

New Trends in Clinical Genetics: Genomic Medicine

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LF MU 2025

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Outline

- ✓ Genomic medicine: motivation for MDs
- ✓ Genomes, genes, genetic variability
- ✓ Genomics and disease: applications
- ✓ Importance for MDs

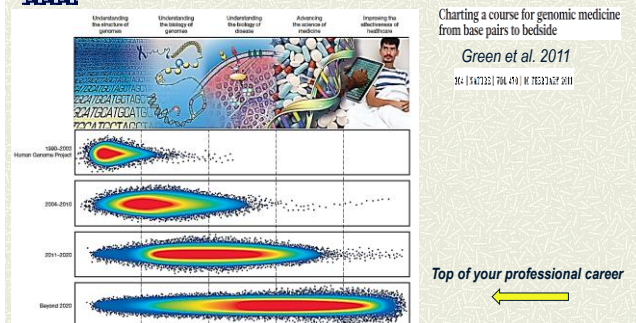
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Genomic medicine: 2011 prediction



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Genomic medicine: clinical practice

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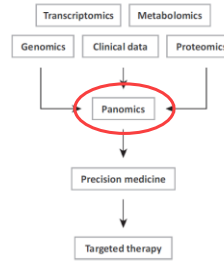
Implementing genomic medicine in the clinic: the future is here

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Precision medicine



Highlights

Genome sequencing costs are rapidly decreasing within the coming decade we might anticipate that whole-genome sequencing may be affordable for patients.

Automated, high-throughput DNA sequencing and probe sequencing platforms are currently creating terabytes of information, referred to as 'big data'.

Big data are characterized by the three V's: a large volume of data, a high velocity of data production occurring in real-time, and the variety of data that can encompass multiple omic subfields.

The analysis of big data has the potential to identify novel biomarkers of disease and targets for therapy. The analysis of large-scale datasets may enable the discovery of diagnostic or prognostic markers that are not readily apparent.

The complexity and vastness of data analysis may ultimately require the development of computational platforms to aid in the discovery of biological pathways underlying health and disease.

Panomics for Precision Medicine

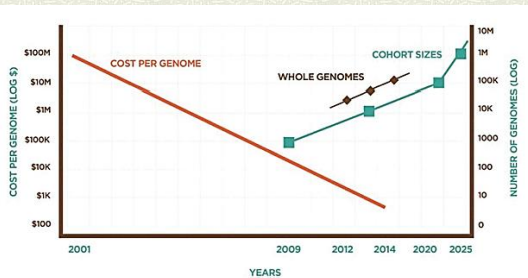
David S. Goff, MD, PhD¹, and Andrew Goff

Figure 1. Proposed Model of Precision Medicine Approaches. Data from omic subfields are integrated (panomics) to guide patient care in a manner that accounts for the genetic variation of each patient.

2. Trends in Molecular Medicine, Month Year, Vol. no, pp

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Genomic medicine - from theory to practice: financial aspects



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Genomic medicine: clinical practice

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<http://dx.doi.org/10.1586/14737159.2016.1146093>

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PERSPECTIVE

OPEN ACCESS

Toward clinical genomics in everyday medicine: perspectives and recommendations
Susan K. Delaney¹, Michael L. Hultner², Howard J. Jacob³, David H. Ledbetter⁴, Jeanette J. McCarthy⁵, Michael Balf⁶, Kenneth B. Beckmann⁷, John W. Belmont⁸, Cinnamon S. Bloss⁹, Michael F. Christman¹⁰, Andy Cosgrove¹¹, Stephen A. Damljan¹², Timothy Dantis¹³, Massimo Delledonne¹⁴, Michael J. Dougherty¹⁵, Joel T. Dudley¹⁶, W. Andrew Faucett¹⁷, Jennifer R. Friedman¹⁸, David H. Haase¹⁹, Tom S. Hays²⁰, Stu Heilsberg²¹, Jeff Huber²², Leah Kaminsky²³, Nikki Ledbetter²⁴, Warren H. Lee²⁵, Elissa Levin²⁶, Ondrej Libiger²⁷, Michael Lindenman²⁸, Richard L. Love²⁹, David C. Magnus³⁰, AnneMarie Martland³¹, Susan L. McClure³², Scott E. Megliff³³, Helen Messier³⁴, Robert L. Nussbaum³⁵, Latha Palaniappan³⁶, Bradley A. Patay³⁷, Bradley W. Popovich³⁸, John Quackenbush³⁹, Mark J. Savant⁴⁰, Michael M. Sur⁴¹, Sharon F. Terry⁴², Steven Tucker⁴³, William T. Wong⁴⁴ and Robert C. Green⁴⁵

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Recommendations for health care providers

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Genet Med. 2016 November ; 18(11): 1075-1084. doi:10.1038/gim.2016.17.

Recommendations for the Integration of Genomics into Clinical Practice

Sarah Bowdin, M.D.², Adel Gilbert, M.S.², Emma Bedoukian, M.S.³, Christopher Carew, M.B.A.², Margaret P Adams, M.D.⁴, John Belmont, M.D., Ph.D.⁵, Barbara Bernhardt, M.S.⁶, Leslie Biesecker, M.D.⁷, Hans T. Bjornsson, M.D., Ph.D.⁸, Miriam Blitzer, Ph.D.⁹, Lisa C. A. D'Alessandro, M.D.¹⁰, Matthew A. Dourado, M.D., Ph.D.¹¹, Laurie Demmer, M.D.¹², Alison Elliott, Ph.D.¹³, Gerald L. Feldman, M.D., Ph.D.¹⁴, Ian A. Glass, M.B.Ch.B., M.D.¹⁵, Gail Herman, M.D., Ph.D.¹⁶, Lucia Hindorf, Ph.D.¹⁷, Fuki Hisama, M.D.¹⁸, Louanne Hudgins, M.D., Ph.D.¹⁹, Bruce Korf, M.D., Ph.D.¹⁷, David H. Ledbetter, Ph.D.²⁰, Mindy Li, M.D.²¹, Shirley Likson, M.S.¹, Christian Marshall, Ph.D.²², Livia Medina, M.S.¹, M. Stephen Meyn, M.D., Ph.D.²³, Nassim Montaredi, M.Sc.¹, Cynthia Morton, Ph.D.²⁴, John J. Mulvihill, M.D.²⁵, Sharon E. Plon, M.D., Ph.D.²⁶, Heidi Rehm, Ph.D.²⁷, Amy Roberts, M.D.²⁸, Cheryl Shuman, M.S.^{1,2}, Nancy B. Spinner, Ph.D.¹⁰, D. James Stavropoulos, Ph.D.²⁹, Kathleen Valverde, M.S.³⁰, David J. Waggaman, M.D.³¹, Alisha Wilkens, M.S.¹, Ronald D. Cohn, M.D.^{1,2,7}, and Ian D. Krantz, M.D.^{2,27}

Translating and realizing the comprehensive clinical benefits of genomic medicine remains a key challenge for the current and future care of patients. With the increasing application of CGES, it is necessary for geneticists and other health care providers to understand its benefits and limitations, in order to interpret the clinical relevance of genomic variants identified in the context of health and disease. Establishing new, collaborative working relationships with specialists across diverse

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New philosophy in medicine: genomics as a holistic approach



Slide courtesy of Prof. Jamie McLeod, UK Lexington

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Holism and genomics: Genome is more than the sum of its genes

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1aigtgccgc cgcgggcct cctctgtg gcatctgg tctoctaa cacctggac
61 cacctagtt tggcaggaa cctcccaca gccacacag gccaggat
gttcagtg 121 ctcaacct ccaaaaact gctgaggacc gtcagcaaca
cgctcagaa gcccaggcaa 181 acctagaat tctactctg cactctgaa
gagatgac algaggat cacaagaac 241 aagagcagca cgtggcggc
ctgcctccc ctggaactg cccgaacga gattgcctg 301 gcttcagag
agatcttt cataactat gggagtgc tgaccccg aaaggcct 361
tctatgta cgctgtct tagcagc atgaggact tgaagatga ccagtgag
421 tcaaggcca tgaatgcca gctgtgata gatctcaga gccagatct
tclgtag 481 aacatgcta cagcaltga caagctgat caggcccta
actcaacag tgagactgt 541 ccaaaaagc cctccctga aggaclgat
tttataaaa claaagtaa gctctgac 601 ctctcatg cctcagaat
cgcgcagtg accatcaaca ggatgatgg cttctgat 661 gctcttaa
    
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Tools and resources

- ✓ DNA Sanger (1-2 kb)
- ✓ DNA NGS (whole genomes)
- ✓ DNA NGS LR: „HiFi“ (50 kb)
- ✓ **DNA exome**
- ✓ RNA IsoSeq: full-length cDNA

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Recent achievements

- ✓ T2T genome(s)
- ✓ Multiomics
- ✓ Pangenomics, pangenomes

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Multiomics

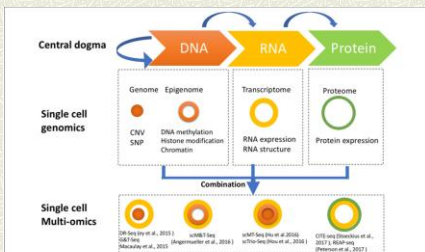


FIGURE 2 | Strategies for multi-omics profiling of single cells. Three main types of molecules relating to biological control systems (Fig. 1): Single-cell genomics methods profile the genome, epigenome, transcriptome, and proteome are shown by different shapes with variable colors (**Module**). Single-cell multi-omics methods are built by combining different single-cell sequencing methods to simultaneously profile multiple types of molecules of the single cell genome sets (**Bottom**). For example, scRNA-seq was built by combining genome (orange) and transcriptome (yellow) to simultaneously detect DNA and RNA of the same cell genome sets.

<https://doi.org/10.3389/fcell.2018.00028>

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Multiomics

Analysis of complex phenotypes/diseases at all levels

- ✓ Genome
- ✓ Epigenome
- ✓ Transcriptome
- ✓ Proteome
- ✓ Metabolome
- ✓ Microbiome

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Pangenomes

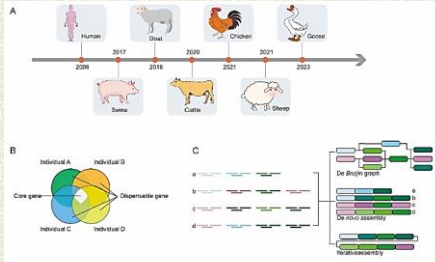


Figure 2. The development process and construction methods of pan-genomic research. (A) Numerous species have developed pan-genomes, including emiliania huxleyi. (B) Pan-genomes comprise core genes, dispensable genes, and strain-specific genes. (C) Pan-genome construction strategies include iterative assembly, de novo assembly, and graphical pan-genomes.

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Microbiome and immunogenome

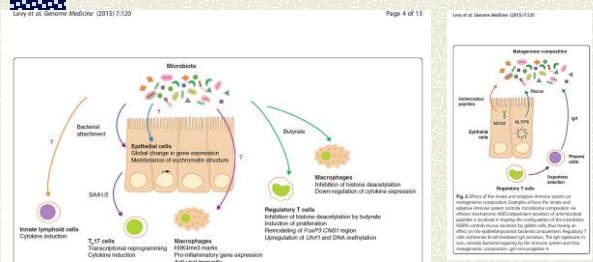
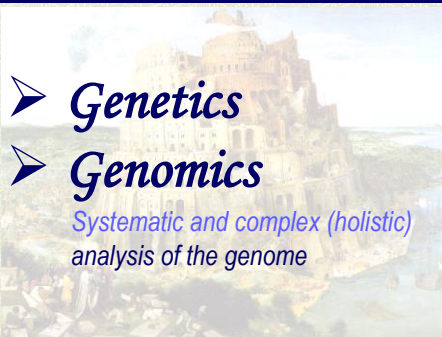


Fig. 1 Effects of the microbiome on host gene regulation. Examples of epigenetic and transcriptional changes induced by commensal colonization in the intestine. Arrows denote bacterial signals involved in the genetic programming of immune cells subsets and intestinal epithelial cells. Question marks indicate unknown microbial signals involved in the regulation of gene expression in macrophages, innate lymphoid cells, and intestinal epithelial cells. [27] [28]

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Terminology: confusion of languages



- **Genetics**
- **Genomics**
Systematic and complex (holistic) analysis of the genome

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Genetic variability: mutations vs. polymorphisms

- ✓ Polymorphisms as “established” mutations
- ✓ Mutations as causes of disease
- ✓ Genetic polymorphisms as causes of the variability in susceptibility/resistance (resilience) to disease

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Genetic variability in disease: different roles

- ✓ *Inherited diseases: causative genes*
- ✓ *Genetic susceptibility/resistance to disease provoked by environmental factors*

Both may be inherited in the Mendelian and/or non-Mendelian way

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An example: infectious diseases

Infectious agent	Clinical phenotype	Immunological phenotype	Gene
<i>Neisseria</i>	Invasive disease	MAC deficiency	C5, C6, C7, C8A, C8B, C9C, C9 PFC
<i>Mycobacteria</i>	Invasive disease MSMD Disseminated tuberculosis	Properdin deficiency IL-12/23-IFN- γ deficiency	<i>IFNGR1</i> , <i>IFNGR2</i> , <i>STAT1</i> , <i>NEMO</i> , <i>IL12B</i> , <i>IL12RB1</i>
<i>Streptococcus pneumoniae</i> Epstein-Barr virus	Invasive disease X-linked lymphoproliferative disease	IRAK-4 deficiency SAP deficiency	<i>IRAK4</i> <i>SH2D1A</i>
Human papillomavirus	Epidemiodyplasia verruciformis	EVER1 or EVER2 deficiency	<i>EVER1</i> , <i>EVER2</i>
<i>Plasmodium vivax</i> Human immunodeficiency virus-1	Natural resistance Natural resistance	Lack of receptor for pathogen Lack of receptor for pathogen	<i>DARC</i> <i>CCR5</i>
Norovirus	Natural resistance	Lack of receptor for pathogen	<i>FUT2</i>

Picard et al Curr Opin Immunol 2008

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Mutations vs. polymorphisms

- ✓ *Strong mutations: simple Mendelian inheritance*
- ✓ *Single nucleotide polymorphisms: underlie complex (quantitative) variability of traits/diseases*

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Inherited disease: two types of inheritance

- ✓ Mendelian: individual strong mutations
- ✓ Complex: interactions of multiple gene variants (**SNPs**) with moderate effects

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Reminder: individual variability of the human genome

Single nucleotide polymorphisms (SNPs): 10 M throughout the genome

cgcgggcctcctcttgggcatcctggctcctctaaaccacctggac

cgcgggcctcctccttgggtcatcctggctcctctaaaccacctggac

Insertions/deletions (indels)

cgcgggcctcctccttgggcatcctggctcctctaaaccacctggac

cgcgggcctcctccttggg-----ctggctcctctaaaccacctggac

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Single nucleotide polymorphisms (SNPs)

✓ Nucleotide sequence

cgcgggcctcctcttgggcatcctggctcctctaaaccacctggac

cgcgggcctcctcttgggtcatcctggctcctctaaaccacctggac

✓ Alleles

C, T

✓ Genotypes

CC, CT, TT

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Genomic medicine - from theory to practice: technical advances

Miniaturization and automation: chips and arrays

High Density (HD) Single Nucleotide Polymorphism (SNP) chips



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Mendelian vs. non-Mendelian inheritance, simple vs. complex traits

cgcgggcctcctcttgggcatcctggctcctctaaaccacctggac
cgcgggcctcctccttgggtcatcctggctcctctaaaccacctggac



Strong effect on the phenotype
Mendelian inheritance

cgcgggcctcctccttgggtcatcctggctcctctaaaccacctggac
cgcgggcctcctccttgggtcatcctggctcctctaaaccacctggac

Weak individual effects with no phenotypic manifestation



Strong effect on the phenotype
Non-Mendelian inheritance

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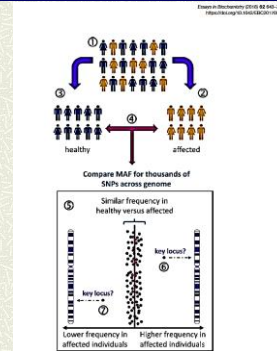
Genetics in complex diseases

Genomes in disease

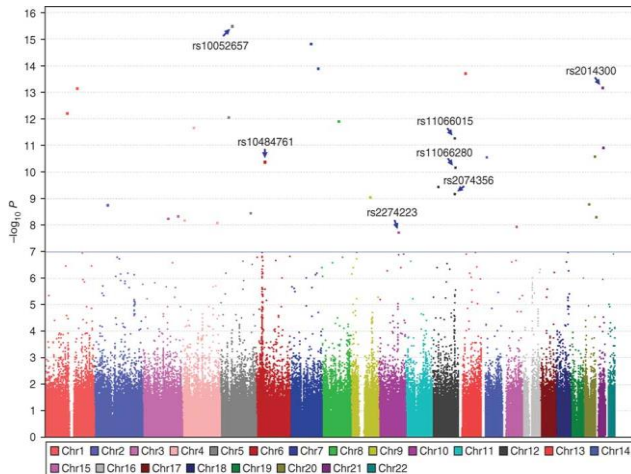
- ✓ 0.6% chromosome abnormalities
- ✓ 8% Mendelian diseases,
- ✓ 90% Multifactorial (complex) disease,
- ✓ 1.4% other than genetic problem

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A tool: Genome-wide association studies (GWAS)



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Example of a really complex disease: Genes associated with atherosclerosis/hypercholesterolemia and Alzheimer's disease

Family	Gene
Cholesterol and lipoprotein-related	A2M, ABCA1, APOA1, APOA4, APOC1, APOC2, APOC3, APOE , CD36, CETP, HMGCR, LDLR, LIPA, LRP1, LRP6, LPA, LPL, OLR1, SREBF1
Cytokines	CCL2, CCR2, IL1B, IL1RN, IL6, IL18, TGFB1, TNF
Oxidative stress	ALDH2, GSTM1, GSTT1, HFE, MPO, NOS3, PON1, PON2
Nuclear receptor and related	CYP19A1, ESR1, PPARA
Proteases	ACE, CST3, MMP1, MMP3, SERPINE1
Miscellaneous	BCH2, CBS, CD14, CRP, GNB3, HLA-A2, HTR6, ICAM1, MEF2A, MTHFR, PTGS2, TLR4

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ARTICLES

A genome-wide association study with 1,126,563 individuals identifies new risk loci for Alzheimer's disease

Table 1. The 28 genomic risk loci identified from 95,138 (6,617 proxy) cases and 1,028,225 (38,246 proxy) controls

Genomic locus	Gene	Position (Mb)	Lead variant	Allele frequency	P-value	R ²	
1	ACE	108,177	rs10443970	T	0.004	8.22 × 10 ⁻¹¹	176,279
2	APP	10,717,034	rs19795	C	0.001	2.62 × 10 ⁻¹¹	16,726
3	ACE2	2,351,225,435	rs1056637	C	0.0235	1.21 × 10 ⁻¹¹	17,737
4	APP	2,029,097,627	rs1044705	C	0.01	3.62 × 10 ⁻¹¹	109,242
5	APP	2,234,492,377	rs107763	C	0.01	4.23 × 10 ⁻¹¹	187,531
6	APP	41,611,822	rs1054765	G	0.18	5.21 × 10 ⁻¹¹	108,153
7	TNFR	8,158,422,386	rs107249	T	0.02	1.27 × 10 ⁻¹¹	108,954
8	APP	9,156,526,137	rs107964	G	0.07	7.91 × 10 ⁻¹¹	109,229
9	IL1A	6,212,612,012	rs107451	A	0.02	2.24 × 10 ⁻¹¹	79,141
10	APP	4,421,842,791	rs1073459	G	0.007	1.26 × 10 ⁻¹¹	191,428
11	CD3AP	4,422,222,001	rs107971	T	0.27	7.29 × 10 ⁻¹¹	122,226
12	APP	712,366,758	rs107934	C	0.01	2.30 × 10 ⁻¹¹	103,178
13	CD3AP	7,022,122,001	rs107451	T	0.01	6.21 × 10 ⁻¹¹	104,136
14	APP	7,942,124,127	rs107307	G	0.02	4.09 × 10 ⁻¹¹	117,525
15	APP	8,218,616,326	rs107370	T	0.01	1.22 × 10 ⁻¹¹	103,843
16	APP	8,141,182,011	rs107323	G	0.06	3.14 × 10 ⁻¹¹	102,383
17	CD3AP	12,217,762,752	rs107451	T	0.04	7.62 × 10 ⁻¹¹	102,387
18	CD3AP	10,411,781,522	rs107307	T	0.04	3.68 × 10 ⁻¹¹	126,188
19	APP	10,126,186,188	rs107451	T	0.04	6.21 × 10 ⁻¹¹	102,383
20	APP	10,622,027,048	rs107370	G	0.02	3.42 × 10 ⁻¹¹	122,324
21	APP	10,622,027,048	rs107370	G	0.02	1.24 × 10 ⁻¹¹	122,324
22	APP	10,121,829,187	rs107343	T	0.06	1.33 × 10 ⁻¹¹	102,383
23	APP	10,121,829,187	rs107343	T	0.06	6.21 × 10 ⁻¹¹	108,954
24	APP	10,121,829,187	rs107343	T	0.06	4.23 × 10 ⁻¹¹	176,162
25	APP	10,121,829,187	rs107343	T	0.06	6.21 × 10 ⁻¹¹	108,954
26	APP	10,121,829,187	rs107343	T	0.06	4.23 × 10 ⁻¹¹	176,162
27	CD3AP	12,217,762,752	rs107451	T	0.01	7.29 × 10 ⁻¹¹	102,383
28	APP	17,421,442,344	rs107307	T	0.05	1.81 × 10 ⁻¹¹	122,422
29	APP	17,421,442,344	rs107307	T	0.05	6.21 × 10 ⁻¹¹	108,954
30	CD3AP	17,421,442,344	rs107307	T	0.05	7.62 × 10 ⁻¹¹	102,383
31	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324
32	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324
33	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324
34	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324
35	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324
36	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324
37	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324
38	APP	17,421,442,344	rs107307	T	0.05	1.24 × 10 ⁻¹¹	122,324

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Applications

- ✓ Genetic prevention: prenatal screening
- ✓ Genetic counselling
- ✓ Genetic diagnostics

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Genomics and diagnostics

- ✓ Cytogenetic diagnostics (karyotype, FISH, CGH)
- ✓ Molecular diagnostics (sequencing, candidate gene and GWAS markers)

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Genomics in Mendelian diseases: Examples of practical applications

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Table 1. Summary of genetic testing.

Test type	Purpose description	Current example(s)
Diagnostic testing	To precisely identify a disease and assist in clinical decision-making	Creatine kinase (CK) level testing for Duchenne muscular dystrophy
Predictive testing	To predict the likelihood of developing a disease	HIT gene test for Huntington disease; BRCA gene testing for breast cancer
Carrier testing	To understand the likelihood of passing a genetic disease to a child	CFTR gene testing for cystic fibrosis
Prenatal testing	To identify disease in a fetus	Expanded alpha-fetoprotein (AFP) for risk of neural tube defects, such as spina bifida and Down syndrome
Newborn screening	To determine if a newborn has a disease known to cause problems in health and development	All states must screen for at least 21 disorders by law, and some states test for 30 or more. Metabolic (e.g. classic galactosemia (GALT)), endocrine (e.g. congenital hypothyroidism) and other disorders tested
Pharmacogenomics (PG) testing	To determine the optimal drug therapy and dose given a person's metabolic response	The vitamin K epoxide reductase complex subunit 1 (VKORC1) test for likely response to the anticoagulant warfarin; TPMT gene testing for likely response to thiopurine immunosuppressive therapies
Research testing	To contribute to our understanding of underlying cause of disease	Genome-wide association studies (GWAS) to determine the association of a variant with a trait

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Massive molecular testing: panels

- ✓ The carrier status (heterozygosity)
- ✓ Infertility, donors of sexual cells and embryos
- ✓ More than 830 most common mutations in 77 genes causing more than 60 AR DO
- ✓ Oncological panel „CZECANCA“ (CZEch CAncer paNel for Clinical Application: 226 genes associated with inherited predisposition (population specific again)
- ✓ Whole exome sequencing

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Prenatal genetic testing

1122

Human Genetics (2020) 139:1121–1130

Fig. 1 Prenatal genetic testing and screening timeline: a Pre-genomic era, b genomic era

1956: Amniocentesis for Gender, Rh status	Low resolution
1966: Culture of amniotic fluid cells	
1967: First prenatal Down syndrome diagnoses	
1970's: Amniocentesis trials: US, Canada, UK	Limited Number of conditions
1980's - early 1990's: chorionic villus sampling (CVS) trials	
Late 1980's-1990's: MSAFP, serum screening T21, T18	
Late 1990's-2000's: First trimester screening T21, T18, (T13)	Genomics
2000's: Chromosomal microarray (CMA)	
2012: NICHD CMA trial & emergence of cfDNA screening	High resolution More conditions
2010's: Expanded carrier screening	Fetal Precision Diagnosis
2014-2019 and beyond: fetal exome sequencing begins	
2019: fetal genome sequencing studies start	
FUTURE: Non-invasive fetal genome analysis?	

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Molecular diagnostics in reproductive medicine

- ✓ Fetal cell free cfDNA in maternal blood: non-invasive testing NIPT
- ✓ Karyomapping: *in vitro* testing of embryos
- ✓ High-resolution non-invasive fetal exome screening and WGS

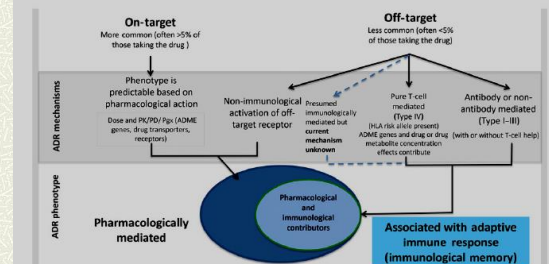
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Preimplantation genetic diagnostics (PGD)

- ✓ During assisted reproduction procedures - IVF
- ✓ Diagnostics of embryos: targeted or screening
- ✓ PCR and linkage analysis using STR markers
- ✓ Selection of embryos
- ✓ Opportunity to get rid of a familial burden

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Pharmacogenetics: ADR



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Variability related to side-effects of drugs

“On-target”

Is due to polymorphisms in genes encoding proteins involved in mechanisms of drug action, e.g. signaling molecules and/or cell metabolism pathways

“Off-target”

Is due to polymorphisms in genes affecting reactions of the organism to a drug. However, these reactions are not related to its curative effects. They are mostly represented by undesirable immune reactions (hypersensitivity) to the drug and associated with underlying immune response genes

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Pharmacogenetics: a commercial offer

Inhibitory protonové pumpy: Dexlansoprazol (A02BC06), Lansoprazol (A02BC03), Omeprazol (A02BC01), Pantoprazol (A02BC02), Raboprazol (A02BC04), **Antiemetika:** Dronabinol (A04AD10), Meloklopramid (A03FA01), Ondansetron (A04AA01), Tropisetron (A04AA03), **Perorální antidiabetika:** Glibenzklamid (A10BD01), **Antifibrinolytika/Antikoagulantia:** Avatrombopas (E02D0308), Kaspogrel (E01AC04), Warfarin (B01AA03), **Antiaritmiika:** Flecainid (C01BC04), Propafenon (C01BC03), **Hypotenziiva:** ACE inhibitory (C09A), Hydrochlorothiazid (C03EA01), **Inhibitory HMG-CoA reduktazy (statiny):** Aclorvastatin (C10AA05), Pravastatin (C10AA03), Rosuvastatin (C10AA07), Simvastatin (C10AA01), **Gynekologika:** Elibarsetin (G02CX02), Hormonální antikoncepce (G03A), **Antinfekční látky:** Fluoxacinil (J01CF05), Vorikonazol (J02AC03), **Tuberkulóstatika:** Ethambutol (J04AK02), Isoniazid (J04AC01), Pyrazinamid (J04AM05), Rifampicin (J04AB03), **Antivirotika:** Abacavir (J05AF06), Efavirenz (J05AG03), Nevirapin (J05AG01), Peginterferon alfa-2a/b (L03AB11), Ribavirin (J05AP01), Telaprevir (J05AF02), **Cytostatika:** Asparaginasa (L01DX02), Erdafitinib (L01EX16), Fluorouracil (L01BC02), Gefitinib (L01EB01), Gemcitabin (L01BC05), Irinotecan (L01CE02), Kapecitabin (L01BC06), Lapatinib (L01EH01), Merkaptopurin (L01BB02), Methotrexat (L01BA01), Platínové preparáty (L01XJ01X), Tamoxifen (L02BA01), Tegalur (L01BC03), Trogidanin (L01BB03), **Imunoterapeutika:** Azathioprin (L04AX01), Eflunersip (L04AB01), Siponimod (L04AX02), Takrolimus (L04AD02), Takrolimus (L04AD02), Ustekinumab (L04AC05), **Nesteroidní protizánětlivé láky (NSAID):** Celekoxib (M01AH01), Flurbiprofen (M01AE09), Ibuprofen (M01AE01), Lornoxicam (M01AC05), Meloxicam (M01AC06), Piroxicam (M01AC01), Tenoxicam (M01AC02), **Urikostatika:** Allopurinol (M04AA01), Rasburicasa (V03AF07), **Inhaláční anestetika:** Inhaláční anestetika (N01AB), Mivacurium (N03AC10), Succinylcholin (N03AB01), **Analgika:** Dihydrokodein (N02AA08), Fentanyl (N01AH01), Fentanyl (N01AH01), Kodein (N02AA09), Lofedolín (N02DC04), Oxycodón (N02AA05), Tramadol (N02AX02), **Antiepileptika:** Brivaracetam (N03AX23), Fenitoin (N03AB02), Fenytoin (N03AB02), Karbamazepin (N03AF01), Oxcarbazepin (N03AF02), **Jiná psychofarmaka:** Arpiprazol (N05AX12), Brexpiprazol (N05AX16), Clozapin (N05BA09), Clozapin (N05AH02), Hoperidol (N05AX14), Thionidazin (N05AC02), Venlafaxin (N06AX16), Vortioxetin (N06AX26), **Tricyklická antidepresiva:** Amitriptylin (N06AA09), Clomipramin (N06AA04), Desipramin (N06AA12), Imipramin (N06AA02), Nortriptylin (N06AA10), Trimipramin (N06AA06), **Selektivní inhibitory zpětného vychytávání serotoninu (SSRI):** Citalopram (N06AB04), Escitalopram (N06AB10), Sertralin (N06AB01), Fluvoxamin (N06AB08), Paroxetin (N06AB05), **Jiná léčiva nervového systému:** Amifampidin (N07X05), Alonoxetin (N06BA09), Pimozid (N05AG02), Tetrabenazin (N07XX13), **Antimalarika:** Primačin (P01BA03), Tafenočin (P01BA07)

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The future of genome editing (?)

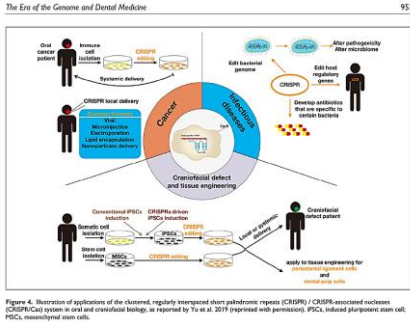


Figure 4. Illustration of applications of the clustered, regularly interspaced short palindromic repeats (CRISPR) / CRISPR-associated nucleases (CRISPR/Cas) system in oral and craniofacial biology, as reported by Yu et al., 2019 (reprinted with permission). iPSC, induced pluripotent stem cell; MSC, mesenchymal stem cell.

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The near future in genomic medicine

- ✓ *Inherited diseases: causative genes*
- ✓ *Genetic susceptibility/resistance to disease provoked by environmental factors*

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Disease

Reaction of an organism to pathogenic insults

Affected by the nature of the insults, environmental factors, current condition of the organism and its genetic make-up

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Mechanisms of immunity-related diseases studied with genomic tools

- ✓ Infections
- ✓ Allergies
- ✓ Autoimmunity
- ✓ Complex immunopathologies

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A model example: genetics of susceptibility to infections

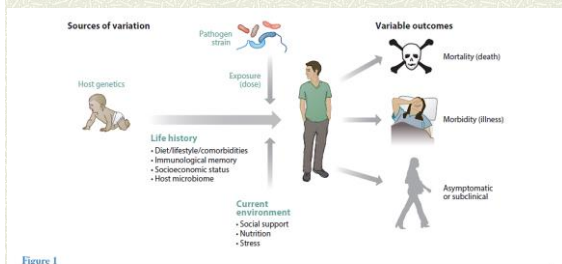


Figure 1

Sources of variable infection outcomes. Host genetics, which is fixed at conception, life history and current environment generate differing susceptibilities in exposed individuals. Beyond host susceptibility, pathogen genetics (virulence) as well as dose also contribute to a wide range of clinical outcomes from most infectious diseases.

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Genetic susceptibility to disease as a complex trait

Leading Edge
Essay

Cell

Infctogenomics: Insights from the Host Genome into Infectious Diseases

Paul Kellum¹ and Robin A. Weiss^{1*}
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 DOI: 10.1016/j.cell.2008.02.003

Five years into the human postgenomic era, we are gaining considerable knowledge about host-pathogen interactions through host genomes. This "infctogenomics" approach should yield further insights into both diagnostic and therapeutic advances, as well as normal cellular function.

Cell 124, February 24, 2008 ©2008 Elsevier Inc. 695

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Genetics of vaccination

Table 3. Heritability estimates of vaccination responses in twin studies

Vaccine	Parameter	DZ ^a	MZ ^a	Population	Age	Study	Heritability, %	95% CI %	References
Measles	antibody	55	45	USA ^b	2-18 years	cross-sectional	89	≥ 52 ^c	18
Mumps	antibody	55	45	USA ^b	2-18 years	cross-sectional	39	≥ 2 ^c	18
Rubella	antibody	55	45	USA ^b	2-18 years	cross-sectional	46	≥ 2 ^c	18
HAV	antibody	95	96	Germany	18-65 years	prospective	36	-2-73	15
HBsAg	antibody	95	96	Germany	18-65 years	prospective	61	-1-81	15
HBsAg	antibody	159	48	Gambia	5 months	prospective	77	-3-85	12 ^d
Polio	antibody	159	48	Gambia	5 months	prospective	60	-3-73	12
Tetanus	antibody	159	48	Gambia	5 months	prospective	44	-6-70	12
Tetanus	IL-13	159	48	Gambia	5 months	prospective	64	-0-75	12
Diphtheria	antibody	159	48	Gambia	5 months	prospective	49	-7-77	12
Hib	antibody	147	43	Gambia	5 months	prospective	51	-2-66	14
Pertussis									
Pertactin	IFN-γ	159	48	Gambia	5 months	prospective	53	-5-67	12
FHA	IFN-γ	159	48	Gambia	5 months	prospective	65	-0-76	12
Toxin	IL-13	159	48	Gambia	5 months	prospective	57	-0-71	12
BCG									
PPD	IFN-γ	159	48	Gambia	5 months	prospective	41	-10-71	12
KMTB	IFN-γ	159	48	Gambia	5 months	prospective	39	-3-71	12

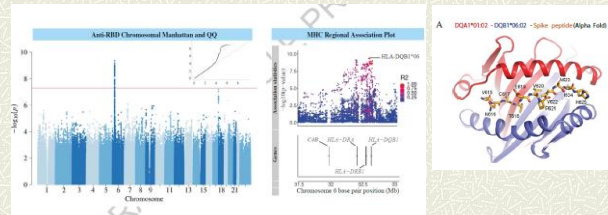
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Genetics of vaccination: Covid-19

nature medicine

Accelerated Article Preview

Human leukocyte antigen alleles associate with COVID-19 vaccine immunogenicity and risk of breakthrough infection



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Ethical issues: how to cope with information generated by genomic techniques

Examples

- ✓ Mendelian diseases:
e.g. *carrier tests, PGD*
- ✓ Complex diseases
e.g. *interpretation of GWAS, DTC*

Only people understanding principles can cope with this problem

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Outline

- ✓ *Genomic medicine: motivation for MDs*
- ✓ *Genomes, genes, genetic variability*
- ✓ *Genomics and disease: applications*
- ✓ *Importance for MDs*

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Practical applications

Minimum variant for you

- ✓ *To know, when and where to refer a patient for a genetic consultation*
- ✓ *To know how to interpret clinical geneticist's reports*
- ✓ *To know when not to refer a patient for a genetic consultation*

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Questions even at this moment?



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