



A North African perspectives on the commission's work

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Public “debate” and genomics in North Africa



Tunis January 14th, 2011

*The International Commission on the Clinical Use
of Human Germline Genome Editing*



Inauguration of the space “DNA for All”, CST, April 25th, 2018



<http://www.cst.rnu.tn/>

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Prenatal diagnosis and IVF in North Africa

- IVF available (Public/Private sectors)
- Prenatal diagnosis available (Public/Private)
- Cultural and religious acceptability: allowed anytime during pregnancy but more easily accepted if <12 weeks.



The Experience of a Tunisian Referral Centre in Prenatal Diagnosis of *Xeroderma pigmentosum*

From a legal point of view, we expected to have more families to investigate. Indeed, in Tunisia, abortion has been allowed since 1973 (Act No. 73-2 of September 26, 1973). Tunisia is one of the few Arab countries that imposes no legal abortion during the statutory period (excluding time and medical staff), which makes the country one of the exceptions of the African continent and among Arab countries. After the 12th week of pregnancy, certain conditions must be met for an abortion. From a religious point of view, contrary to common belief, Islam does not prohibit abortion. It is permitted if the pregnancy is aged less than 120 days and only in cases where the medical staff states that the foetus will suffer from a severely disabling and life-threatening disease. Nevertheless, many families choose not to have an abortion even if they know that the foetus will suffer from a severe disease. If the diagnosis is established after the period of 120 days of pregnancy (4 lunar months: when the soul has been ‘breathed into the foetus’), then abortion is not allowed, unless the mother’s life is in danger (from Ahkaam al-Janeen fi’l-Fiqh al-Islami, by ‘Umar ibn Muhammad ibn Ibraaheem Ghaanim).

The prenatal genetic counselling was done without specific mention to religion. Each couple was informed about the risk of having an affected child and being confronted with the decision to terminate pregnancy, if prenatal molecular diagnosis shows that the foetus is homozygous for the mutation. In case the parents did not accept to abort the affected foetus, PND was not chosen because of the low benefit for the couple and to avoid the risk of miscarriages associated to foetal cell sampling. The counselling geneticist should be neutral without having sociocultural or religious implications.



Pre-implantation Genetic Diagnosis in North Africa

Available in the private sector for a limited set of diseases

Les maladies monogéniques

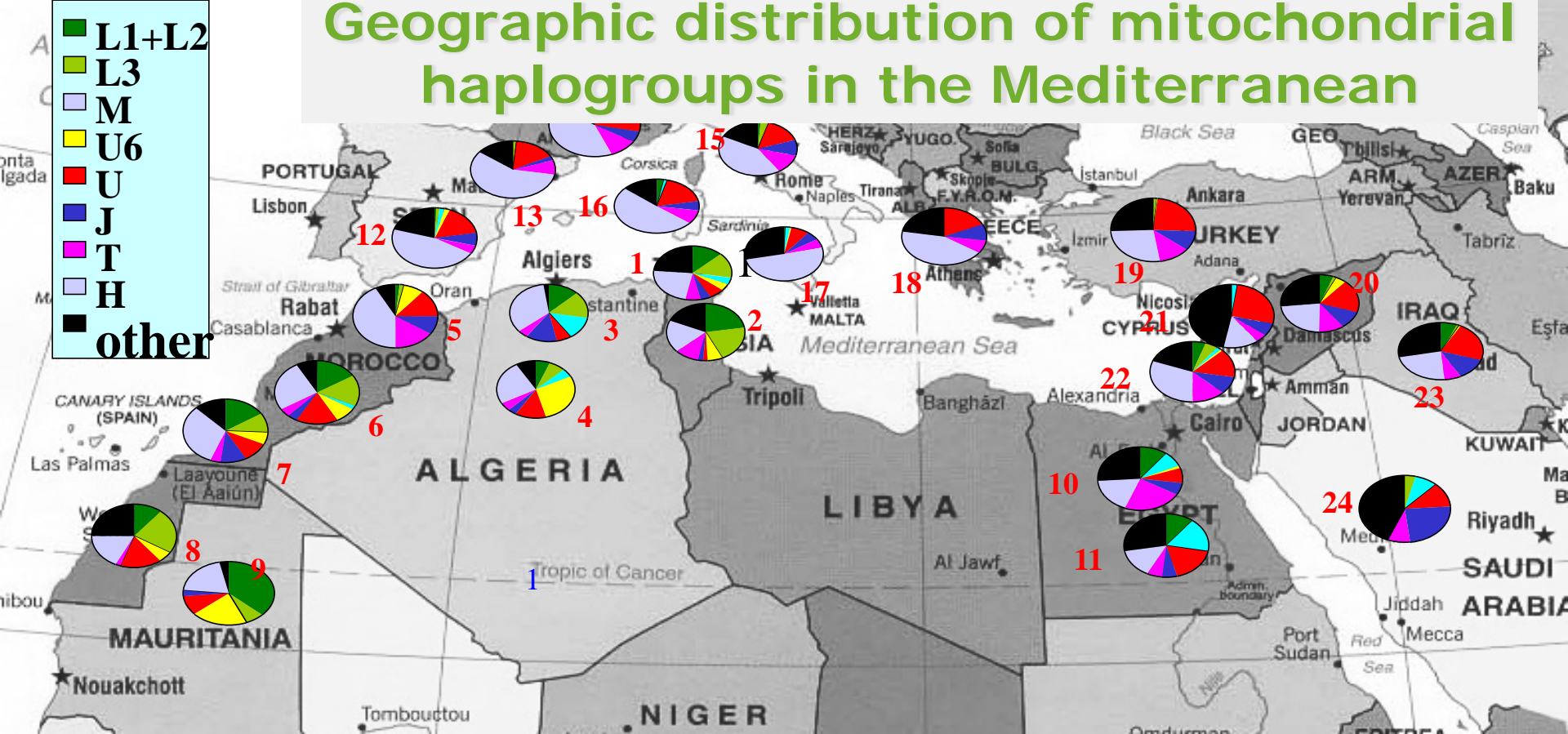
- Myopathie
- Mucoviscidose
- Neurofibromatose
- Béta-thalassémie
- Rétinite pigmentaire
- Dystrophie musculaire de Becker
- Hémophilie
- Maladie de Huntington

Anomalie chromosomique

Le **DPI** peut être indiqué lorsque l'un des partenaires d'un couple est porteur d'une anomalie chromosomique de structure équilibrée chez lui, mais pouvant aboutir à un génotype déséquilibré pathogénique ou létal chez le fœtus (fausses couches):

- Translocation
- Inversion
- Dans d'autres cas, la sélection d'un embryon d'un sexe donné permet de garantir l'absence d'une maladie si cette dernière ne concerne qu'un seul sexe (**maladie liée au sexe**).

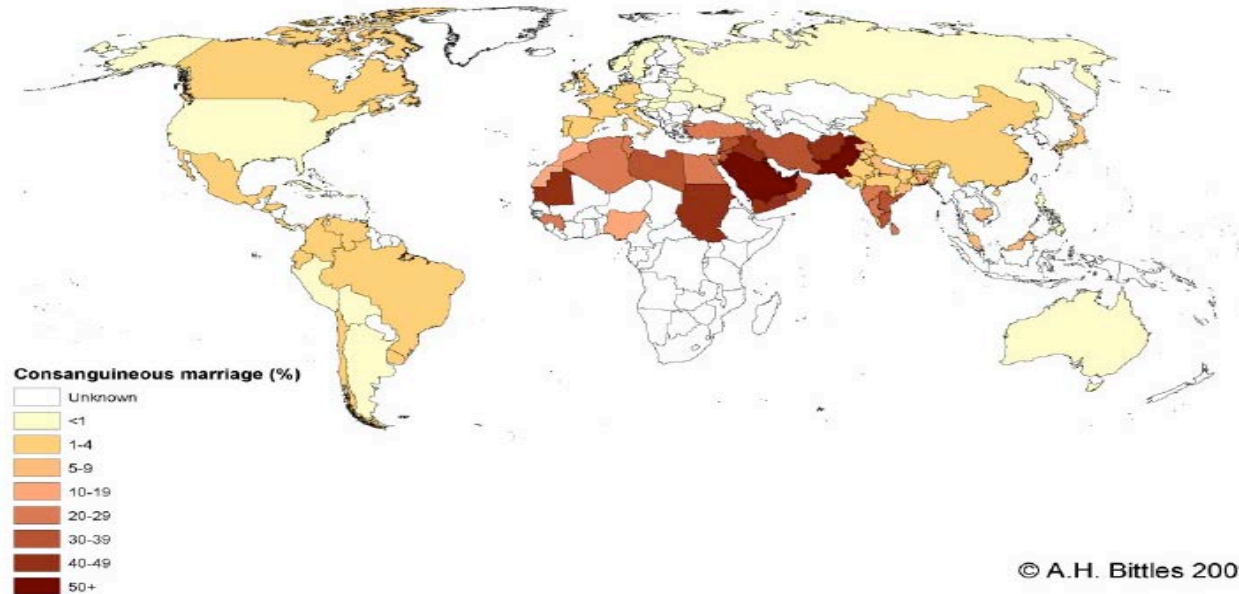
Geographic distribution of mitochondrial haplogroups in the Mediterranean



1:TUN, 2:MAK, 3: ALG, 4: MOZ, 5: MBN, 6: MAR, 7: SOU, 8: SAH, 9: MAU, 10: EGY, 11: GUR, 12: AND, 13: CAT, 14: FR, 15: ITA, 16: SAR, 17: SIC, 18: GRE, 19: TUR, 20: SYR, 21: DRU, 22: PAL, 23: IRA, 24: BED

Consanguineous marriages in MENA region

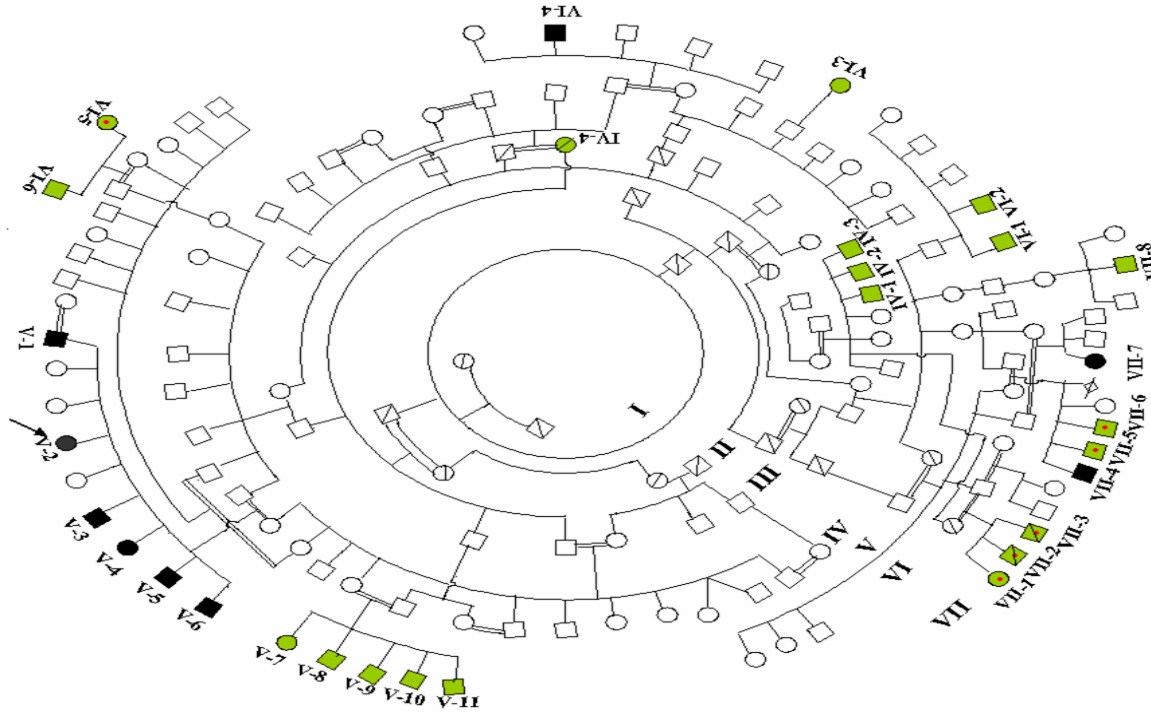
If we have beauty, intelligence and wealth in the family, why look outside?



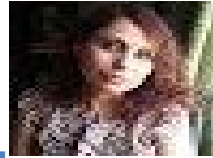
© A.H. Bittles 2009



Pedigree of a family affected by achromatopsia mental impairment and/or myopathy

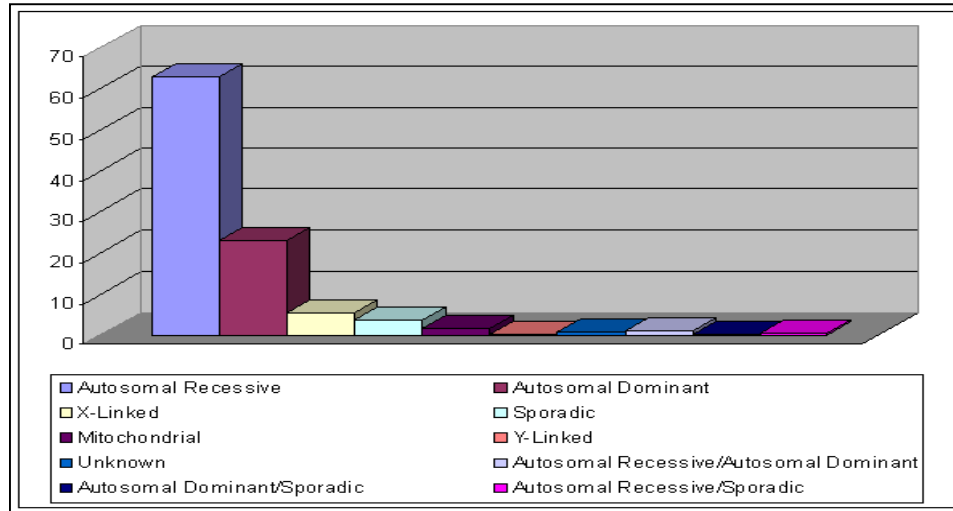


Genetic diseases in Tunisia: > 400

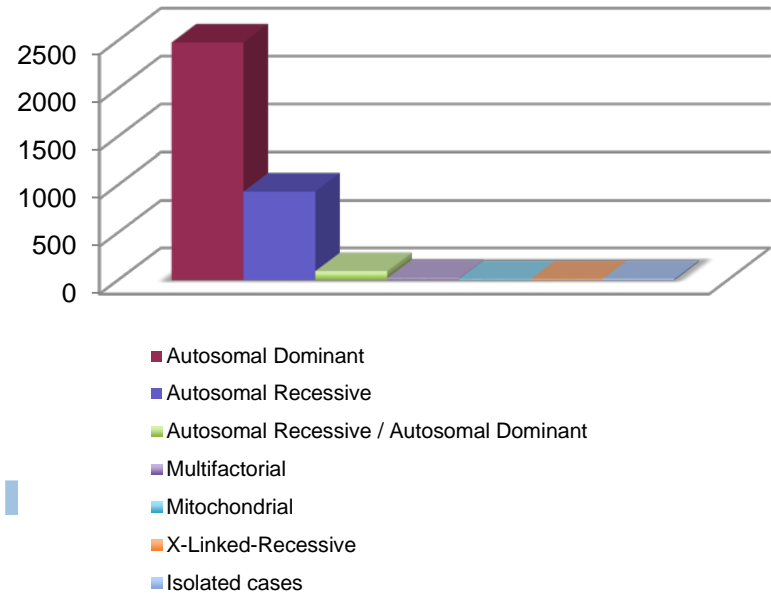


Distribution of genetic diseases by the mode of inheritance

In Tunisia



In OMIM



RESEARCH REVIEW

AMERICAN JOURNAL OF
medical genetics

Genetic Diseases in the Tunisian Population

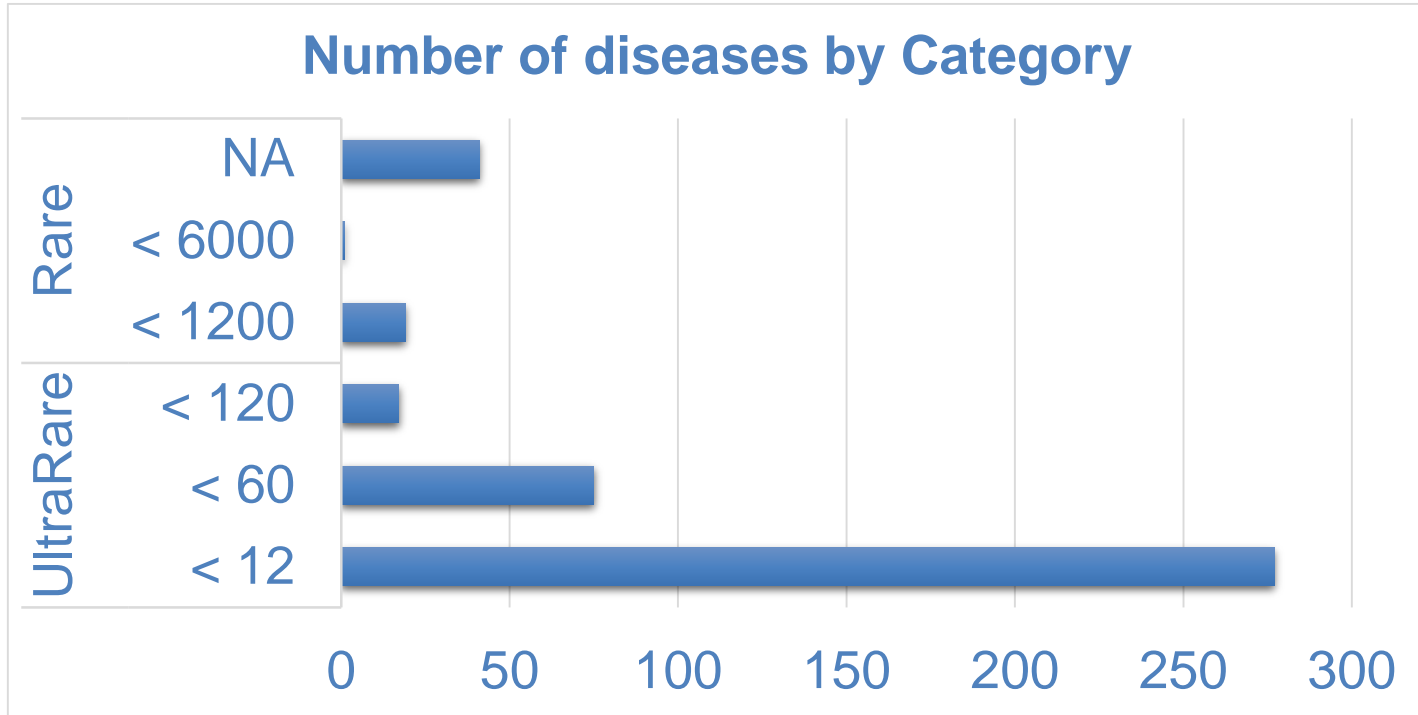
Lilia Romdhane, Sonia Abdelhak* for the Research Unit on Molecular Investigation of Genetic Orphan Diseases[†] and Collaborators[‡]

Research Unit on "Molecular Investigation of Genetic Orphan Diseases" Institut Pasteur de Tunis, Tunis, Tunisia

Received 6 September 2009; Accepted 25 August 2010



Number of Rare Diseases in Tunisia according to the number of patients/disease



Romdhane L, Mezzi N, Abdelhak S unpublished data



Will the GM individual have no (other) (genetic) disease?

- Neo-mutation? Mosaicism? Co-occurrence of 2+ diseases?

Original Paper

Public Health Genomics 2013;16:251–254
DOI: 10.1159/000354584

According to our experience in rare diseases in Tunisia, in some cases, 2 or more diseases cosegregate within the same family [9]. Even if this event is rare, the genetic counsellor should be aware of this possibility, in order to avoid the very unlikely case that the foetus is excluded of having the screened mutation but bares another mutation which is responsible for another disease.



Original Article

Comorbidity in the Tunisian population

Romdhane L., Messaoud O., Bouyacoub Y., Kerkeni E., Naouali C., Cherif Ben Abdallah L., Tiar A., Charfeddine C., Monastiri K., Chabchoub I., Hachicha M., Tadmouri G.O., Romeo G., Abdelhak S. Comorbidity in the Tunisian population. Clin Genet 2015. © John Wiley & Sons A/S. Published by John Wiley & Sons Ltd, 2015

Genetic diseases in the Tunisian population represent a real problem of public health as their spectrum encompasses more than 400 disorders. Their frequency and distribution in the country have been influenced by demographic, economic and social features especially consanguinity. In this article, we report on genetic disease association referred to as comorbidity and discuss factors influencing their expressivity. Seventy-five disease associations have been reported among Tunisian families. This comorbidity could be individual or familial. In 39 comorbid associations, consanguinity was noted. Twenty-one founder and 11 private mutations are the cause of 34 primary diseases and 13 of associated diseases. As the information dealing with this phenomenon is fragmented, we proposed to centralize it in this report in order to draw both clinicians' and researcher's attention on the occurrence of such disease associations in inbred populations as it makes genetic counseling and prenatal diagnosis challenging even when mutations are known.

L. Romdhane^{a,b}, O. Messaoud^a, Y. Bouyacoub^a, E. Kerkeni^c, C. Naouali^a, L. Cherif Ben Abdallah^a, A. Tiar^a, C. Charfeddine^a, K. Monastiri^d, I. Chabchoub^e, M. Hachicha^a, G.O. Tadmouri^f, G. Romeo^g and S. Abdelhak^a

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Do we really know that much about genetic diseases?

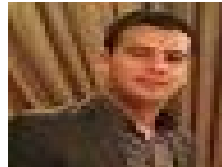


Long Runs of Homozygosity Are Enriched for Deleterious Variation

Zachary A. Szpiech,^{1,2,*} Jishu Xu,³ Trevor J. Pemberton,^{2,4} Weiping Peng,³ Sebastian Zöllner,^{5,6} Noah A. Rosenberg,^{2,7} and Jun Z. Li^{3,7}

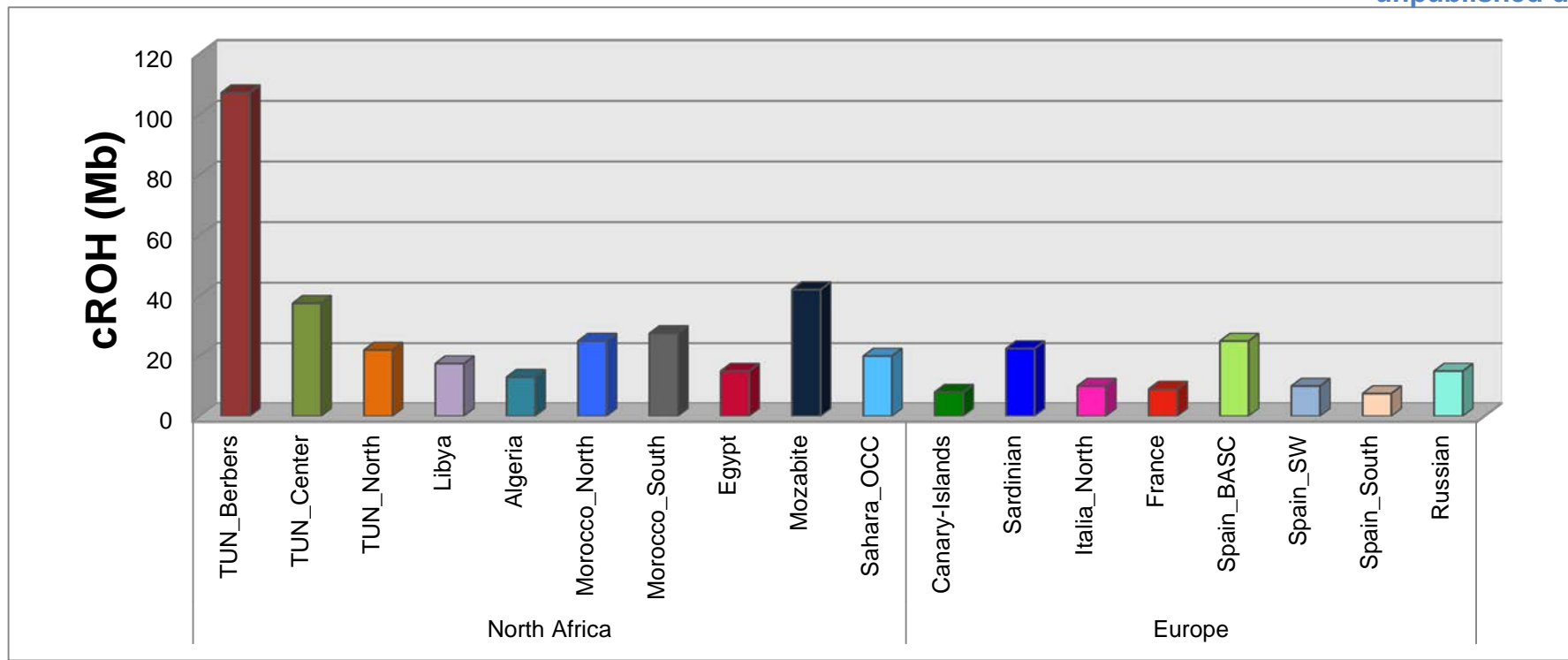
Exome sequencing offers the potential to study the population-genomic variables that underlie patterns of deleterious variation. Runs of homozygosity (ROH) are long stretches of consecutive homozygous genotypes probably reflecting segments shared identically by descent as the result of processes such as consanguinity, population size reduction, and natural selection. The relationship between ROH and patterns of predicted deleterious variation can provide insight into the way in which these processes contribute to the maintenance of deleterious variants. Here, we use exome sequencing to examine ROH in relation to the distribution of deleterious variation in 27 individuals of varying levels of apparent inbreeding from 6 human populations. A significantly greater fraction of all genome-wide predicted damaging homozygotes fall in ROH than would be expected from the corresponding fraction of nondamaging homozygotes in ROH ($p < 0.001$). This pattern is strongest for long ROH ($p < 0.05$). ROH, and especially long ROH, harbor disproportionately more deleterious homozygotes than would be expected on the basis of the total ROH coverage of the genome and the genomic distribution of nondamaging homozygotes. The results accord with a hypothesis that recent inbreeding, which generates long ROH, enables rare deleterious variants to exist in homozygous form. Thus, just as inbreeding can elevate the occurrence of rare recessive diseases that represent homozygotes for strongly deleterious mutations, inbreeding magnifies the occurrence of mildly deleterious variants as well.





Nagara et al.
unpublished data

Cumulative Runs of Homozygosity (cROH) in Europe and in different Southern Mediterranean country



Unanticipated findings in “routine” mutational screening: non penetrant homozygous individuals



Charfeddine C. et al.
unpublished data

“Unaffected” homozygous carriers: individuals in a family screened positive for a deleterious recessive mutation:

- Fanconi anemia (*FANCA* mutated siblings screened for bone marrow transplant).
- Niemann-Pick disease type B (homozygous mothers)
- Primary hyperoxaluria
- Gaucher disease
- Hypogonadotropic hypogonadism (transient fertility/infertility)



**Are we sure to target the right gene?
variant?**

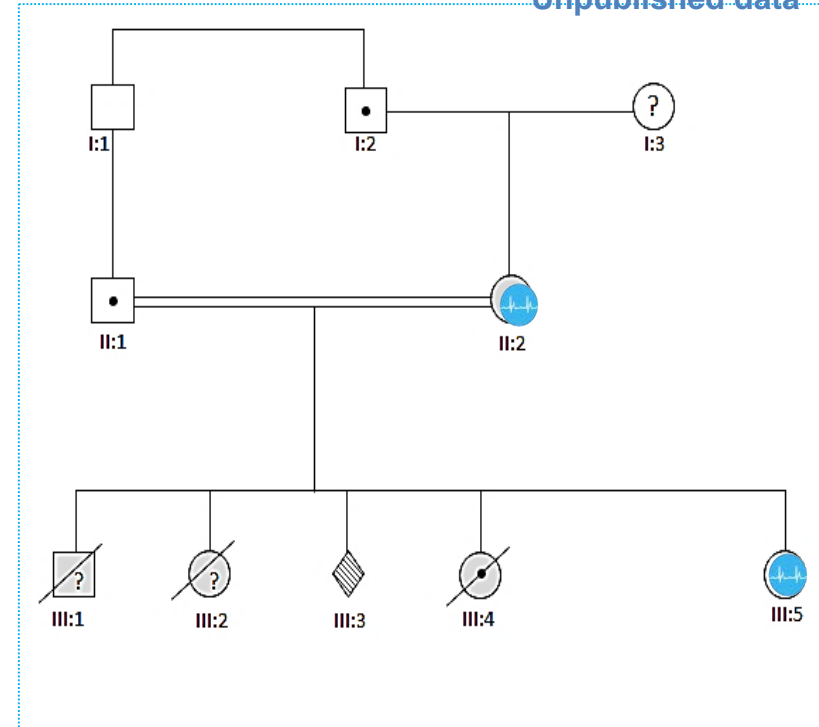


Molecular investigation (WES) of a consanguineous family with Sudden Cardiac Death (SCD)



Jaouadi H et al.
Unpublished data

Variant	Phénotype	Score-CADD
OBSCN : p.Arg6855Ser	CMH CMD	35
DSC2 : p.Ser868Phe	CAVD	31
VCL : p.Leu682Phe	CMH15 CMD	23.3
RBM20 : p.Ser455Leu	CMD	23.3
RYR2 : p.Asp1220Glu	TVPC CAVD	23.2
AKAP9 : p.Arg1609Lys	LQT11	22.8
CACNA1C : p.Gly1795Arg	LQT8 Sd. Timothy	17.26



A “new” gene and a “new” phenotype?

Research Article

2017



EMBO
Molecular Medicine

TECRL, a new life-threatening inherited arrhythmia gene associated with overlapping clinical features of both LQTS and CPVT

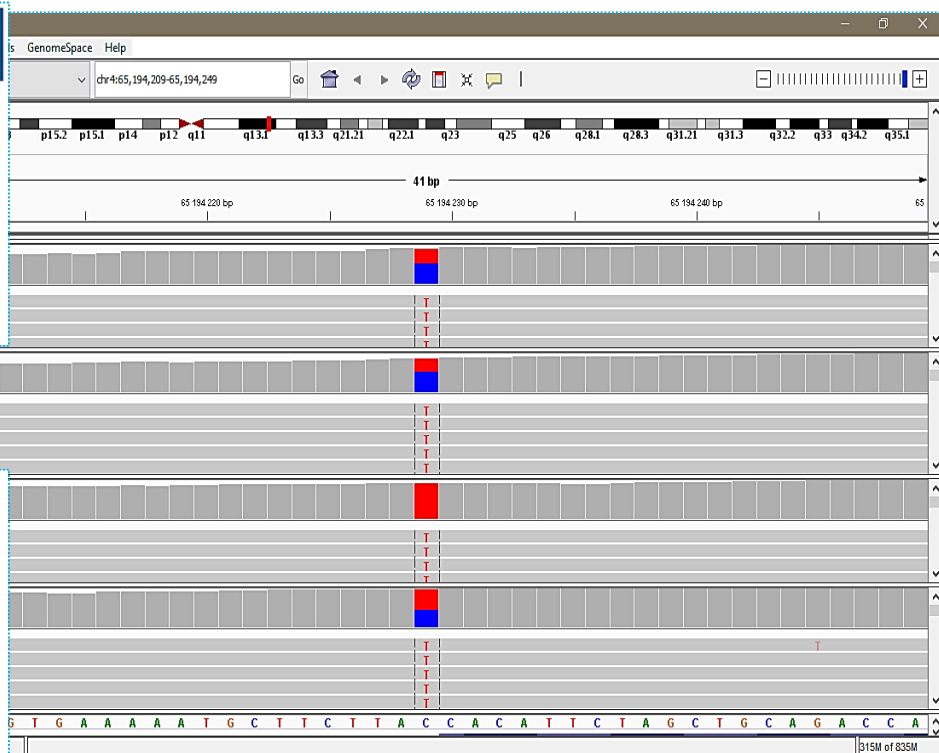
Harsha D Devalla^{1,*†}, Roselle Gélinas^{2,3,†}, Elhadi H Aburawi^{4,†}, Abdelaziz Beqqali^{5,†}, Philippe Goyette², Christian Freund^{1,6}, Marie-A Chaix^{2,3}, Rafik Tadros^{2,3,5}, Hui Jiang^{7,8,9}, Antony Le Béchec¹⁰, Jantine J Monshouwer-Kloots¹, Tom Zwetsloot¹, Georgios Kosmidis¹, Frédéric Latour², Azadeh Alikashani², Maaike Hoekstra², Jurg Schlaepfer^{1,1}, Christine L Mummery¹, Brian Stevenson¹⁰, Zoltan Kutalik^{10,12}, Antoine AF de Vries^{13,14}, Léna Rivard^{2,3}, Arthur AM Wilde^{15,16}, Mario Talajic^{2,3}, Arie O Verkerk^{5,†}, Lihadh Al-Gazali^{4,†}, John D Rioux^{2,3,*†}, Zahurul A Bhuiyan^{17,*†} & Robert Passier^{1,18,*†}

Accepted Manuscript

2019

A compound heterozygosity of Tecrl gene confirmed in a catecholaminergic polymorphic ventricular tachycardia family

Lijian Xie, Cuilan Hou, Xunwei Jiang, Jian Zhao, Yun Li, Tingting Xiao

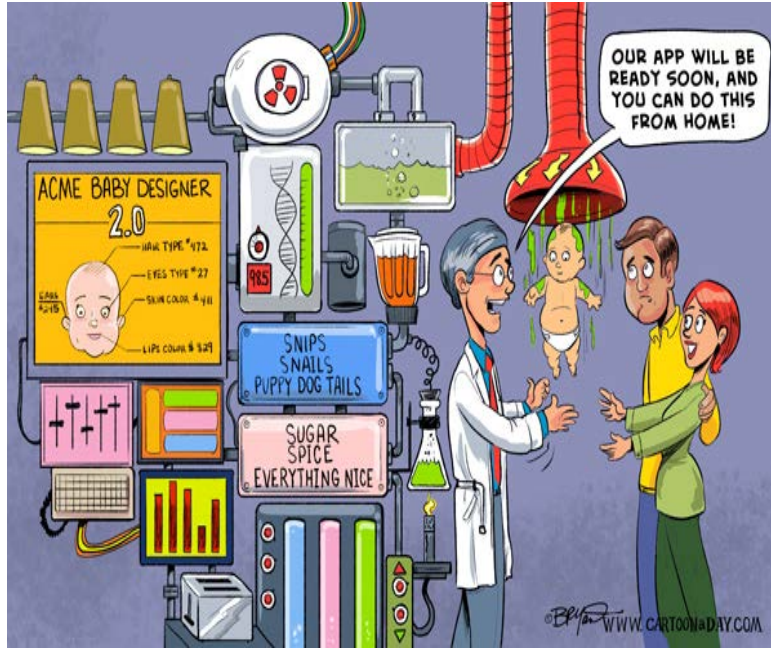


PND, disease phenotypes and socio-economic considerations

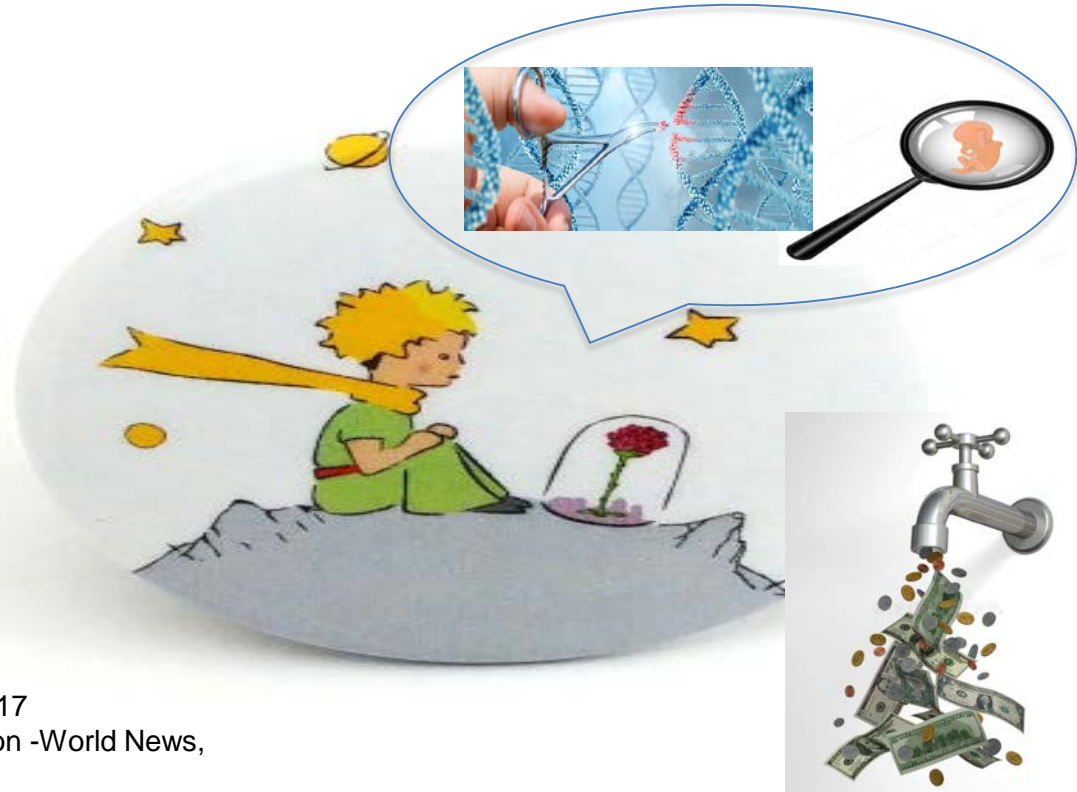
- What could be considered as an “acceptable” or “non acceptable” disease?
- Parents of children with PKU requesting PND
- Patients/parents/family resilience.



Capable to take the risk?



Designer Baby Cartoon By Bryant Arnold Published: May 7, 2017
Posted in: Conceptual Artwork, Digital Painting, Editorial Cartoon -World News,
Modbook Artwork, Pen and Ink Cartoons



Dankie Gracias شكراً
Спасибо Merci Takk
Köszönjük Terima kasih
Grazie Dziękujemy Dëkojame
Ďakujeme Vielen Dank Paldies
Kiitos Täname teid 谢谢
Thank You Tak
感謝您 Obrigado Teşekkür Ederiz
Σας Ευχαριστούμ 감사합니다
Бодхон
Bedankt Děkuje vám
ありがとうございます
Tack

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