

بِسْمِ اللَّهِ الرَّحْمَنِ الرَّحِيمِ
وبعد حمد الله والثناء عليه والصلوة على رسوله محمد وآله فان
هذه الكتب التي صنعناها في الطب التي **الاول** منها هو في الاحكام
الكلية من الطب والثاني منها هو هذا الكتاب المجمع في الادوية
المفردة وتسمنا هذا الكتاب **مقالتين الاول** منهما في
القوانين الطبيعية التي يجب ان يعرف من امر الطب في قوى الادوية
الجزوية **اما الاول** فقسناها الى ستة فصول **ا** في تعريف امزجة
الادوية المفردة **ب** في تعريف امزجة الادوية المردة بالتجربة
ج في تعريف امزجة الادوية المفردة بالقياس **د** في تعريف
افعال قوى الادوية المفردة **ك** في احكام بعض الادوية
في خارج **ق** في النقاط الادوية وادخالها واحا الثانية
فان جعلت الادوية المفردة فيها الواح **ا** الاسماء الادوية
المفردة وتعريف ماهياتها **ب** لاحتيا الجيد منها **ج** لذكر
كيفيةها وطبايعها **د** لخواص افعالها واحوالها الكلية
مثل التحليل ومثل الانضاج والتعريف والتخدير وما شبه ذلك
من الافعال التي ذكرناها في المقالة الاولى وخواص اجزاء كانت
لها وجعلت لكل واحد منها كتابه بصيغ
حتى سهل المقاطع **هـ** في افعالها
التي يتعلق بالزمن وعلمت على كل شيء



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KUWAIT GENOME PROJECT

G2MC Greece



Fahd Al-Mulla B.Sc., M.B.Ch.B., Ph.D. PCTM, FRCP

Professor of Molecular Pathology at Kuwait University

Head of Functional Genomics at Dasman Diabetes center

Director of Genomic Medicine Center “GENATAK” “جيناتك”

Kuwait



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Area:

Total: 17,820 sq km

Population:

Total: 3,442,945

Kuwaiti nationals: 1,102,485

Non-nationals : 2,340,460

(Public Authority of Civil Information, 2009)

6-Governorates

One public many private Universities
Centralized specialized Free public Health
Service:

- Kuwait Cancer Control Center
- Kuwait Medical Genetics Center/maternity
- Private free Dasman Diabetes Center

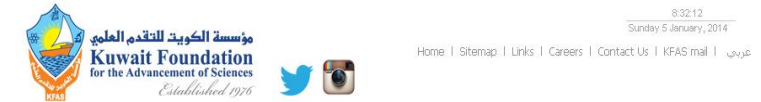
Research and External funding



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<http://kfas.org/index.html>



- Kuwait Foundation for the Advancement of Sciences. Directed Dr. Adnan Shihab Eldin
 - 1% of profit from local businesses
 - Research, programs and educational-based funding
- Kuwait institute for Scientific research another source of research Funding
- Research funding dropped \$30M-300k 2017

Research funding not a priority



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Also this week

- Nature 2006 issue on Islam and Science
- Most Gulf states spend 0.1-1% of GDP towards research and development
- Better trends now with Qatar 5% and Saudi Arabia matching this and more
- Kuwait-Bahrain-UAE-Oman remain on low spending side

OIL RICH, SCIENCE POOR

The wealthy Arab states offer scant support for science and technology.

Jim Giles finds out whether this indifference to research is likely to change.

When *Nature* surveyed the prospects for science in the Arab world in 2002, our reporter picked out three subjects in which the region excelled¹. One was, and still is, important: desalination technologies to combat water shortages. But the other two highlight the region's threadbare research record. Camel reproduction and falconry research might excite Arab sports enthusiasts, but they are unlikely to set the scientific world on fire.

The monarchies of the Gulf are the richest of all Muslim nations, but little of that wealth is spent on research. Saudi Arabia, Qatar and Kuwait spend about 0.2% of their gross domestic product (GDP) on science — less than one-tenth of the developed-country average of 2.3% and about a third of that spent by less wealthy Iran. The oil monarchs have the





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Another Revolution Needed?

Counting the many plagues that threaten research in the Middle East and North Africa region

By Fahd Al-Mulla | March 1, 2011

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4. Suspected Effects of Vitamin D
5. Immune Role in Brain Disorder?

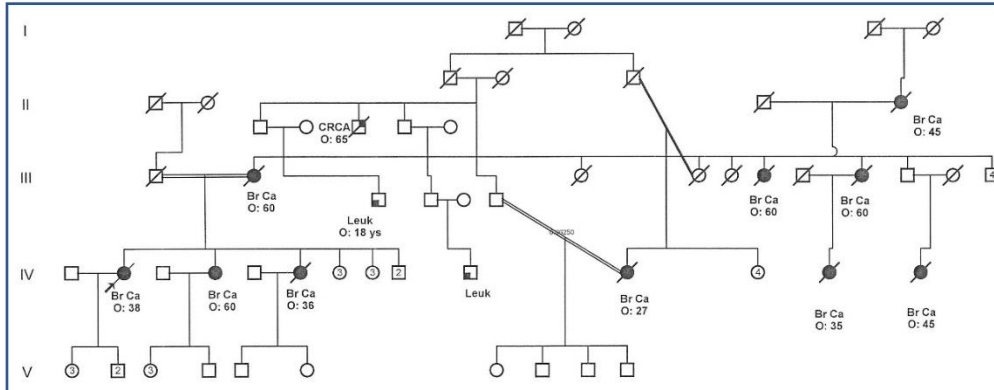
Current Issue



- Very difficult research environment
- Delayed tenders/ethical approvals etc
- Please read our cry for help in theScientist

<http://www.the-scientist.com/?articles.view/articleNo/29545/title/Another-Revolution-Needed-/>

Rare allele avenue!



This family cost Government +3 million KD
 Genetic screening/ prediction costs only few thousands

- Enormous time depth of human habitation (second only to sub-Saharan Africa)
- 50-70% Consanguineous marriages
- Source of major genetic discoveries
 - Autozygosity mapping
 - Linkage analysis
- Clusters of familial disorders and cancers
 - 50% of 50-years aged adults T2DM
 - 30% of the population are obese
- Arabs are not represented in the HapMap, 1000 Genome project

Original Article

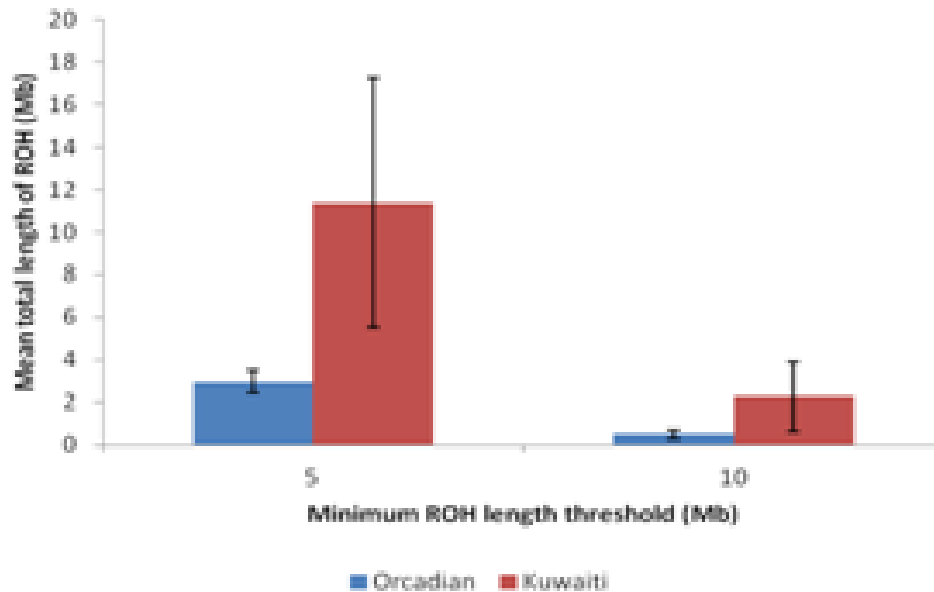
Journal of Human Genetics **59**, 615-622 (November 2014) | doi:10.1038/jhg

The influence of admixture and consanguinity on population genetic diversity in Middle East

Xiong Yang, Suzanne Al-Bustan, Qidi Feng, Wei Guo, Zhiming Ma, Makia Marafie, Sindhu Jacob, Fahd Al-Mulla and Shuhua Xu



Mean Total Length of ROH > 5 and 10 Mb in Kuwait and Orkney



- Considerable higher proportion of ROH over 5 Mb was observed in the Kuwaiti samples when compared to the Orkney population.
- Over **three times** as many Kuwaitis had at least one ROH > 10 Mb in length than Orcadians.
- Indicating recent inbreeding loops in their pedigrees.

Genome Arabia

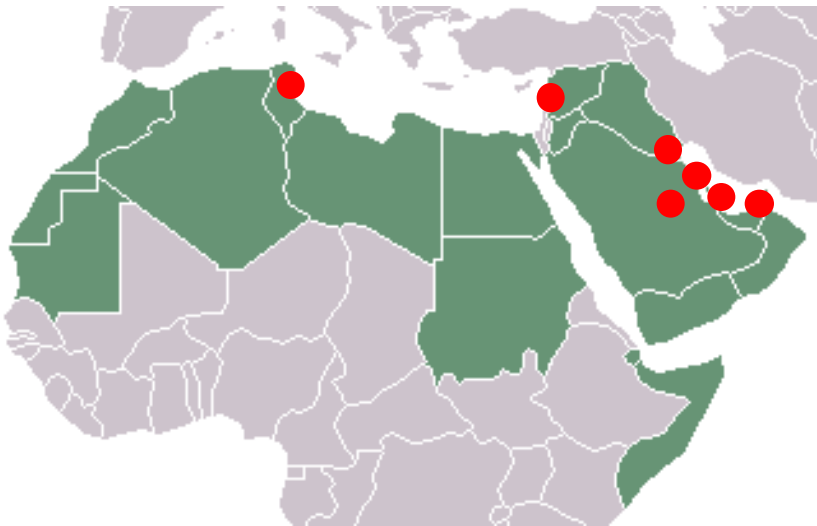


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- In 2012:
Set up Genome Arabia working group to
whole genome sequence 1000 normal
Arabs.
Grant funded by QNRF

2013-stopped??



Gulf | Qatar

Qatar Genome launched

Project is road map for future treatment of personalized medicine

By Habib Toumi, Bureau Chief

Published: 12:08 December 10, 2013

GULF NEWS



Manama: Shaikha Moza Bint Nasser, the Chairperson of the non-profit Qatar Foundation for Education, Science and Community Development has announced the launch of the 'Qatar Genome'.

"In Qatar, when we strived to build our all-inclusive culture of health, we transformed our health centers into research and academic centers, which incorporate hands on experience," Shaikha Moza said.

"As a result of the integration of scientific research and the clinical realities, I am pleased to announce the project 'Qatar Genome', a project that consists of a road map for future treatment of personalized medicine," she said as she opened the World Innovation Summit for Health (WISH) in the Qatari capital Doha on Tuesday.

Mapping the Qatari genome to prevent inherited diseases

January, 2014



Dr. Ron Crystal, chairman of genetic medicine at WCMC-NY, is leading a group of research projects investigating the Qatari genome

A Weill Cornell Medical College study that analyzed the DNA of Qatar's native population has discovered genetic variations that could help doctors target interventions to reduce the prevalence of a variety of debilitating hereditary disorders.

Researchers at WCMC-Q and Weill Cornell Medical College New York (WCMC-NY), working with colleagues from Cornell University in Ithaca and Hamad Medical Corporation, identified 37 genetic variants in 33 genes known to play causal roles in a total of 36 diseases, including such devastating conditions as cystic fibrosis, sickle cell anemia and muscular dystrophy. The study points the way to more

Saudi Genome



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9 December 2013 Last updated at 01:33 GMT



Hundred thousand genomes to be mapped in Saudi Arabia

By Helen Briggs
BBC News



Saudi Arabia is launching a national research project to study the genetic basis of disease in its population

Up to 100,000 people in Saudi Arabia are to have their genetic codes mapped in a new human genome project.

Related Stories



ARTICLE

Clinical exome sequencing: results from 2819 samples reflecting 1000 families

Daniel Trujillano^{*,1,10}, Aida M Bertoli-Avella^{1,10}, Krishna Kumar Kandaswamy^{1,10}, Maximilian ER Weiss¹, Julia Köster¹, Anett Marais¹, Omid Paknia¹, Rolf Schröder¹, Jose Maria Garcia-Aznar¹, Martin Werber¹, Oliver Brandau¹, Maria Calvo del Castillo¹, Caterina Baldi¹, Karen Wessel¹, Shivendra Kishore¹, Nahid Nahavandi¹, Wafaa Eyaid^{2,3}, Muhammad Talal Al Rifai^{3,4}, Ahmed Al-Rumayyan^{3,4}, Waleed Al-Twajiri^{3,4}, Ali Alothaim^{3,5}, Amal Alhashem⁶, Nouriya Al-Sannaa⁷, Mohammed Al-Balwi^{3,4}, Majid Alfadhel^{2,3}, Arndt Rolfs^{1,8} and Rami Abou Jamra^{*,1,9}

We report our results of 1000 diagnostic WES cases based on 2819 sequenced samples from 54 countries with a wide phenotypic spectrum. Clinical information given by the requesting physicians was translated to HPO terms. WES processes were performed according to standardized settings. We identified the underlying pathogenic or likely pathogenic variants in 307 families (30.7%). In further 253 families (25.3%) a variant of unknown significance, possibly explaining the clinical symptoms of the index patient was identified. WES enabled timely diagnosing of genetic diseases, validation of causality of specific genetic disorders of *PTPN23*, *KCTD3*, *SCN3A*, *PPOX*, *FRMPD4*, and *SCN1B*, and setting dual diagnoses by detecting two causative variants in distinct genes in the same patient. We observed a better diagnostic yield in consanguineous families, in severe and in syndromic phenotypes. Our results suggest that WES has a better yield in patients that present with several symptoms, rather than an isolated abnormality. We also validate the clinical benefit of WES as an effective diagnostic tool, particularly in nonspecific or heterogeneous phenotypes. We recommend WES as a first-line diagnostic in all cases without a clear differential diagnosis, to facilitate personal medical care.

European Journal of Human Genetics (2017) 25, 176–182; doi:10.1038/ejhg.2016.146; published online 16 November 2016

Top-to-bottom model



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- Kept knocking
- No major reaction from policymakers
- Unlike Qatar GP. We have no champion.
- Few doctors/specialists understood our GM initiative
- Doctors/specialists send-out

GM and the private sector



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- Bottom-to-top model
- Direct to customer model
- Deliver state-of the art services
- Limited bureaucracy

Kuwait Public and Private Genome Projects



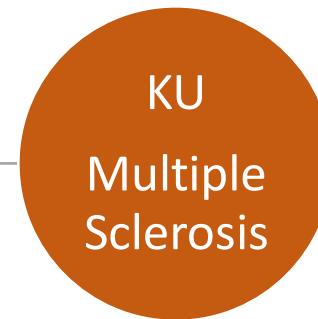
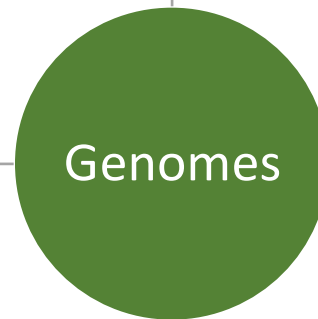
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200 Families



Counseling
Phenotyping
1000 genomes 30x
400 rare diseases



176 samples/families



25,000 samples Biobank
Plan for 10,000 genomes
Functional studies

Bioinformatics/EHR made simple



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Patient View

Genome View

Body View

Personal Genomics

Body View:

Genome Report

Chromosome	Position	Normal	Tumor	Frequency	Class	Predicted Effect	Pass Filter	Gene	Primary Site
1	3989004	1	L		Mitosome	TOLUATED	F	GCPC1	Brainstem
1	20420951	1	1			FNK3	CNS		
4	527676	1	1			FRS3	CNS		
4	1882303	1	1	0.020	Synonymous	TOLUATED	F	FRS3	Skin
6	32342054	2	1	0.006	Synonymous	TOLUATED	F	FRS3B	CNS
5	3991778	1	1	0.007	Synonymous	TOLUATED	F	CNAG2	Skin
5	21225709	1	0	0.028	Synonymous	TOLUATED	F	AAC	Large Intestine
6	32360200	2	2	0.033	Mitosome	TOLUATED	F	DNES1	CNS
7	10000883	1	1			TOLUATED	F		Ovary
7	34084034	1	1		Mitosome	TOLUATED	F	FRS2	CNS
8	35233961	1	1			FUNCTION/CHANGING	F		
9	23862434	1	0	0.020		FUNCTION/CHANGING	F	GENA3A	Gastrophage
9	23861818	2	2			FUNCTION/CHANGING	F	GENA3A	Gastrophage
9	7876184	0	1			FUNCTION/CHANGING	F	DNF76	Ovary
9	18818006	1	1	0.003		FUNCTION/CHANGING	F	DNF76	Ovary
9	18877862	1	0		SpliceRegion	FUNCTION/CHANGING	F	CACNA1B	Brain
10	76207407	1	1			FUNCTION/CHANGING	F	AVR19C	CNS
10	89702918	1	1			FUNCTION/CHANGING	F	PRR19	CNS

Gene Overview:

5S9S_CAGATC_L001_sorted Coverage

ReadAlign

Pile-up

dbSNP 137, UC SC

RefSeq Genes 63, UC SC

Reference Sequence GRCh37 hg19, UC SC

Genes and Regulation - Public Annotations

CDH1 E W G N R F K K L A D M Y G

p.ARG868CYS

Association with Dr. Darrol Baker
Golden helix

5S9S_CAGATC_L001_sorted Coverage

ReadAlign

Pile-up

dbSNP 137, UC SC

RefSeq Genes 63, UC SC

Reference Sequence GRCh37 hg19, UC SC

Genes and Regulation - Public Annotations

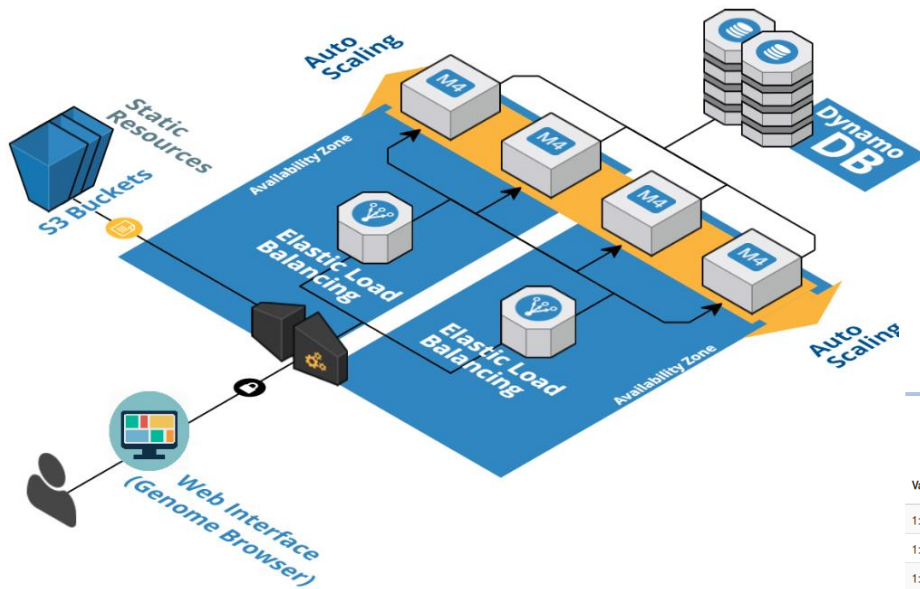
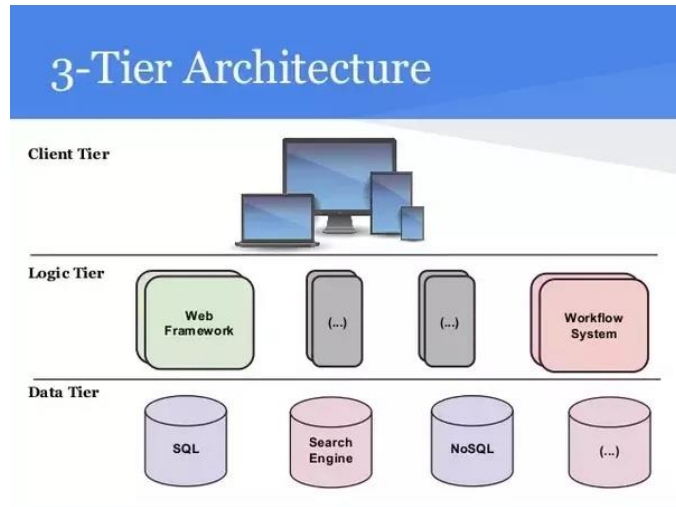
CDH1 E W G N R F K K L A D M Y G

p.ARG868CYS

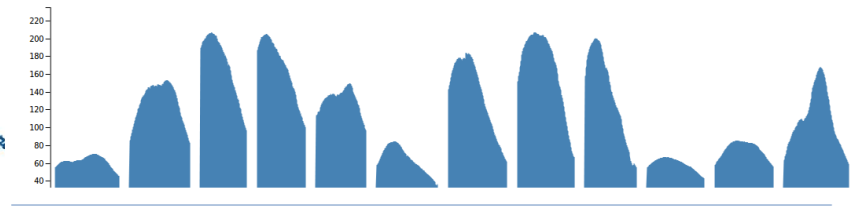
Data generation and databases



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- Building online Kuwait genomics portal



Variant	Chrom	Position	Consequence	Filter	Annotation	Flags	Allele Count	Allele Number	Number Of Homozygotes	Allele Frequency
1:55512190 C / T	1	55512190	c.400-6C>T	PASS	splice region	test	1	121374	0	0.082
1:55512192 G / T	1	55512192	c.400-6C>T	FAIL	splice acceptor		1	121374	0	0.082
1:55509511 G / T	1	55509511	c.400-6C>T	FAIL	splice acceptor		3	121374	119198	0.838
1:55505537 C / T	1	55505537	p.Ser9Ser	PASS	synonymous		5	23606	166	0.838

Kuwait Genome Project



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Inherited disease	Inheritance mode	SNP ID	Mutation	KGP_MAF	ExAC MAF
21-hydroxylase deficiency	Autosomal recessive	rs6471	p.V282L	0.0056	0.01
Adenosine deaminase 2 allozyme	Autosomal recessive	rs73598374	p.D8N	0.087	0.13
Alport syndrome	X-linked recessive	rs104886192	p.M898V	0.0034	0.0003
Arrhythmogenic right ventricular cardiomyopathy type 8	Autosomal dominant	rs121912998	p.V30M	0.0056	0.0031
Metachromatic leukodystrophy	Autosomal recessive	rs2071421	p.N352S	0.24	0.21
Metachromatic leukodystrophy	Autosomal recessive	rs74315479	p.E384K	0.0028	0.000025
Asphyxiating thoracic dystrophy 2	Autosomal recessive	rs138004478	p.G104R	0.0028	0.00009
Autoimmune lymphoproliferative syndrome type 2	Autosomal dominant	rs80358239	p.I406L	0.0085	0.0049
Congenital ichthyosis 1	Autosomal recessive	rs41295338	p.S42Y	0.0056	0.004
Bartter syndrome antenatal type 2	Autosomal recessive	rs59172778	p.M338T	0.0056	0.008
Becker muscular dystrophy	X-linked recessive	rs1800279	p.H2798R	0.051	0.026
Bethlem myopathy	Autosomal dominant/recessive	rs117725825	p.P932L	0.0028	0.0029
Biotinidase deficiency	Autosomal	rs35976361	p.I296V	0.011	0.004

Kuwait Genome project: Breast Cancer



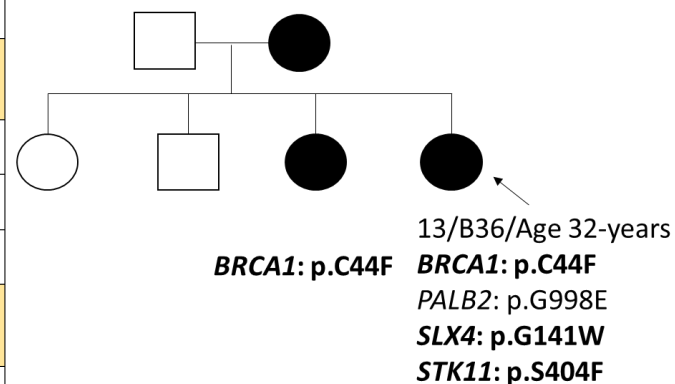
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Next-generation sequencing in familial breast cancer patients from Lebanon

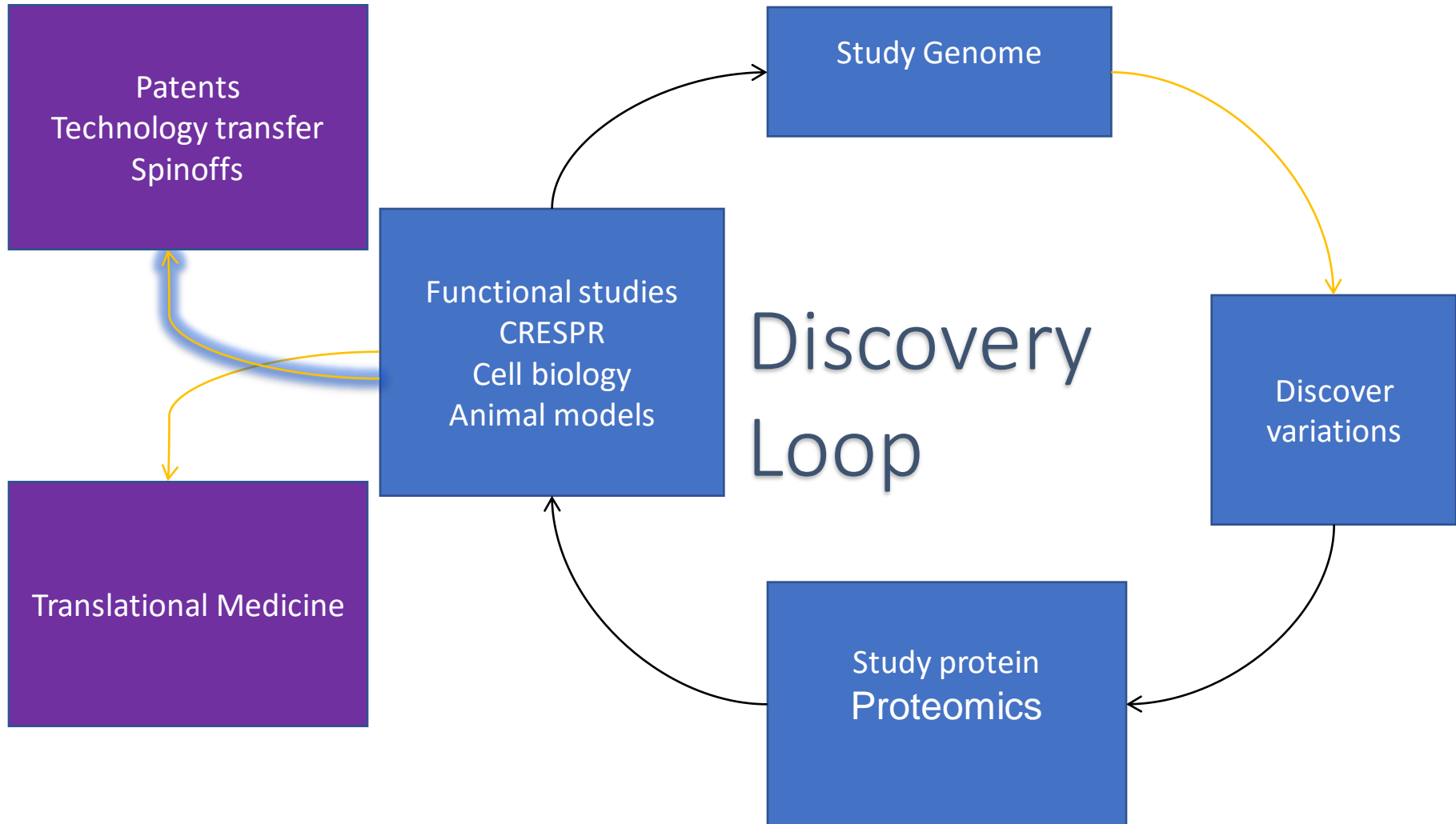
Nadine Jalkh¹, Eliane Chouery¹, Zahraa Haidar¹, Christina Khater², David Atallah³, Hamad Ali^{4,5}, Makia J. Marafie⁶, Mohamed R. Al-Mulla⁷, Fahd Al-Mulla^{5,8*} and Andre Megarbane^{9*}

Family 13



Gene	Variation	BIC database Clinically Importance/ Clinical Classification	COSMIC	Leiden Open Variation Database (LOVD)	BRCA Exchange
<i>BRCA1</i>	c.G131T p.C44F FOUNDER	unknown/ pending	Not found	Affects function	Not found
	c.A536G p.Y179C	unknown/ pending	Not found	Does not affect function	Benign
	c.C4327T p.R1443*	yes/ class 5	Neutral	Affects function	Not found
	c.A1067G p.Q356R	unknown/ pending	Pathogenic	Does not affect function	Benign
	c.5090_5093del GTTA p.L1697fs	Not found	Not found	Not found	Not found
<i>BRCA2</i>	c.C65T p.A22V	unknown/pending	Not found	Effect unknown	Not found
	c.G223C p.A75P	unknown/ pending	Not found	Does not affect function	Benign
	c.658_659delGT p.V220I*	yes/ class 5	Not found	Affects function	Not found
	c.C4061T p.T1354M	unknown/ pending	Neutral	Does not affect function	Benign
	c.G4258T p.D1420Y	no/ pending	Neutral	Does not affect function	Benign
	c.C5744T p.T1915M	no/ class 1	Neutral	Does not affect function	Not found
	c.G8775C p.Q2925H	unknown/ pending	Not found	Effect unknown	Not found
	c.A1114C p.N372H	no/ class 1	Neutral	Not found	Benign
	c.C1151T p.S384F	no/ pending	Not found	Not found	Benign

Discovery Loop



Lessons Learned



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Implementation of GM in the Kuwait public sector is challenging

Collaborations should be based on sincere partnerships

Significant opportunities for GM and discovery in the area