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Genetic Technologies Limited

March 2019

Forward Looking Statements

This presentation may contain forward-looking statements within the meaning of Section 27A of the U.S. Securities Act of 1933 and Section 21E of the U.S. Securities Exchange Act of 1934 with respect to the financial condition, results and business achievements/performance of Genetic Technologies Limited and certain of the plans and objectives of its management. These statements are statements that are not historical facts.

Words such as “should”, “expects”, “anticipates”, “estimates”, “believes” or similar expressions, as they relate to Genetic Technologies Limited, are intended to identify forward-looking statements. By their nature, forward-looking statements involve risk and uncertainty because they reflect Genetic Technologies’ current expectations and assumptions as to future events and circumstances that may not prove accurate. There is no guarantee that the expected events, trends or results will actually occur. Any changes in such assumptions or expectations could cause actual results to differ materially from current expectations.

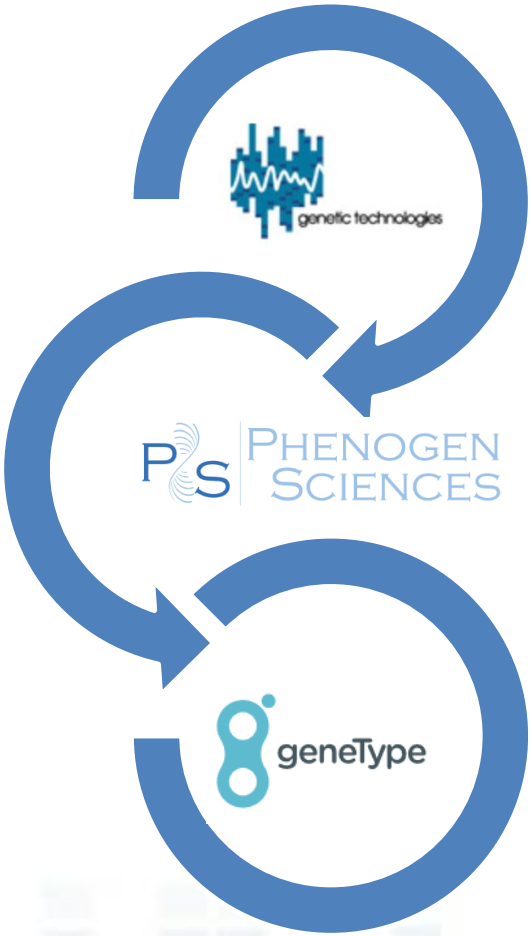
Who we are

Research and Development leader in the genomics sector

- Developing and commercialising a suite of genetic risk assessment products to prevent morbidity and mortality across a range of diseases
- 20 years experience bringing genomics products to market
- Progressive R&D and commercialisation partner to
  - Universities
  - Research organisations
  - Companies exploring new delivery technologies for genomic solutions

Dual listed on both the NASDAQ (GENE) and ASX (GTG)

Corporate Overview



Genetic Technologies Limited
Melbourne, Victoria, Australia

Technical and corporate support with laboratory globally certified to ISO, RCPA, NATA and CLIA

Phenogen Sciences Inc.
Charlotte, North Carolina, U.S.

Sales and marketing, customer support, reimbursement management and sample accessioning to Laboratory Information Management System in Australia

PHENOGEN SCIENCES

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Breast Cancer Risk Assessment

BREVAGen*plus*®, is a first-to-market, clinically validated risk assessment test for non-hereditary breast cancer

- **Simple cheek swab based test** that helps determine a woman's risk of developing sporadic breast cancer
- **First test of its kind** to be clinically validated to evaluate risk for sporadic breast cancer
- **Validated and CLIA-approved** for use in Caucasian, Hispanic and African-American women aged ≥ 35

BREVAGenplus - Our flagship first-in-class risk assessment test for sporadic breast cancer

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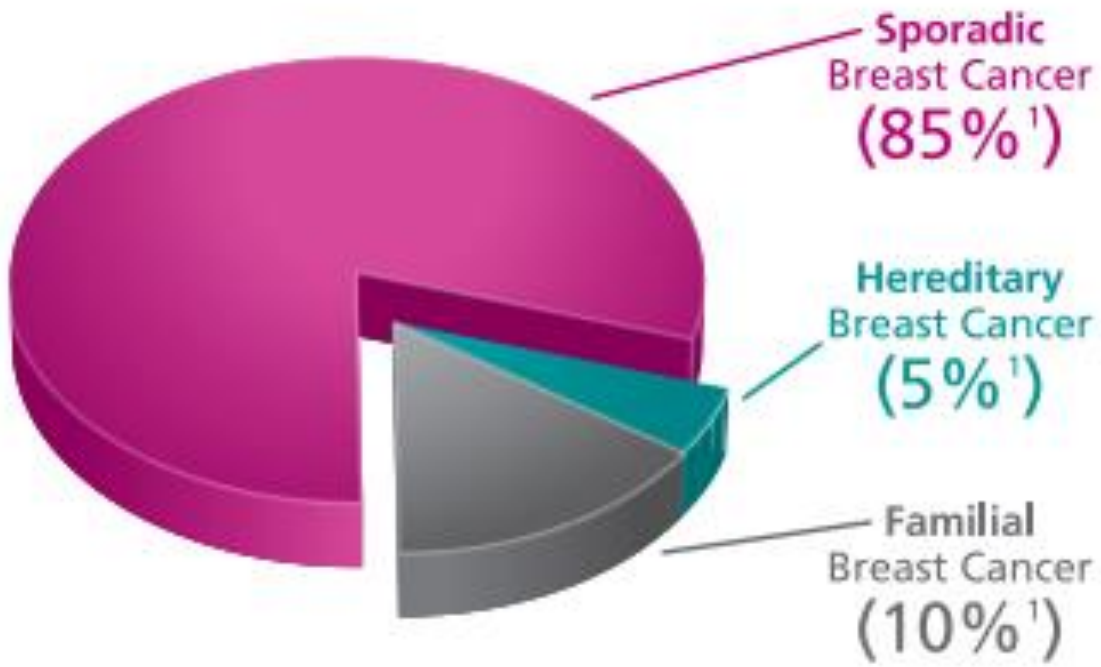
Enhanced Breast Cancer Test

- 15% of breast cancers are hereditary
  - 5-10% of breast cancers are caused by BRCA1 / BRCA2 mutations
  - 5-10% are unknown hereditary cancers
- 85% of breast cancer cases are non-hereditary (sporadic)
  - Less than 15% of women who get breast cancer have a family history
  - Only half will test positive for a BRCA mutation

Our enhanced breast cancer test covers all non-BRCA related cancers.

Combined with BRCA testing, we cover ~100% of women.

Sporadic Breast Cancer Statistics



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Precision Medicine

- 1 in eight women will get breast cancer in their lifetime
- Screening programs that test all women at the same intervals will be overscreening 7 women and underscreening 1 woman.

Our breast cancer risk assessment test offers the potential for more efficient use of screening resources, such as mammography and MRI, through precision genetic risk profiling across the entire population of women.

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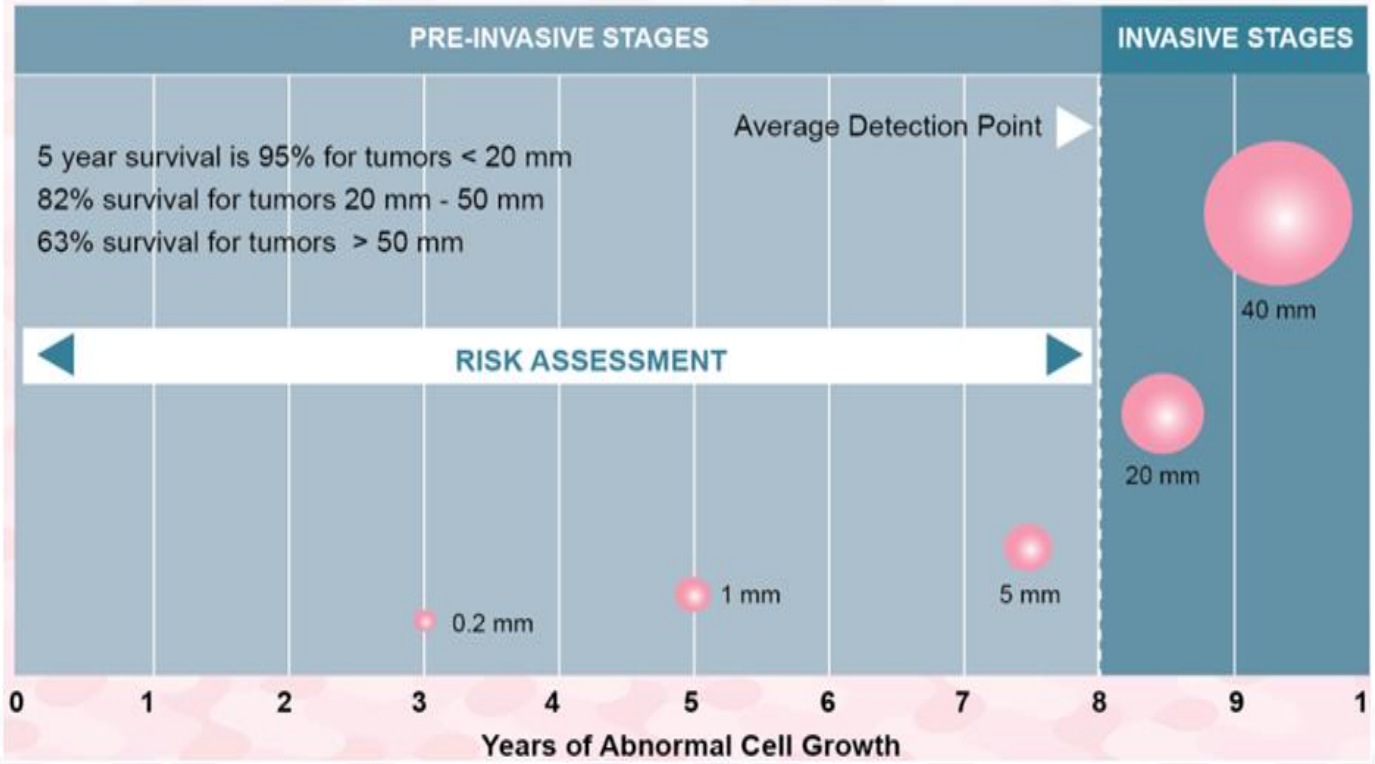
Early Detection = Better Outcomes

- Each year, 240,000+ new breast cancer cases are diagnosed in the US.
- 40,000+ will die.
- With early detection, >95% of these women can survive.*

Breast Cancer Develops Before It Is Detected – "Know Your Risk"



*http://www.cancer.org/cancer/breastcancer/detailedguide/breast-cancer-key-statistics

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GTG Market Advantage

- All of our tests are clinically validated.
  - Physicians are authorised to action the results without further testing.
  - Higher level of trust in the accuracy of our tests as compared to competitive genomic testing
- Our laboratory holds a range of accreditations.
  - CLIA - Clinical Laboratory Improvement Amendments license required for all laboratories offering test in the US
  - CLEP - Clinical Laboratory Evaluation Program license, an additional certification required to offer tests in the state of New York
  - MDEL - Medical Device Establishment License required for Canada
  - ISO - International Organisation for Standardisation compliance enables us to accept test samples from anywhere in the world

GTG's Intellectual Property

- 4 Patents granted in U.S.
  - Patent Nos. 9,051,617 and 9,068,229 covering three of the core genetic markers included in the BREVAGen*plus* risk assessment test
  - Patent No. 7,127,355 offering broad protection re: methods of genetic analysis (the concept of combining clinical risk assessment with genetic risk factors to improve predictability over clinical risk assessment alone)
  - Patent No. 6,969,589 covering the identification of informative SNPs
- 6 Patents pending
  - Covering methods for breast cancer risk assessment
  - Methods for assessing risk of developing breast cancer
  - Improved methods for assessing risk of developing breast cancer
  - Markers for breast cancer
  - Methods for genetic analysis
  - Methods for genomic analysis

Scientific Authority

Dr. Richard Allman, GTG Scientific Director

- Strong publication record in genetic epidemiology across multiple disease categories
- Collaboration for peer review and statistical validation

Richard Allman, GTG Scientific Director
BSc Microbiology
PhD Microbiology (Flow Cytometric Analysis of Bacteria)
Honorary Fellow, Centre for Epidemiology and Biostatistics The University of Melbourne

Dr Allman brings over 20 years of scientific and research experience in both the academic arena in the UK and the commercial sector in Australia. He has wide experience in research leadership, innovation management, and intellectual property strategy, covering oncology, diagnostics, and product development. Most recently he was responsible for providing scientific and technical guidance for the launch of the BREVAGen™ risk assessment test to the US market and managing both in-house research programs and external collaborative research projects, which include major academic units and commercial partners. Prior to entering the biotech sector, Dr Allman's academic career encompassed oncology research, drug development, and assay design, with a particular interest in the linkage between onco-genetic profile and treatment response.

National Health and Medical Research Council

University of Melbourne NHMRC Partnership Grant

- National Health and Medical Research Council is Australia's peak funding body for medical research.
- Collaboration with Professor John Hopper

Genetic Technologies Announces Grant from NHMRC Awarded to University of Melbourne to Substantially Improve Breast Cancer Risk Prediction and Increase Accessibility

Globe Newswire 1-May-2018 5:30 AM

MELBOURNE, Australia, May 01, 2018 (GLOBE NEWSWIRE) -- Genetic Technologies Limited (ASX:GTG) (NASDAQ:GENE↗) ("Company"), a diversified molecular diagnostics company embracing blockchain technologies across genomic testing platforms, is pleased to announce the award of an NHMRC Partnership Grant to a research team led by Professor John Hopper from the Centre for Epidemiology and Biostatistics, Melbourne School of Population & Global Health at The University of Melbourne.

https://marketchameleon.com/PressReleases/i/620446/GENE/genetic-technologies-announces-grant-from-nhmrc-awarded

Professor John Hopper

- PhD in Mathematical Statistics
- NHMRC Senior Principal Research Fellow
- Director (Research) of the Centre for Epidemiology and Biostatistics in the School of Population Global Health at The University of Melbourne
- Published more than 700 papers

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Collaboration with University of Melbourne

- Australia's peak university
- Ranked #32 in the world
- Research-intensive
- Global collaborations

THE WORLD UNIVERSITY RANKINGS

=27	New York University	United States
=27	Peking University	China
30	Tsinghua University	China Explore
31	University of California, San Diego	United States
32	University of Melbourne	Australia Explore

Research into Clinical Applications

GTG partners with world-leading research hospitals to develop the clinical use of polygenic risk scores in treatment decisions.

Research agreement is in place with Memorial Sloan Kettering (MSK) and University of Cambridge.

- The research is led by Mark E. Robson, MD, Chief of Breast Medicine Service, Memorial Sloan Kettering.
- MSK is the world's oldest and largest cancer treatment and research institution.
- The University of Cambridge's UK Institute is a world leading cancer biotech centre.

Top Cancer Hospitals 2018-2019

1. MD Anderson Cancer Center
2. **Memorial Sloan Kettering Cancer Center**
3. The Mayo Clinic

www.health.usnews.com/best-hospitals/rankings/cancer

Other Key Partnerships

Ohio State University (Columbus, Ohio)

- Research collaboration exploring polygenic risk as a means to more informed decision-making for women with *BRCA* mutations
- Led by Amanda Toland, Director of Clinical Genetics and a leader in the field of breast cancer risk assessment.

Nurses' Health Study

- Harvard University prospective study of the risk factors for major chronic diseases in women
- Collaborating with principle investigators to validate new risk models for breast cancer

In Negotiation:

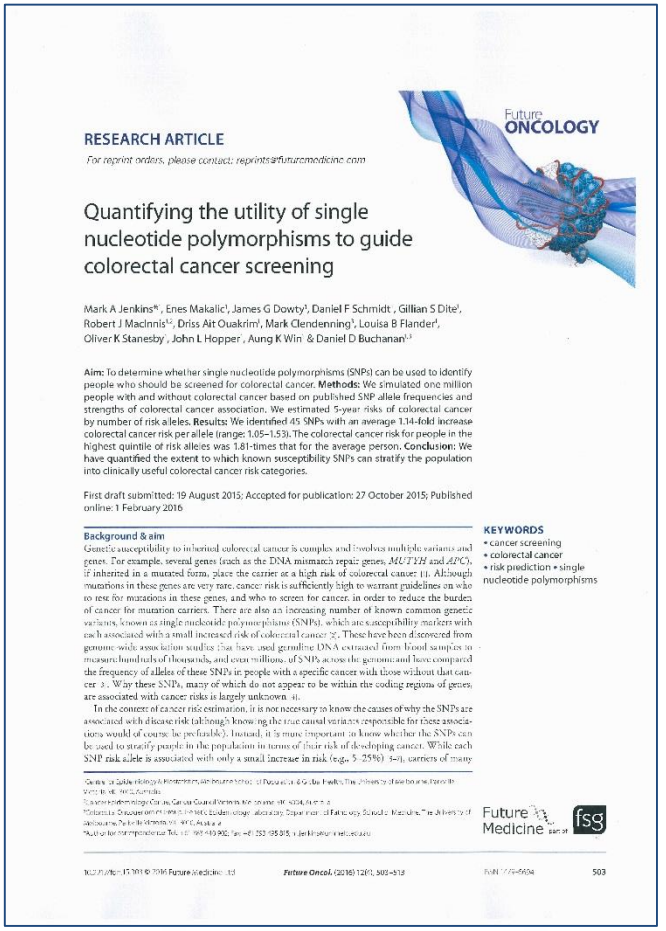
Translational Genomics Research Institute (Phoenix, Arizona USA)

Peter MacCallum Cancer Centre (Melbourne, Australia)

Rapid Deployment of New Products

- Established network of academic collaborators, both in Australia and the US, accelerates the clinical validation process
  - Developing colon cancer test in collaboration with the University of Melbourne
- GTG diagnostic operations and workflow support multiple genetic risk screening protocols

Speed to market is critical in the genomics sector. GTG is uniquely positioned to rapidly introduce new products to a global market.



Future ONCOLOGY

RESEARCH ARTICLE

For reprint orders, please contact: reprints@futuremedicine.com

Quantifying the utility of single nucleotide polymorphisms to guide colorectal cancer screening

Mark A Jenkins*, Enes Makalic, James G Dowty, Daniel F Schmidt, Gillian S Dite, Robert J MacInnis, Driss Ait Ouakrim, Mark Clendenning, Louisa B Flander, Oliver K Stanesby, John L Hopper, Aung K Win & Daniel D Buchanan

Aim: To determine whether single nucleotide polymorphisms (SNPs) can be used to identify people who should be screened for colorectal cancer. Methods: We simulated one million people with and without colorectal cancer based on published SNP allele frequencies and strengths of colorectal cancer association. We estimated 5-year risks of colorectal cancer by number of risk alleles. Results: We identified 45 SNPs with an average 1.14-fold increase colorectal cancer risk per allele (range: 1.05–1.53). The colorectal cancer risk for people in the highest quintile of risk alleles was 1.81-times that for the average person. Conclusion: We have quantified the extent to which known susceptibility SNPs can stratify the population into clinically useful colorectal cancer risk categories.

First draft submitted: 19 August 2015; Accepted for publication: 27 October 2015; Published online: 1 February 2016

KEYWORDS
• cancer screening
• colorectal cancer
• risk prediction • single nucleotide polymorphisms

Background & aim

Genetic susceptibility to inherited colorectal cancer is complex and involves multiple variants and genes. For example, several genes (such as the DNA mismatch repair genes, *MUTYH* and *APC*), if inherited in a mutated form, place the carrier at a high risk of colorectal cancer [1]. Although mutations in these genes are very rare, cancer risk is sufficiently high to warrant guidelines on who to test for mutations in these genes, and who to screen for cancer, in order to reduce the burden of cancer for mutation carriers. There are also an increasing number of known common genetic variants, known as single nucleotide polymorphisms (SNPs), which are susceptibility markers with each associated with a small increased risk of colorectal cancer [2]. These have been discovered from genome-wide association studies that have used germline DNA extracted from blood samples in research bundreds of thousands, and even millions, of SNPs across the genome and have compared the frequency of alleles of these SNPs in people with a specific cancer with those without that cancer [3]. Why these SNPs, many of which do not appear to be within the coding regions of genes, are associated with cancer risks is largely unknown [4].

In the context of cancer risk estimation, it is not necessary to know the causes of why the SNPs are associated with disease risk (although knowing the true causal variants responsible for these associations would of course be profitable). Instead, it is more important to know whether the SNPs can be used to stratify people in the population in terms of their risk of developing cancer. While each SNP risk allele is associated with only a small increase in risk (e.g., 5–25%) [5–6], carriers of many

Future Medicine

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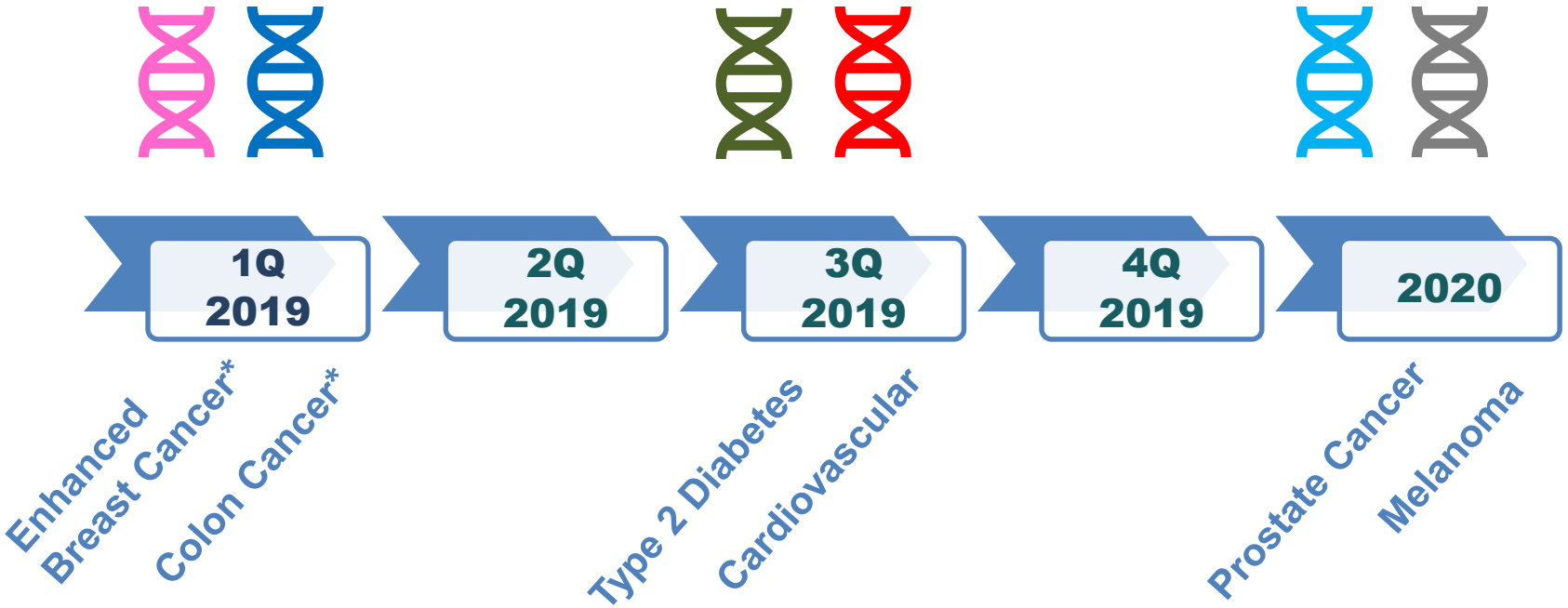
GTG Product Roadmap



* Tests are developed and market launch is scheduled.

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Our Vision

To empower individuals to manage and reduce their risk of contracting cancer and other chronic diseases

We continually strive to maintain our standing as a global leader in genomics by investing in our own research capabilities and by forming partnerships with world-class/expert organisations.

Making a Difference in China

Improved health outcomes for individuals

- People who know their risk of developing disease take steps to prevent it
  - Lifestyle changes such as weight loss, physical activity and nutrition
- Healthcare professionals can prescribe pharmaceutical treatments to high-risk patients
- Individuals and physicians can develop screening programs based on risk

Efficient use of healthcare resources

- Screening regimens can be targeted based on genetic risk
- People at increased risk receive more frequent screening so that disease can be identified and treated early
  - Lower cost of interventions and treatment
  - Reduce loss of productivity due to illness

Higher survival rates and a healthy Chinese population

Cancer in China

Science News *from research organizations*

Nearly half of China cancer deaths attributable to potentially modifiable risk factors

Date: July 6, 2017

Source: American Cancer Society

Summary: More than half of all cancer deaths in men in 2013 in China and more than a third of those in women were attributable to a group of potentially modifiable risk factors.

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- Lung Cancer

Science & Society

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- Education and Employment
- Disaster Plan
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FULL STORY

A new report finds more than half of all cancer deaths in men in 2013 in China and more than a third of those in women were attributable to a group of potentially modifiable risk factors: smoking, alcohol, nutrition, weight, physical activity, and infections. The study appears in *Annals of Oncology*, and concludes that effective public health interventions to eliminate or reduce exposure from these risk factors can have considerable impact on reducing the cancer burden in China.

Cancer is the leading cause of death in China, with 4.3 million new cancer cases and 2.8 million cancer deaths estimated to occur each year. That burden is expected to increase in the coming decades because of aging of the population as well as changes in lifestyle that increase cancer risk, such as excessive calorie intake and physical inactivity.

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Breast cancer in China is increasing at a rate of 3.5% per year.

https://www.sciencedaily.com/releases/2017/07/170706071915.htm

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Diabetes in China

Diabetes in China: Epidemiology and Genetic Risk Factors and Their Clinical Utility in Personalized Medication

Cheng Hu[1,2] and Weiping Jia[1]⇑

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Diabetes 2018 Jan; 67(1): 3-11.
https://doi.org/10.2337/dbi17-0013

Check for updates

Abstract

The incidence of type 2 diabetes (T2D) has rapidly increased over recent decades, and T2D has become a leading public health challenge in China. Compared with European descents, Chinese patients with T2D are diagnosed at a relatively young age and low BMI. A better understanding of the factors contributing to the diabetes epidemic is crucial for determining future prevention and intervention programs. In addition to environmental factors, genetic factors contribute substantially to the development of T2D. To date, more than 100 susceptibility loci for T2D have been identified. Individually, most T2D genetic variants have a small effect size (10–20% increased risk for T2D per risk allele); however, a genetic risk score that combines multiple T2D loci could be used to predict the risk of T2D and to identify individuals who are at a high risk. Furthermore, individualized antidiabetes treatment should be a top priority to prevent complications and mortality. In this article, we review the epidemiological trends and recent progress in the understanding of T2D genetic etiology and further discuss personalized medicine involved in the treatment of T2D.

Introduction

The increasing prevalence of type 2 diabetes (T2D) has become a global public health concern in the 21st century. Previously, T2D was mostly prevalent in affluent "Western" countries; however, currently, T2D occurs worldwide. According to the latest report in the International Diabetes Federation *Diabetes Atlas* (1), the overall prevalence of diabetes in adults is 9.1%, implying that 415 million adults suffer from diabetes globally. Moreover, 318 million adults have impaired glucose regulation and are at a high risk for developing diabetes in the future. China ranks number one, with the highest number of people with diabetes.

Environmental factors, including obesity, aging, diet, and physical activity; genetic factors; and epigenetic modification contribute to the accelerating diabetes epidemic. Knowledge of the risk factors that affect the incidence of T2D and the complications of T2D can advance the understanding of the pathophysiology of this disease and the development of effective preventive measures. Previously, numerous T2D susceptible loci have been successfully

T2D has become a leading public health challenge in China.

In addition to environmental factors, genetic factors contribute substantially to the development of T2D.

China ranks number one, with the highest number of people with diabetes.

http://diabetes.diabetesjournals.org/content/67/1/3

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Screening and Early Detection

- Breast cancer death rates declined 39% from 1989 to 2015 among women. The progress is attributed to improvements in early detection and screening.
- Prostate cancer death rates declined 52% from 1993 to 2015 among men. Attributed to national screening programs
- Colorectal cancer death rates declined 52% from 1970 to 2015 among men and women because of increased screening and improvements in treatment.

Collaboration with Chinese Research

- Contribution to science is a core value.
- Collaboration with experts in genomics
  - Population geneticists
  - Disease-specific investigators
  - Pharmaceutical research organisations
- Research partnerships help us to continually refine our test protocols and bring new products to market.

Our intent is to collaborate with Chinese research organisations and investigators to develop cutting-edge genetic products for disease prediction and prevention.

Next Steps

- Develop collaborative relationships within China
  - Clinical validation
  - Regulatory approval
  - Commercial channels
  - Laboratory testing
- Deliver the benefits of genetic screening into China
  - Go-to-market plan for additional genetic screening tests
  - Engagement with Key Opinion Leaders
  - Collaboration with Chinese research organisations

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