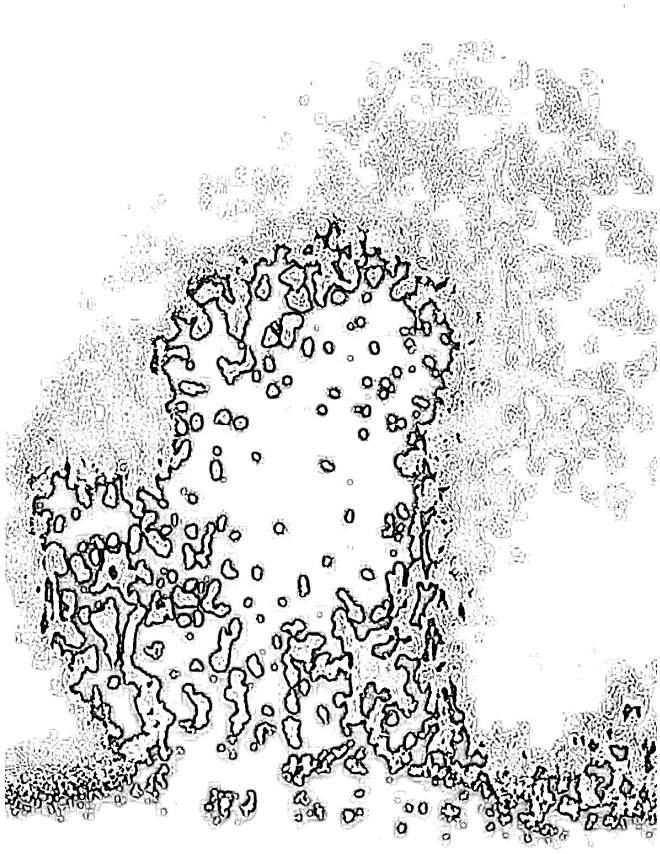
Img 1



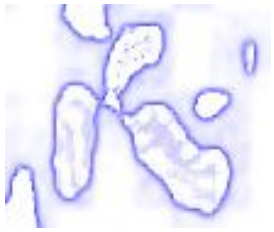
Img 1 a



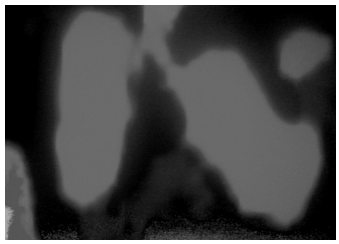




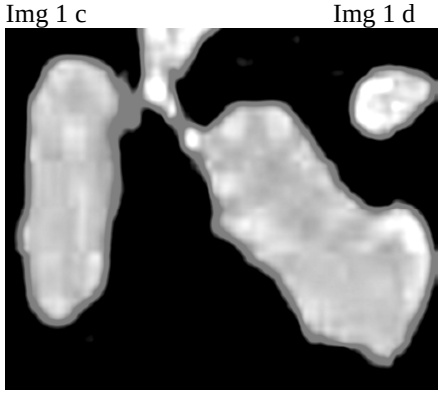
Img 1 b



Img 1 c

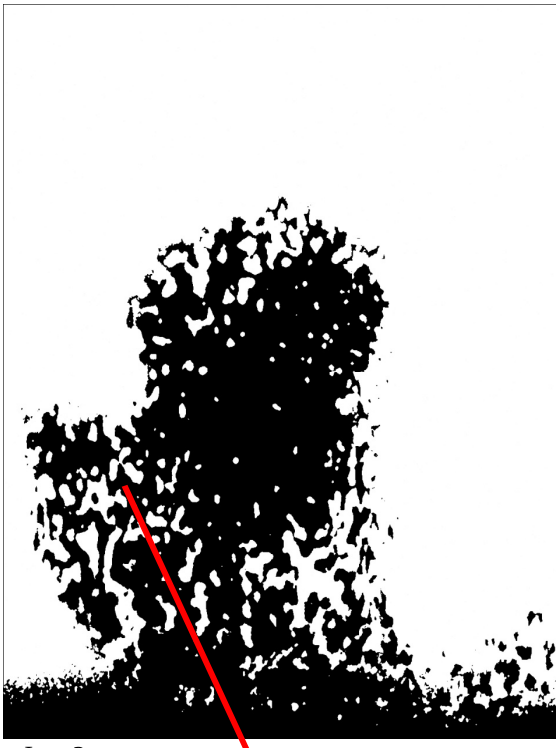


Img 1 d



Img 1 e

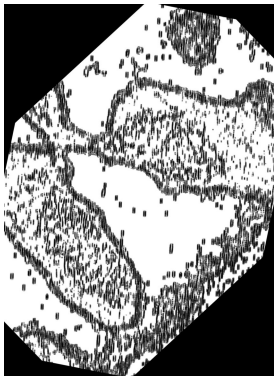
These images were already presented in my first publication<<vitreous imaging system a new method for medical diagnostic >> the images, that will appear, will display chromosomes DNA



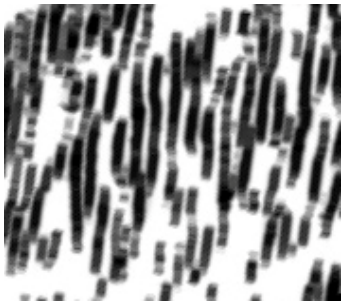
Img 2

Img 3

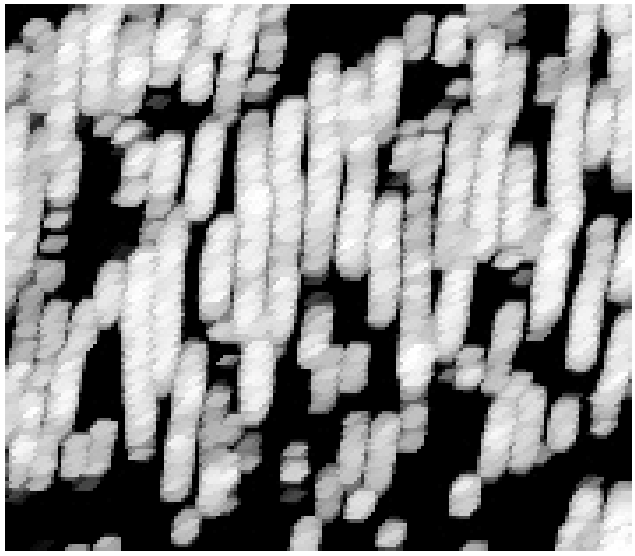
In the vitreous humor, we have the map of organs affected by pathologies. We select an organ to be studied in the glazed humor and we proceed to the second technique which consists of the display (visualization) of the chromosomes of this organ.



Img 4



img 5

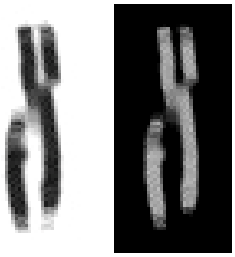


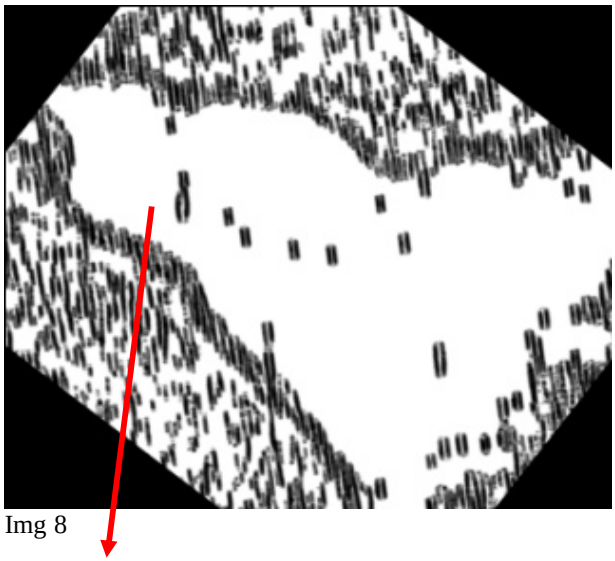
Img 6

Img 7

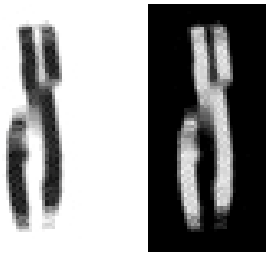
You will notice that we visualize display the chromosomes which are in the same direction, this will allow us to decrease considerably the number of chromosomes to be able to isolate them and study them easily.

We clearly see appearing chromosomes, we isolate a chromosome and we enlarge the image.



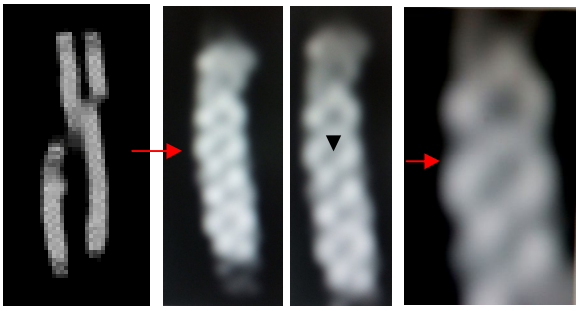


Img 8



Img 9 img 9

The chromosome that we study is the chromosome X , ewpanding the image we , we can see very clearly the double helix of DNA.



Img 9 img 10 img 11 img 12

We clearly see appearing chromosomes, we isolate a chromosome and we enlarge the image.

The double helix of DNA appears clearly in the form of two rolled up stalks the one on the other one. The comparison with a comparative plan is identical and remarkable; I open a bracket here by letting know that there is no image at present showing to us exactly the double helix of DNA**.**

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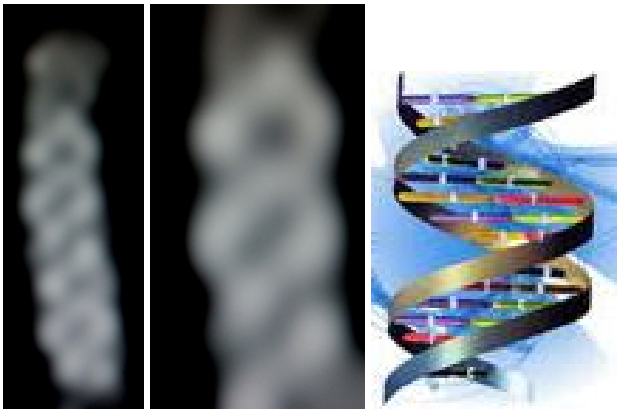

Img 11 img 12 img 13

Img 1 : photo of the eye
Img1a :vizualisations of pathological organ in humor vitreous
Img 1 b : organs visibles in vitreous humor
Img 1c et Img 1d : lung
Img 1 e : elargment
Img 2 : vitreous humor
Img 3 : lung
Img 4 : rotation of image and vizualisation to chromosomes
Img 5 : amas de chromosomes
Img 6 : chromosomes clusters
Img 7 : visualisation of chromosomes
Img 8 : rotation and ellargment
Img 9 : ellargment (visualisation of chromosome X)
Img 10 : strand of chromosome showing the double helix
img11 :ellargment of strand of chromosome
img 12 : visualisation of the double helix of chromosome
img 13 : diagram showing the double helix of DNA

The technique of visualization of DNA by the V.I.S.system is little expensive, simple and much faster than traditional techniques. After extraction, the genomic DNA is cut by sonication in fragments from 50 to 200 kb then cloned in a vector adapted as the artificial bacterial chromosomes, or B.A.C.

The number of clones has to allow a cover from 5 to 10 times the total length of the studied genome. The overlapping and the organization of clones are realized either by hybridization of specific probes, or by analysis of the profiles of limitation, or more frequently by an organization after sequencing and hybridization of the extremities of the B.A.C... After the organization of clones, they are split up and sequenced individually, then assembled by bioIT alignment

. The advantages of this method are a bigger ease of assembly of fragments thanks to the overlapping of B.A.C ., the possibility of comparing fragments with the available data

banks, and the possibility of sharing the work of sequencing between several laboratories, each being in charge of a chromosomal region.

the major drawback is the difficulty to clone fragments containing repeated sequences very common in some genomes, which makes difficult the final bioIT analysis .Contrary t the VIS system, which consists of applying the technique of DNA visualization in the first place, and making magnifications in order to be able to see the double helix, chromosomes are observed in real images. (as we, have explained in our previous publication in Worldcomp 2011, the difference between a real image and an approximate one. The real image contains an infinite number of images themselves (Bank data) , unlike the, approximate image that contains only a single one.

Les avantages de cette méthode sont une plus grande facilité

2.4 Nucleotides

The DNA double helix consists of a set of elements containing the genetic information, called nucleotides. A nucleotide is a complex molecular assembly and includes a sugar linked to a phosphate group and a nitrogenous base. This base can be cytosine, guanine, and thymine, and adenine, adenine pairs with thymine and cytosine with guanine. Nucleotides thus related form a kind of scale rolled up in double helix. DNA molécule consists of 13 pairs of nucléotides**.**

2.5 Sequencage

2.5.1 Méthode de Sanger

The principle of this method is to initiate the polymerization of DNA using a small oligonucleotide (primer) complementary to a portion of the DNA fragment to be sequenced. The elongation of the primer is made by the Klenov fragment (DNA polymerase I lacking exonuclease activity of 5 '---> 3') and now by thermostable DNA polymerases, those used for PCR. The four deoxyribonucleotides (dATP, dCTP, dGTP, dTTP) are added, as well as a weak concentration of one of the four dideoxynucleotides (ddATP, ddCTP, or ddTTP). These didesoxynucléotides act as <<poisons >> chain terminators, once incorporated into the new synthesized stand, they prevent further elongation. This termination is specifically at the nucleotides corresponding to didesoxyribonucleotide incorporated into the reaction. For the complete sequencing of the same DNA fragment, this reaction is repeated four times in parallel, with four different didesoxyribonucleotides. For example ,in the reaction where we added ddGTP , the synthesis stops at G . The reactional mixture contains at the same time dGTP and a little ddGTP . The ending is statistically depending on whether the DNA polymerase uses one or more of these nucleotides. The result is a mixture of DNA fragments of increasing sizes, which all end in one of G in the sequence. These fragments are then separated by polyacrylamide gel electrophoresis, thus, making it possible to pinpoint the location of the Gs in the sequence.
The detection of fragments so synthetized is made by incorporating a tracer into the synthetized DNA**.** Initially**,** this tracer was radioactive; today, we use fluorescent, attached tracers either in the oligonucléotide, or in the didésoxyribonucléotide.

2.5.2 Méthode de Maxam et Gilbert

Specifics. The single-stranded DNA are subject to reactions. This method is based on a chemical degradation of DNA and uses the different reactivities of the four bases A, T, G and C to make selective cuts. By reconstructing the sequence of cuts, one can trace the sequence of nucleotides of the corresponding DNA . We can decompose the chemical sequencing into successive six stages.
Marking : the ends of two strands of DNA to be sequenced are marked by a radioactive tracer (32 p). This reaction is generally done using radioactive ATP and polynucleotide kinase.
Isolation of DNA fragment to be sequenced: it is separated by electrophoresis on a polyacrylamide gel. The DNA fragment is cut from the gel and recovered by diffusion.

- **Séparation of strands** : : the two strands of each DNA fragment are separated by thermal denaturation, and then purified by another electrophoresis

Chimical changes : specific of different basic types. Walter Gilbert has developed several types of specific reactions, performed in parallel on a fraction of each labeled DNA strand, for example, a reaction for G (alkylation by the sulphate of dyméthyle), a reaction for G and A (dépurification), a reaction for the C , as well as a reaction for the C and T (alkaline hydrolysis). These different reactions are carried out under very arranged conditions , so that on average each DNA molecule carries only zero or one modification.

- **Cut** : After these reactions, the DNA is cleaved at the modification by reaction with a base, piperidine.

- **Analysis:** for each fragment, the products of different reactions are separated by electrophoresis under denaturing conditions and analyzed to reconstruct the sequence of DNA. This analysis is similar to that which is carried out for the Sanger's method.

2.5.3 Pyroséquencing ultra broadband

suitable for sequencing <<novo>> and <<re sequencing>>

2.6.4 Séquençage par re synthèse
Utilisant un terminateur réversible adapté au re séquençage

1.1.5 Séquençing by hybridization / ligation

Adapted to the re sequencing, the detection of the SNP and the study of the organization of genomes.

2.6 V.I.S and technical of visualization of the DNA

The V.I.S. system allows us a direct visualization of chromosomes in real images, a real image , as we explained it previously, is an image < < data bank > > which means that it contains all the information relative to this image at the moment T when this image was taken.
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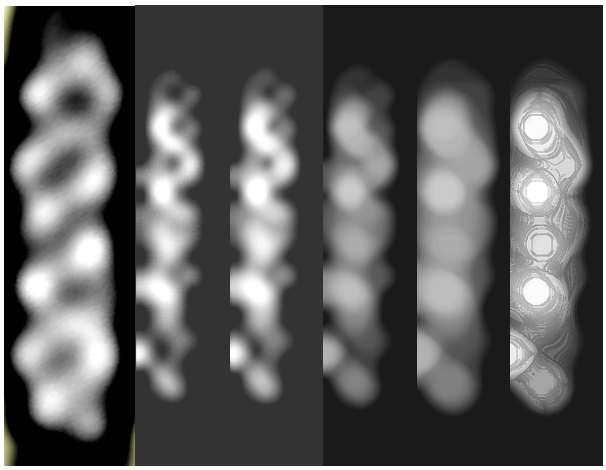
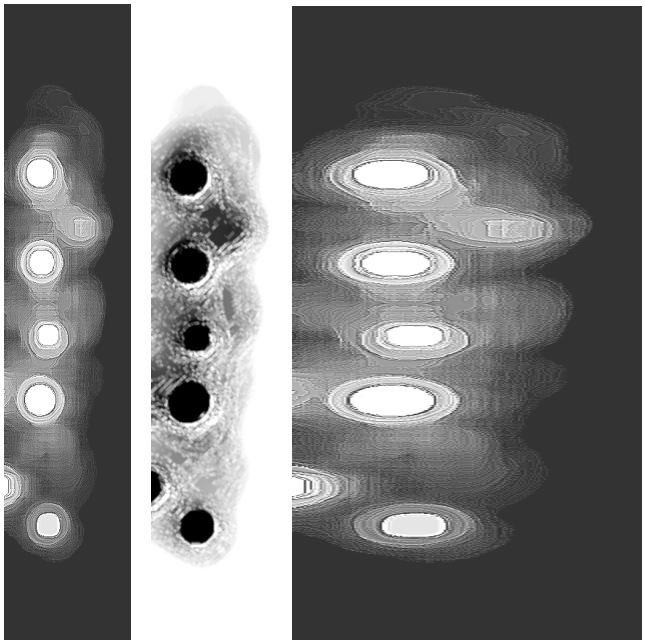


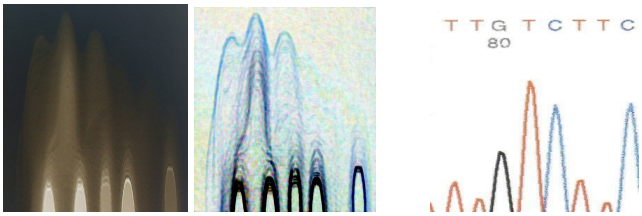
Img 14 img 15 img 16 img 17 img 18 img 19



Img 20 img 21 img 22

We visualize nucléotides at the level of the stalk of DNA; every nitrogenous base has a precise position with regard to the others, and every nitrogeneous base has a curve different from the others; we can read the image by widening it on the horizontal plan and by shrinking it on the vertical plan .We obtains the technical sequencing by the V.I.S. system. We can easily read it, with, in front of every nitrogenous base, its graphic curve the explanation of which is given by these images.

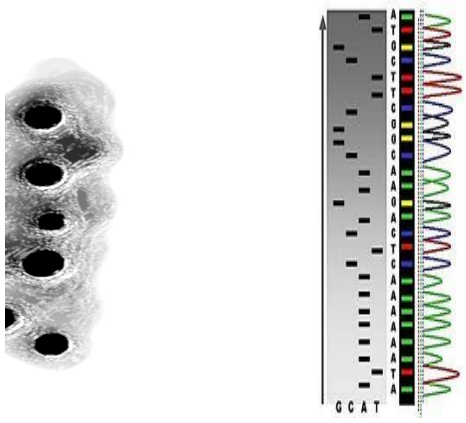
Img14 :strand of chromosome helix DNA
img15 : vizualisation to the double helix of DNA
img 16, img 17 ; img 18 ; img 19 : visualization of nucleotides
img20, img 22 : nucléotides reading
img 22 : image V.I.S sequencing of DNA



Img 23 img 24 img 25

Img 23 , img 24 : each nucleobase is a graphical wave

Img 25 : graphical of comparatif of sequencing DNA



C T C A C G A comparatif

The reading by VIS syteme is :

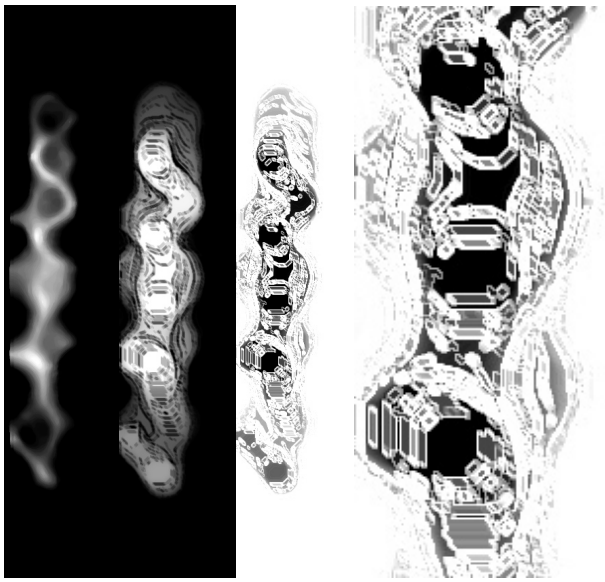
C : cytosine T : thymine C : cytosine A : adenine C : cytosine G : guanine A : adenine

2.8 Images of nucléotides by V.I.S

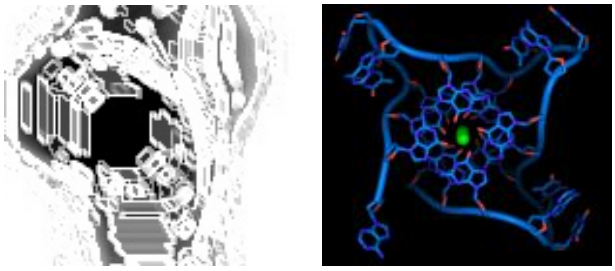
The imagery obtained by the nucleotide V.I.S. system is unique, where the current science provides only theories,

diagrams and graphs to illustrate these theories .The V.I.S .system gives us real images of the infinitely small, and these images are not images of synthetic data computer, then by mathematical algorithm, these images are real ones .

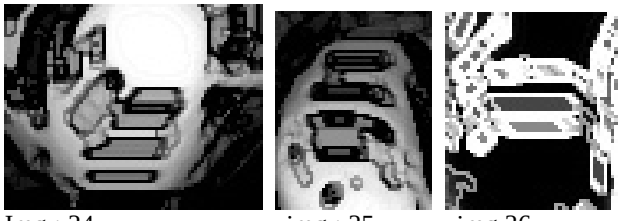
From the image of chromosome obtained by the V.I.S .system technical, we can go farther by providing images with real details of the structure of the nucleotide as it has never been given.



Img 26. 27. 28. 29.



Img 32 img 33: comparative



Img : 34 img : 35 img 36

Img: 26, 27, 28, 29, 30, vizualisation of nucleotides in the double helix of DNA.
Img 32: internal view of the nucleotide
Img 33: diagram of nucleotide
Img 34: internal view of nucleotide
Img 35: other internal view of nucleotide
Img 36 : view of nucleobase

The images of the V.I.S. system show with high accuracy the external and internal configuration of a nucleotide, the image of sugars, phosphates and nitrogenous bases.

3 Conclusion

This publication is the continuity of the first one which is a new technique of medical and diagnostic imaging. The first technique of the V.I.S. system gives us the images of the pathological organs visible in the vitreous humor of the eye; on the other hand this second publication gives us the imaging of the double helix of DNA as well as the reading of the genetic coding always from the photo of the eye.
It is a new of reading DNA without having recourse to a taking or too long, expensive processes of reading, with a percentage of 99 % success. V.I.S. system gives us an easy, quick, not very expensive reading with a rate of 100 % success.
There will be much change in terms of ethics, for the present moment a legal authorization is needed to proceed to a taking . But with this new process and this new technique, the examiner will need only a photo to read DNA , because for each picture of a person, we can get his DNA.