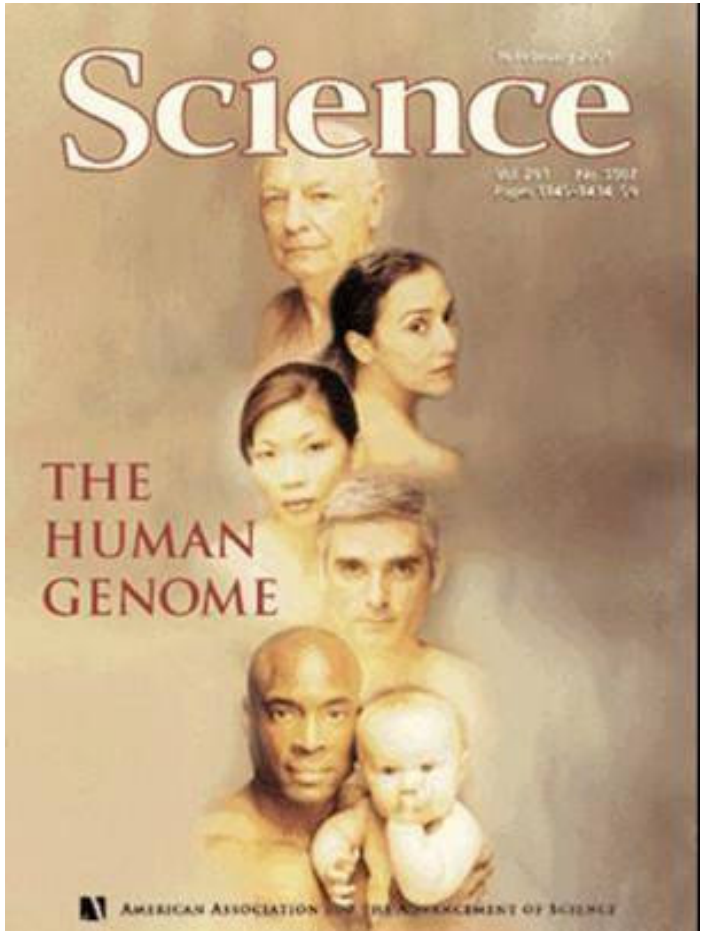
賽亞基因

依「基因體質」的健康風險照護

Yuchi Hwang, PhD

Mar, 2010

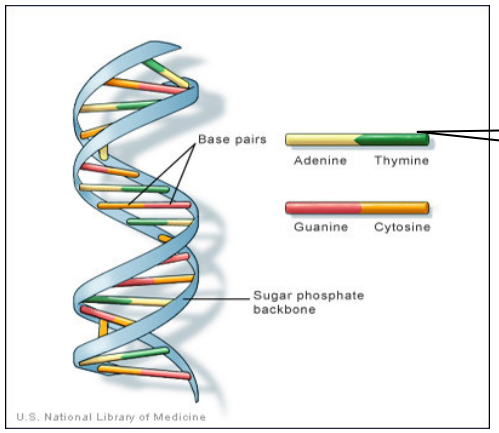
DNA-- 生命密碼



從一出生，每個人的獨特個性、長相、身高體型，生理體質，都記錄在我們的 **DNA** 裡……

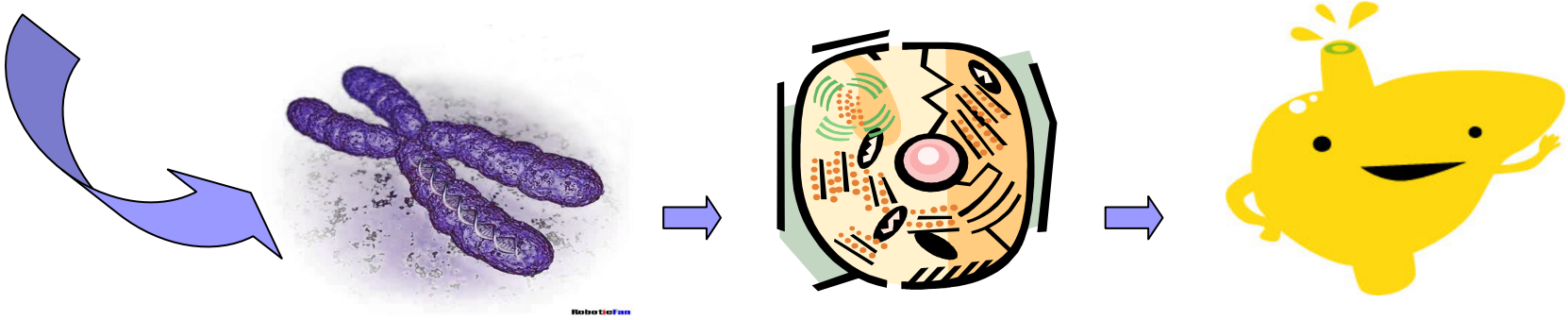
Vita Genomics

DNA--生命的起源



AGCT
鹼基

檢測項目再多　仍不出基因
這個最基本也最尖端的範圍

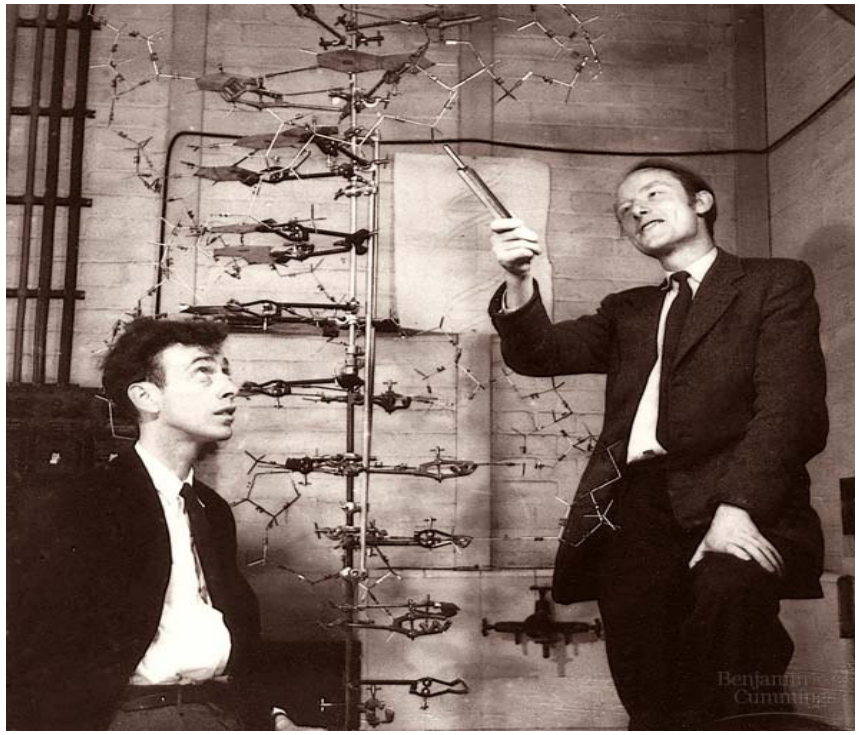


染色體　　細胞　　器官及生理功能

Vita Genomics

從前,我們由占星預測自己的命運;
現在發現,
我們的命運大部分註寫在基因中.

--詹姆士.華生(1962諾貝爾獎得主)



James D. Watson and Francis H. Crick

No. 4553 April 25, 1953 NATURE 737

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 Corey[1]. 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-ray diagrams is the salt, not the free acid. Without the acidic hydrogen atoms it is not clear what forces would hold the structure together, especially as the negatively charged phosphates near the axis will repel each other. (2) Some of the van der Waals distances appear to be too small.

Another three-chain structure has also been suggested by Fraser (in the press). In his model the phosphates are on the outside and the bases on the inside, linked together by hydrogen bonds. This 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-deoxyribofuranose residues with 3′,5′ linkages. The two chains (but not their bases) are related by a dyad perpendicular to the fibre axis. Both chains follow right-handed helices, but owing to the dyad the sequences of the atoms in the two chains run in opposite directions.

Each chain loosely resembles Furberg's[2] model No. 1; that is, the bases are on the inside of the helix and the phosphates on the outside. The configuration of the sugar and the atoms near it is close to Furberg's 'standard configuration', the sugar being roughly perpendicular to the attached base. There is a residue on each chain every 3·4 A. in the z-direction. We have assumed an angle of 36° between adjacent residues in the same chain, so that the structure repeats after 10 residues on each chain, that is, after 34 A. The distance of a phosphorus atom from the fibre axis is 10 A. 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 the sequence on the other chain is automatically determined.

It has been found experimentally[3,4] that the ratio of the amounts of adenine to thymine, and the ratio of guanine to cytosine, are always very close to unity for deoxyribose nucleic acid.

It is probably impossible to build this structure with a ribose sugar in place of the deoxyribose, as the extra oxygen atom would make too close a van der Waals contact.

The previously published X-ray data[5,6] on deoxyribose nucleic acid are insufficiently accurate for a rigorous test of our structure. So far as we can tell, it is roughly compatible with the experimental data, but it must be regarded as unproved until it has been checked against more exact results. Some of these are given in the 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 stereochemical 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 in building it, together with a set of co-ordinates for the atoms, will be published elsewhere.

We are much indebted to Dr. Jerry Donohue for constant advice and criticism, especially on interatomic distances. We have also been stimulated by a knowledge of the general nature of the unpublished experimental results and ideas of Dr. M. H. F. Wilkins, Dr. R. E. Franklin and their co-workers at King's College, London. One of us (J.D.W.) has been aided by a fellowship from the National Foundation for Infantile Paralysis.

J.D. WATSON
F.H.C. CRICK

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

Pauling, L., and Corey, R. B., nature, 171, 346 (1953); Proc. U.S. Nat. Acad. Sci., 39, 84 (1953).
Furberg, S., Acta Chem. Scand., 6, 634 (1952).
Chargaff, E., for references see Zamenhof, S., Brawerman, G., and Chargaff, E., Biochim. et Biophys. Acta, 9, 402 (1952).
Wyatt, G.R., J. Gen. Physiol., 36, 201 (1952).
Astbury, W.T., Symp. Soc. Exp. Biol., 1, Nucleic Acid, 66 (Camb. Univ. Press, 1947).
Wilkins, M. H. F. and Randall, J. T. Biochim. et Biophys. Acta, 10, 192 (1953).

人生四部曲 基因伴著你……

生:無法選擇

老:延緩老化

病:預防不生病

死:自然落幕…..

保 險 保障你……

Vita Genomics

全基因譜掃描

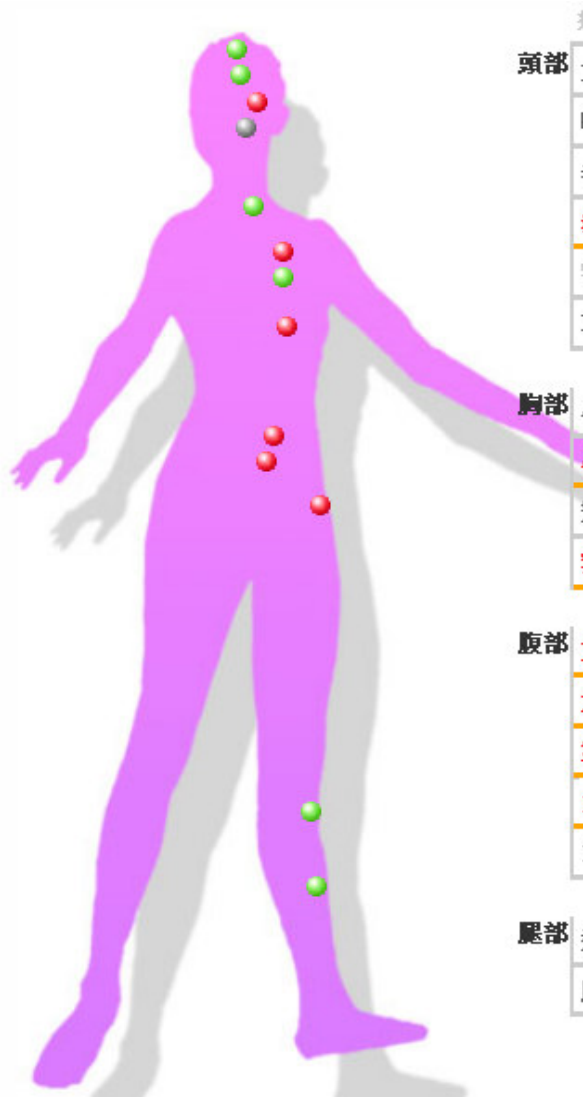
解密獨一無二的生命密碼

顯示全部位 »

疾病名稱	風險*
全身性紅斑性狼瘡	• 1.32%
多發性硬化症	• 2.35%
類風濕性關節炎	• 1.71%
躁鬱症	• 0.52%
慢性淋巴性白血病	• 0.08%
痛風	• 0.06%
肥胖	• 16.77%
憂鬱症	• 38.75%

外在特徵

身高	•



	疾病名稱	風險*
頭部	女性禿髮	• 16.88%
	晚發性阿茲海默症	• 1.45%
	老年性黃斑部病變	• 10.44%
	剝落性青光眼	• 11.85%
	特徵	
	耳垢型態	•
胸部	小兒氣喘	• 6.75%
	心房顫動	• 30.13%
	冠狀動脈硬化	• 34.1%
	乳癌	• 6.36%
腹部	克隆氏症	• 0%
	大腸直腸癌	• 6.55%
	第一型糖尿病	• 7.77%
	第二型糖尿病	• 40.81%
	末期腎病變	• 0.95%
腿部	退化性關節炎	• 27.26%
	腿不寧症候群	• 6.44%

Vita Genomics

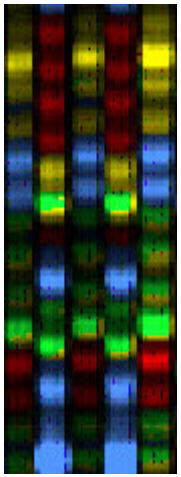
基因加值檢　　健康有保險

高階男性重大疾病基因健康指標	高階女性重大疾病基因健康指標
• 癌症罹患風險基因	• 癌症罹患風險基因
• 心血管疾病罹患風險	• 心血管疾病罹患風險
• 攝護腺癌罹患風險基因	• 乳癌罹患風險基因

Vita Genomics

基因檢測特點

- 個人化
- 一生一次
- 準確度99%



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DNA 解碼

……..ATCGGTGCGTGCATGCAGTGCAGTGCATGCAA
CCGTATATTAATCCCACTGTTTAAAACTGGTTCAT
CAGAATTTATATTTTTTTCTTTCCTCCCTTTTGAATT
TTACTTATGACAGAGGAAGTATTGACCCATGACTT
TTTAAACATAATTTATATTTATACTGGTCAATAATG
AAGGTTTTTTTTTATTATTAAA
GAACTTGATTTTATAATTCT……..

A４二百萬張的內容

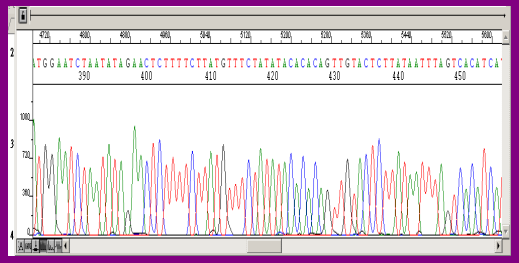
一個DNA佔一位元組
需 3Gb 記憶容量

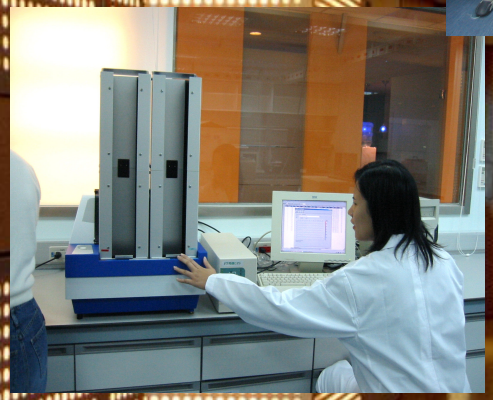
每秒讀10個DNA，約需10年

Vita Genomics

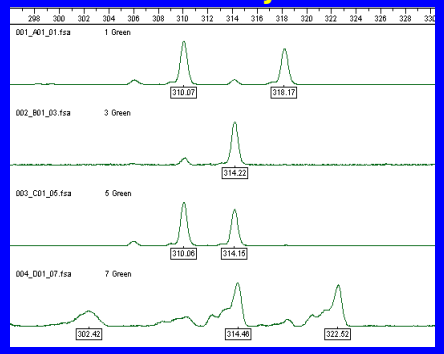
賽亞基因

Genome sequencing on ABI 3700 DNA analyzer





STR analysis on ABI 3700 DNA analyzer



公司沿革

■ 2001年3月成立，資本額23.5億台幣,台灣第一大資本額生技公司，

是亞洲民間第一大以基因體科技為研發重點的生技公司。

■2003年併購上海基康,完成 台北—基因體平台技術研發與生物資訊開發、

上海(基康)—市場開發與技術服務、美國加州—海外業務擴展,

兩岸三地營運佈局與據點。

■2006年，藥物基因體研發中心取得完整國際實驗室認證。

■2006年，工業局認可之公正專業鑑價單位，評鑑無形資產價值達12億美金。

■為歐美生技與藥廠簽約的亞洲首選基因體技術與藥物開發之合作伙伴。

國際學術期刊專文介紹

news

Genomics firm aims to fill Asian gene gap

David Cyranoski, Tokyo

A Taiwanese company last week turned the spotlight on Asian genetic variability when it opened its laboratories in Taipei.

Vita Genomics was formed last year to mine the mass of public and private genetic data in an effort to trace genes among the

tained by the international Human Genome Project and by the US-based company Celera Genomics. Celera, which owns a 5% stake in Vita, helped to set up the company after abandoning its original plan to establish a subsidiary in Taiwan.

"Western drug companies mostly con-

Academia Sinica, which is greatly expanding its functional genomics capacity.

The question of how genetic diversity between different ethnic groups influences human health is a hotly contested one. But many researchers in east Asia believe that distinct sets of SNPs within a region can

Nature 2002 Mar; vol. 416(14):152

Vita Genomics, Inc.

COMPANY PROFILE

Lawrence Shih-Hsin Wu[1], Chun-Lin Su[1] & Ellson Chen[1†]

†Author for correspondence
[1]Vita Genomics, Inc., 7Fl. No.6, Sec.1, Jungshing Rd., Wugu Shiang, Taipei, 248 Taiwan
Tel.: +886 289 769 123;
E-mail: ellson.chen@vitagenomics.com

Vita Genomics, Inc., centered in Taiwan and China, aims to be a premier genomics-based biotechnological and biopharmaceutical company in the Asia–Pacific region. The company focuses on conducting pharmacogenomics research, *in vitro* diagnosis product development and specialty contract research services in both genomics and pharmacogenomics fields. We are now initiating a drug rescue program designed to resurrect drugs that have failed in the previous clinical trials owing to low efficacies. This program applies pharmacogenomics approaches using biomarkers to screen subsets of patients who may respond better or avoid adverse responses to the test drugs.
Vita Genomics, Inc. has envisioned itself as an important player in the healthcare industry offering advanced molecular diagnostic products and services, revolutionizing the drug-development process and providing pharmacogenomic solutions.

Pharmacogenomics 2007; 8(6):669-673

Vita Genomics

Recent Publications

Eugene Lin, **Yuchi Hwang**, **Kung-Hao Liang**, and **Ellson Y. Chen**. (2007) **Pattern-Recognition Techniques with Haplotype Analysis in Pharmacogenomics.** Pharmacogenomics 8 (1): 75-83.

Min-Ji Charng, Kuan-Rau Chiou, **Hua-Mei Chang**, Hao-Ming Cheng, Zhong-Xuan Ye, and Shing-Jong Lin. (2006) **Identification and Characterization of LDLR Mutations in Patients with Familial Hypercholesterolemia in Taiwan.** European Journal of Clinical Investigation 36: 866–874.

Pei-Jer Chen**, Cherry Guan-Ju Lin, Felicia Yi-Fang Lin, Ellson Chen,** and **Lawrence Shih-Hsin Wu** (2006) **Genetic Structure Difference between Responder and Non-Responder of Interferon Therapy for Chronic Hepatitis B Patients.** J Hum Genet 51(11): 915-1036.

Chang-Hsun Hsieh, **Kung-Hao Liang**, Yi-Ren Hung, **Li-Chin Huang**, Dee Pei, **Ya-Tang Liao**, Shi-Wen Kuo, **Monica Shian-Jy Bey**, **Jui-Lin Chen**, and **Ellson Y. Chen**. (2006) **Analysis of Epistasis for Diabetic Nephropathy among Type 2 Diabetic Patients.** Human Molecular Genetics 15: 2701-2708.

Yuchi Hwang, **Ellson Y Chen**, **Z. John Gu**, Wan-Long Chuang, Ming-Lung Yu, Ming-Lung Lai, You-Chen Chao, Chuan-Mo Lee Jing-Houng Wang, Chia-Yen Dai, **Monica Shian-Jy Bey**, **Ya-Tang Liao**, Pei-Jer Chen, and Ding-Shinn Chen. (2006) **Genetic Predisposition of Responsiveness to Therapy for Chronic Hepatitis C.** Pharmacogenomics 7(5): 697-709.

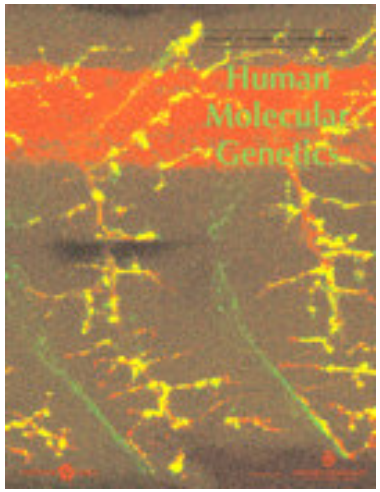
Yuchi Hwang, **Chunlin Su**, Ding-Shinn Chen and Pei-Jer Chen. (2006) **Prospect of Individualized Medicine in Chronic Hepatitis C Therapy by Pharmacogenomics.** Current Pharmacogenomics 4(2): 157-167.

Bin Jiang, Zhongzheng Zhu, Feng Liu, Lifang Hou, **John Gu**, **Ellson Y. Chen**, **Chi-Meng Tzeng**, and **Guanshan Zhu.** (2006) **Prevalence of Mutation in the Epidermal Growth Factor Receptor Gene in Chinese Patients with Non-Small Cell Lung Cancer.** Clinical Oncology 18(8): 635.

Kung-Hao Liang, **Yuchi Huang**, Wan-Ching Shao, and **Ellson Y. Chen**. (2006) **An Algorithm for Model Construction and its Applications to Pharmacogenomic Studies.** J Hum Genet 51: 751-759.

Eugene Lin, **Yuchi Hwang**, and **Chi-Meng Tzeng**. (2006) **A Case Study of the Utility of the HapMap Database for Pharmacogenomic Haplotype Analysis in the Taiwanese Population.** Molecular Diagnosis & Therapy 10(6): 367-370.

Eugene Lin, **Yuchi Hwang**, **Shu-Ching Wang**, **Z. John Gu**, and **Ellson Y. Chen**. (2006) **An Artificial Neural Network Approach to the Drug Efficacy of Interferon Treatments.** Pharmacogenomics 7 (7): 1017-1024.

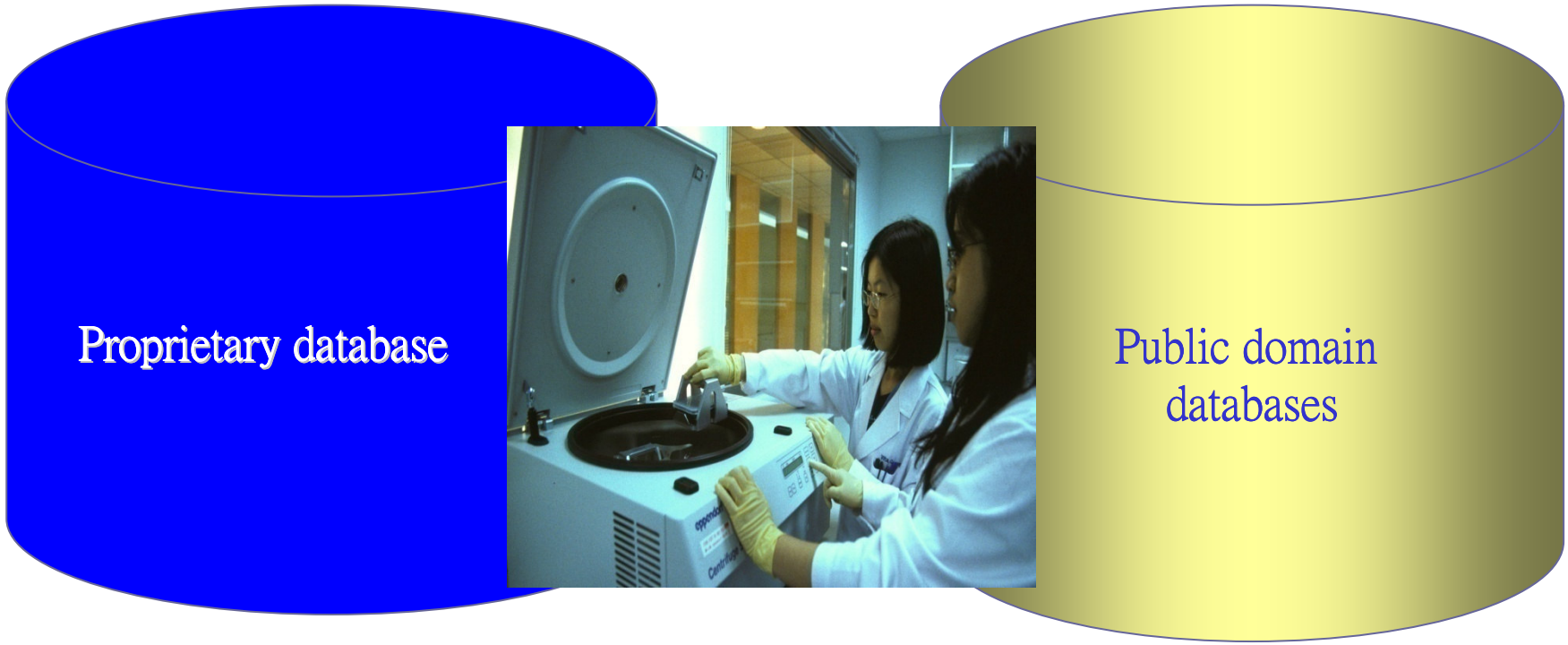


- 51 Papers
- 15 Patents
  - 5 issued,
  - 10 pending

For details: http://www.vitagenomics.com/eng/results.htm

Vita Genomics

國際最具規模華人基因組臨床研究資料庫



Yita Genomics

亞洲十大影響力生命科學公司
BioSpectrum, May 2006

He led CSL from a state-owned overtly cautious entity to a company that created an indigenious biotech success story in Australia. Foreseeing a burgeoning demand for vaccines in the US, he re-focused CSL's in vaccine development by investing nearly 80 million to double the company's output.

The biotech 'gene'ius

TAIWAN-born Dr Ellson Chen is known as the "grandfather of sequencing". Passionate about human genomics and DNA sequencing, he has spent nearly three decades in this field. He has authored over 110 scientific papers and sits on the editorial boards of several major journals, including DNA Sequence, Genome Research and GENE.

His success story can be traced back to the late 70s – armed with a Bachelors in Agricultural Science from National Taiwan University, he headed to Ohio to do his PhD at the Department of Chemistry, Kent State University. He spent the next 25 years in various research positions in reputed companies such as Genentech, Perkin Elmer and Celera Genomics.

Taiwan

After spending nearly 30 years in the US, Mr Chen returned home to Taiwan to set up Vita Genomics. He wanted to create a company that would focus on studying diseases that are common in Asia. Chen's dream was to create global biotech company that could not only find drug targets in Asia but also expand to other countries. From its humble beginnings in 2001 when the company set up its working labs, today Vita Genomics has over 120 employees between its headquarters in Taipei, its international business office in San Diego, Calif. and its research center in Shanghai, China.

Dr Ellson Chen

DESIGNATION & COMPANY: President & CEO, Vita Genomics

ACADEMICS: PhD in Biochemistry, Department of Chemistry, Kent State University, Kent, Ohio (1977)

STARTING POINT: Started work in 1980 as a Senior Scientist & Scientific Manager at Molecular Biology Department, Genentech, Inc., South San Francisco, California, USA.

CAREER HIGHS: In 2000/2001, when the completion of the human genome sequencing was in sight.

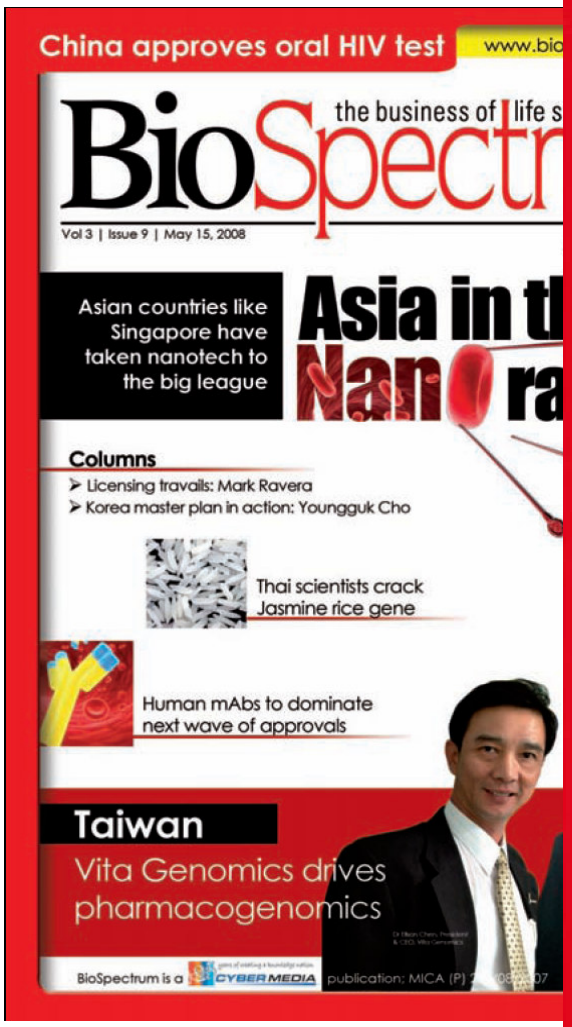
AWARDS & ACCOLADES:
- University Research Fellowship at Kent State University
- Editorial Board Member of DNA Sequence Journal and Genome Research Journal and Editor of Gene Journal

FAMILY: Wife, two daughters

PASSIONATE ABOUT: Basketball. Still plays twice a week

Vita Genomics

Vita Genomics Drives PGx (May & Aug.2008)



Vita Genomics

賽亞基因

BioSpectrum

2010年
亞太
最具爆發力
生技公司

EMERGING COMPANY OF THE YEAR

VITA GENOMICS, TAIWAN

Promising growth of pharmacogenetics

ASIA PACIFIC AWARDS
2ND EDITION
BioSpectrum
ASIA EDITION
2010

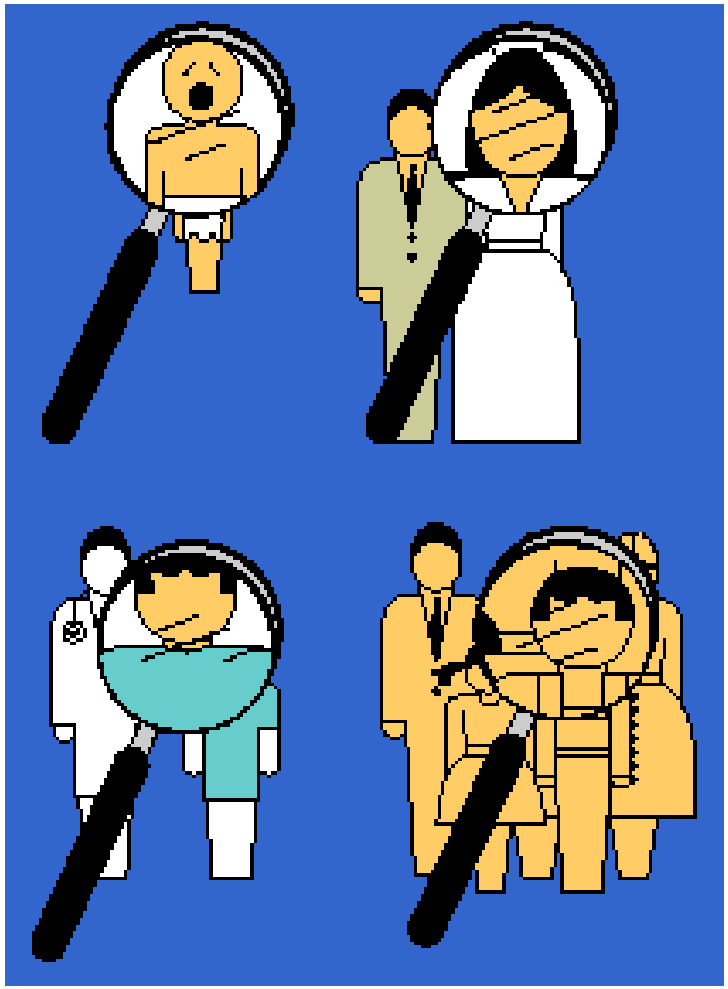
Dr Ellson Chen,
Founder & CEO,
Vita Genomics

"We strongly believe that the role of genomics and pharmacogenomics in the development of personalized medicines is unarguably indispensable"

Vita Genomics

基因科技之應用

胎兒/新生兒篩檢

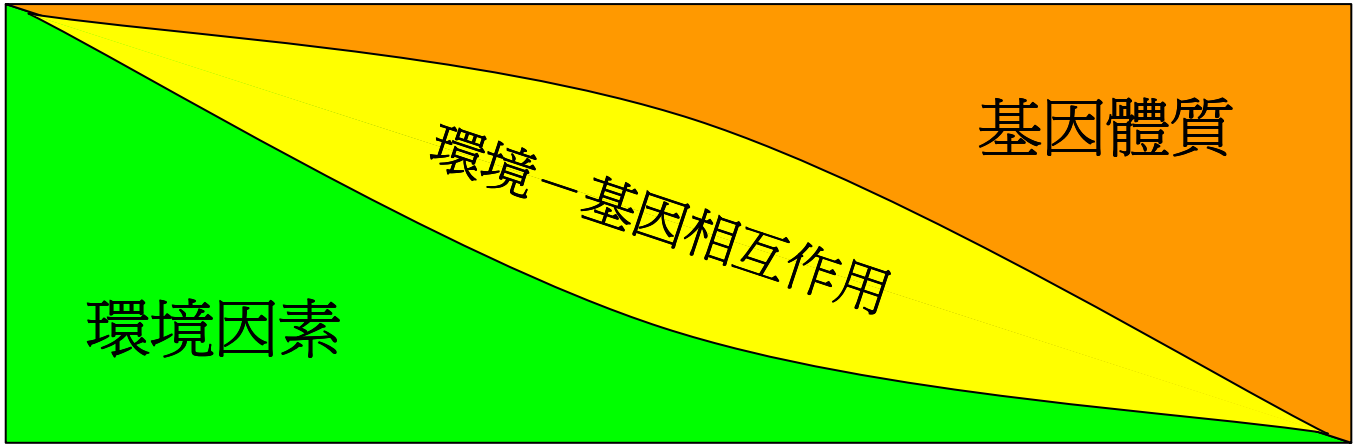


婚前健檢

醫學研究

預防性檢測
藥效預測

基因體質與環境因素互為表裡



感染性疾病
職業傷害

癌症、氣喘、過敏、糖尿病、
心血管、肥胖、精神性疾病..

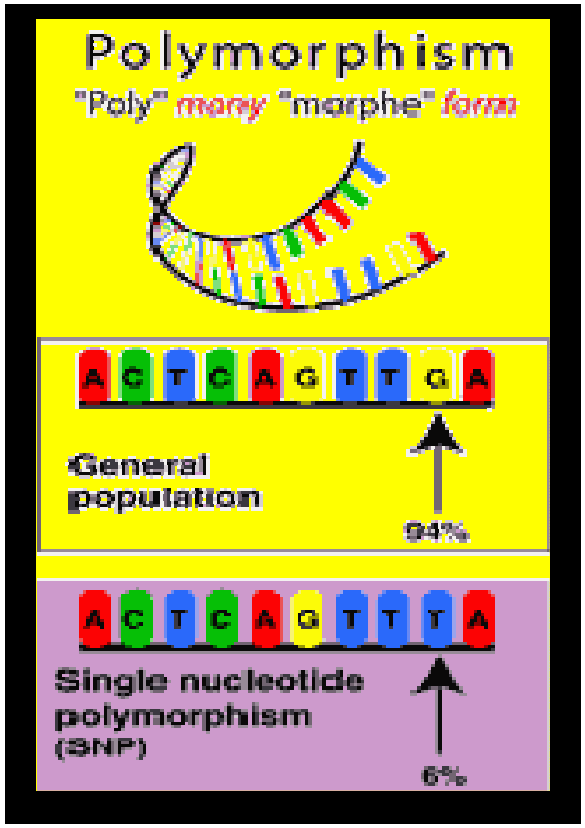
單基因遺
傳性疾病

依「基因體質」量身訂作的
個體化醫學與保健

由〝預防〞到〝保健〞到〝醫學〞

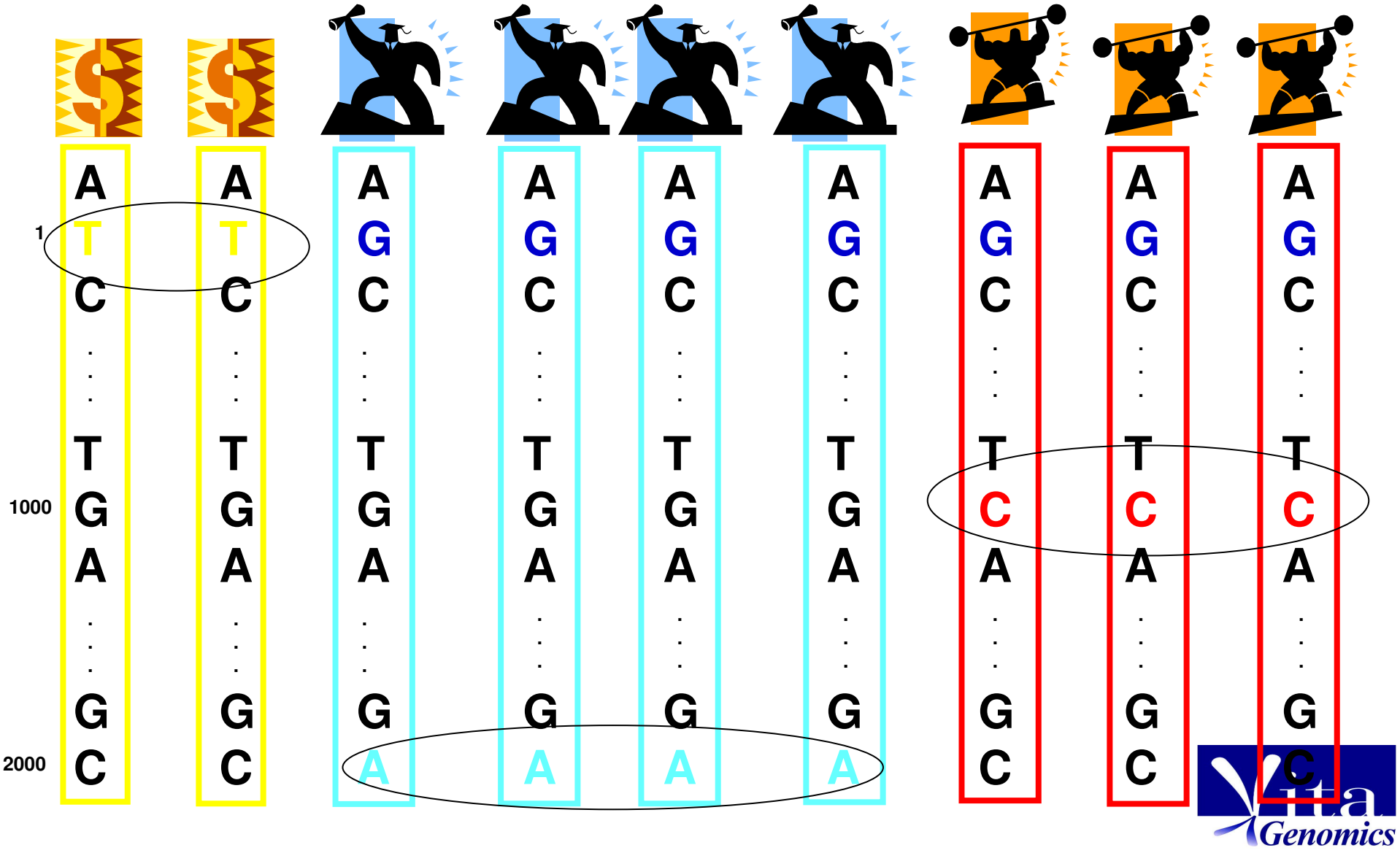
Vita Genomics

基因多型性



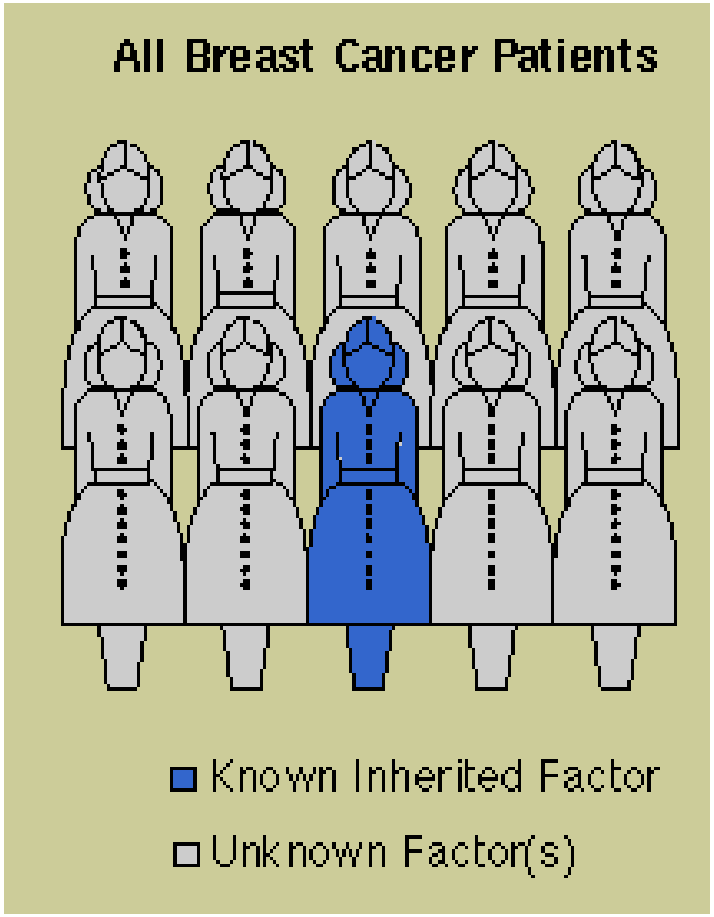
- 每個人的獨特性、長相、身高體型、生理體質，都記錄在三十億鹼基裡。
- 人與人之間 0.1% 的基因多型性 (genetic polymorphism) 造就了個體之間的差異。
- 運用基因體質來掌握個人生理特質、疾病好發傾向與治療應用參考 。

DNA 的微小差異象徵與眾不同的您



疾病風險評估

- 基因檢測發現可能造成疾病之遺傳性危險因子，但並非疾病的本身。
- 檢測出危險因子不一定發病，只要進行有效健康管理。
- 檢測出危險因子，更要加強保險規劃



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心血管疾病基因檢測

- 瞭解自己各項疾病所承擔的風險
- 可依報告結果建議定期回診健康檢查（如進行血脂肪指數檢測）
- 提供健康管理方案，包括日常生活、飲食以及營養補助品

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DNA見證分享(一)

- Angel常為失眠所苦，檢測出「腿不寧症候群」風險偏高，她至醫院檢查。
- 醫生開了藥物，控制睡覺腳會抖動的情形，解決長期失眠的困擾

DNA見證分享(二)

- 一位65歲老人家 檢測出「心血管」風險偏高，到醫院做全身健康檢查後，發現有血管鈣化，一條血管55%塞住，一條血管45%塞住。
- 醫生已開藥讓他服用，控制血管病變情形。

DNA見證分享(三)

- 有位企業家檢測出「剝落性青光眼」風險很高，才回想到似乎有「剝落性青光眼」家族史
- 他很慶幸藉由基因檢測，提醒了疾病的健康風險。

DNA見證分享(四)

- 一位中年女士，檢測出「糖尿病」風險很高，回想起很少吃甜食的她懷孕時，每天吃八顆柳丁，當時被驗出有妊娠性糖尿，並略為早產。
- 「如果事先知道有這麼嚴重的風險，就不會自以為健康的放任自己，還讓下一代承受後果!」她感嘆的說。

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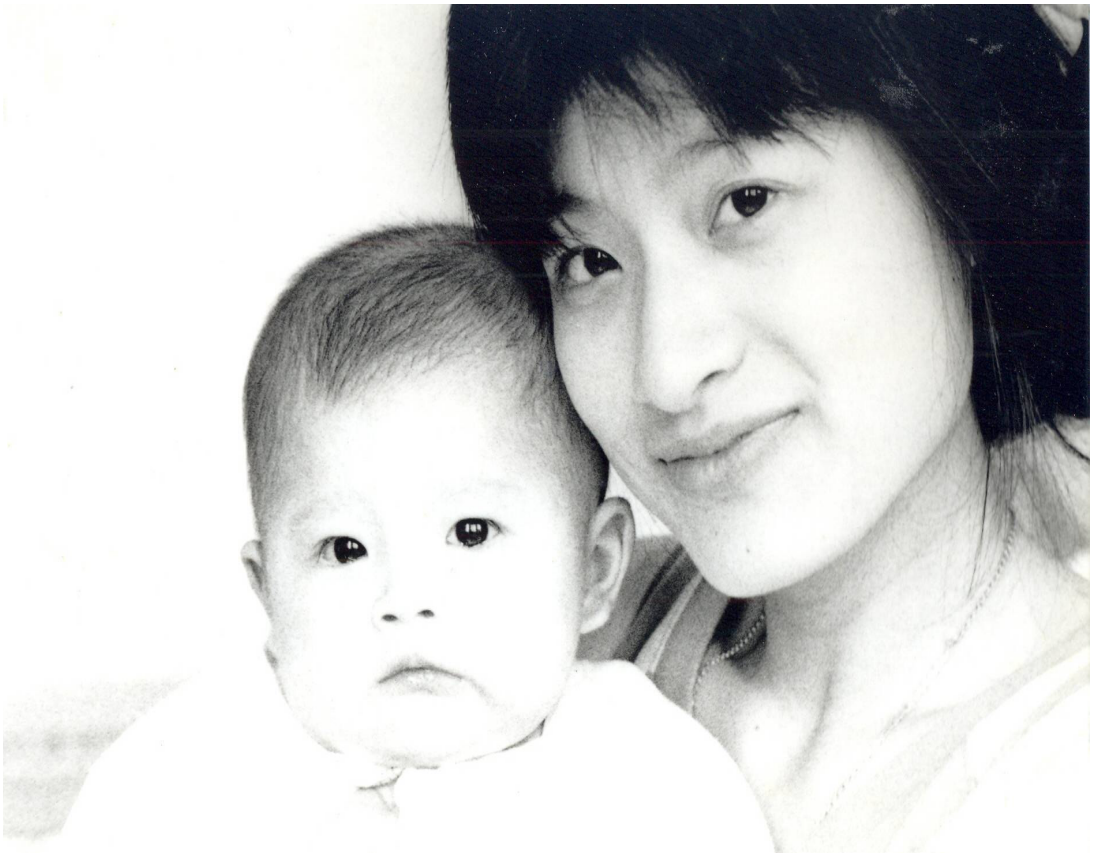

針對個人的脆弱基因來作健康管理。

「就像買了保險一樣，覺得很安心」

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賽亞基因

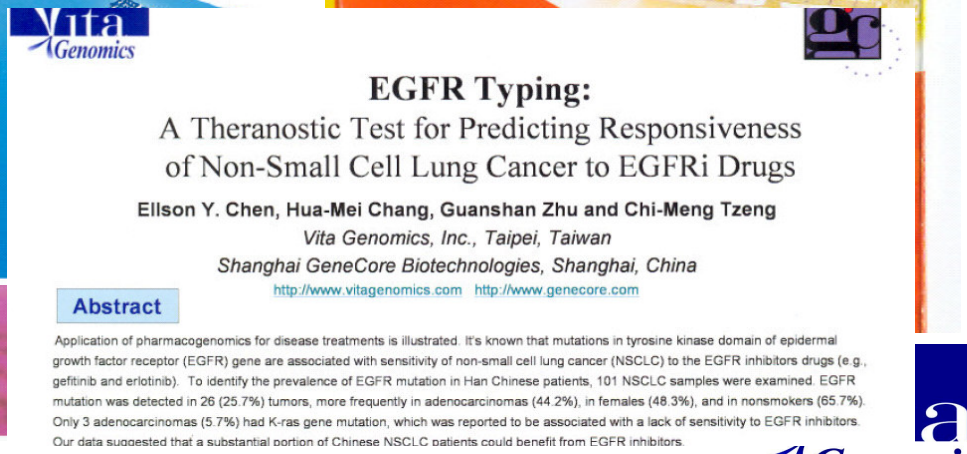
千金換得早知道--

基因科技量身規劃的人生保險

照護您一生的健康

基因健檢

專屬華人基因體質比對開發之檢測



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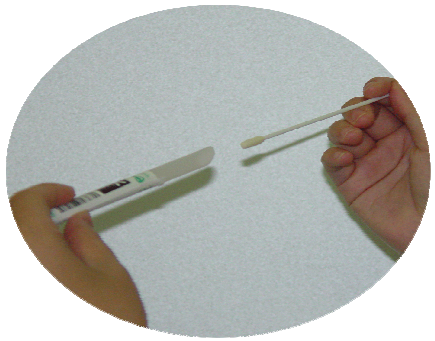
非侵入性檢測 便利安全



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國際品質保證實驗室

Vita Genomics 賽亞基因科技

- 榮登亞洲十大影響力生技公司
- 國際藥廠臨床試驗合作單位
- 榮獲經濟部優等創新企業獎
- 榮獲全國工業總會金炬獎
- 多項專利與科學論文發表

ISO 9001:2000 基因檢測服務認證

ISO 13485:2003 基因檢測試劑設計與製造

ISO 17025:2005 TAF實驗室認證

CRO 經濟部列入國內醫藥研發服務公司

GMP 醫療器材優良製造認證

專業 精確 守密

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賽亞基因

企業與醫界響應

WGScan™

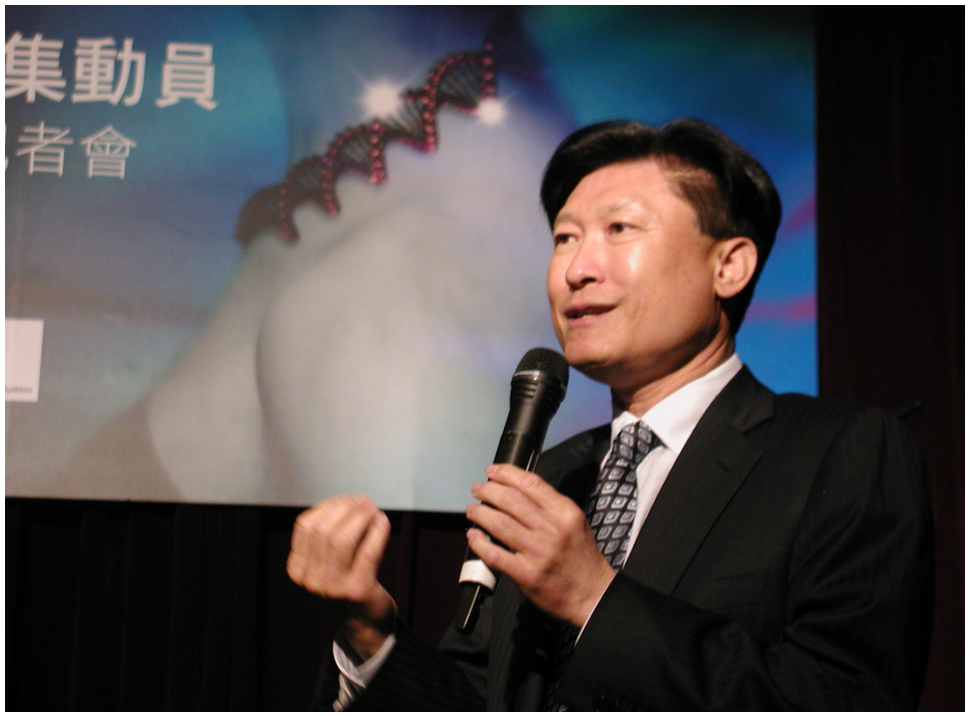
台灣建築、鋼鐵....等各產業工會龍頭 2008 12 3

金仁寶集團董事長許勝雄

中華海峽兩岸健康旅遊促進會
黃明和總裁

Vita Genomics

中華企劃人協會
理事長
翁林澄



亞洲抗老醫學會會長
王桂良醫師