mtDNA disease: recurrence risks & reproductive strategies

Sara Seneca Postgraduate Course in Medical genetics Centrum Medische Genetica, UZ Brussel





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outline

 mitochondrial disorders & oxidative phosforylation

> what - where - how ?

 recurrence risks & appropriate genetic counseling

• future prospects & summary



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mitochondrial disorder (1)?

- single organ or multisystem disease
- dysfunction of oxidative phosphorylation system (OXPHOS)
- clinically very heterogeneous condition, affecting patients
 - at any age (early in infancy or in late(r) adulthood),
 - in any tissue or organ
 - > mild or severe phenotype



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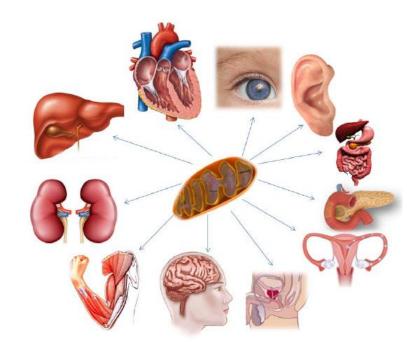
illustration of clinical diversity

might include, but not limited to

- migraine
- deafness
- blindness
- diabetes
- cardiac problems
- epilepsy
- seizures
- dysphagia
- ophthalmoplegia







- respiratory failure
- myopathy
- neuropathy
- gastrointestinal dysmotility
- liver failure
- bone marrow dysfunction



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mitochondrial disorder (2)?

- life limiting (or fatal very early in life)
- incidence of mt cytopathies
 - 1/5.000 affected with mt disorder*
 - >1/200 carriership in life births**
 - * estimated 1/4.000 1/6.000

** investigation in UK of 10 frequent mtDNA mutations in cordial blood of neonates

(Gorman 2015, Chinnery & Taylor in 2000 & 2008, Thornburn 2003)





mitochondrial disorder (3)?

• no cure(s) yet

- early phase drug trials and clinical studies are (a slow) work in progress
- idebenone is licensed in Europe for LHON
- > gene therapy for LHON
- > taurine is licensed in Japan for Melas
- other therapies/treatments alleviation (ptosis, cardio, diabetes, epilepsy...) of symptoms



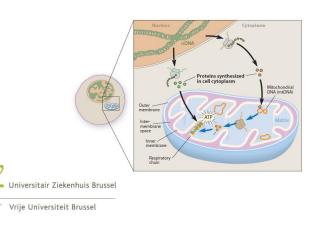


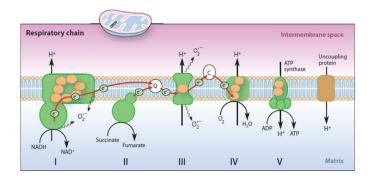


mitochondrial disorder (4)?

What is the cause of a mitochondrial (mt) disorder ?

a defect of the oxphos system

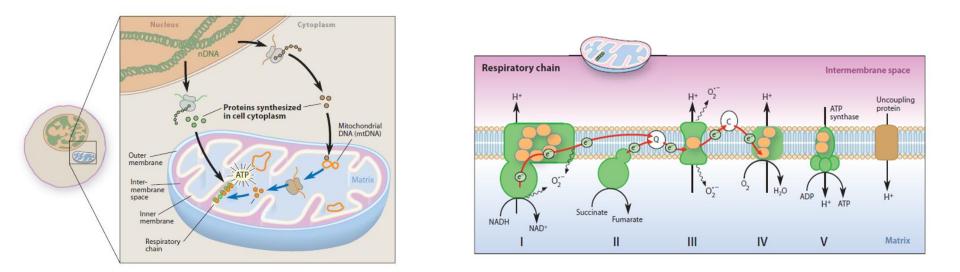






short overview OXPHOS pathway

largest generator of ATP



mitochondria harbour a small genome: mtDNA





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mitochondrial disorder (5)

It is not a single disorder but an 'umbrella' term for dozen of disorders, in which mitochondria are not able to produce (enough) energy for cells to work properly.

OXPHOS system is under dual genetical control of the n & mt genome



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mt disease recurrence risks

 recurrence risk for nuclear encoded gene mutations
 Mendelian rules for dominant, recessive and X-linked inheritance

recurrence risks of mtDNA mutations
 maternal inheritance







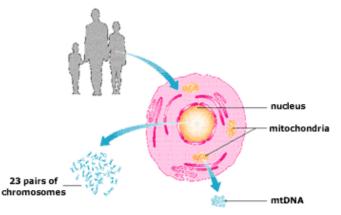
mitochondrial genome (mtDNA)

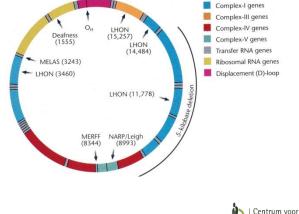
molecular causes of OXPHOS problems are dual :

nuclear DNA: 3 10⁹ bp

versus

mtDNA: 16 569 bp small double stranded molecule only 37 genes essential to OXPHOS compact (no introns) translation system







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unique characteristics of mtDNA

- polyploid genome
- homoplasmic/heteroplasmic
- maternal inheritance
- treshold level
- random mitotic segregation
- high mutation rate (polymorf)
- bottleneck concept





polyploidy : multicopy mt genome

- \Leftrightarrow nuclear genome
- multiple mtDNA copies/cell
- # dependent of cell type & energy demand
 - e.g. sperm cell: ± 10-100 mtDNA molecules
 - e.g. oocytes : $\pm 1-3.10^5$ mtDNA molecules average cell : $\pm 10^3-10^4$ mtDNA molecules

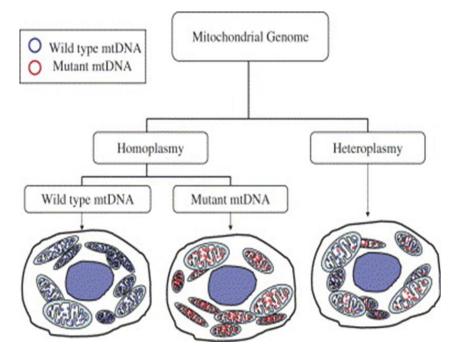




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definition homo-/heteroplasmy

 presence of identical mtDNA molecules or WT or variant



presence of
 different types
 (sequence) of
 mtDNA molecules



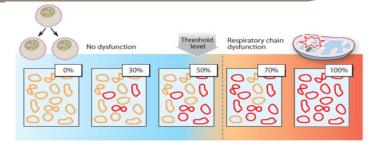
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recurrence risks of mtDNA



heteroplasmy can vary

- ≠ tissues in 1 individual
- ≠ cells of same tissue in 1 individual

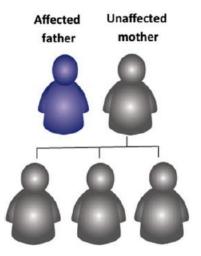


- changes with **time** in 1 individual
- (strong) impact on cell fie >> treshold
 - tissue/organ dependant
 - age of patient dependant
 - variant dependant
- blood levels (often) << post-mitotic tissues



strict maternal inheritance

only maternal (from oocyte) contribution, **no paternal** (from sperm cell) contribution



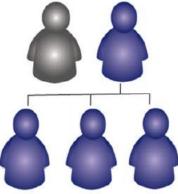
No affected children



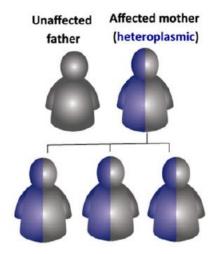


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Unaffected Affected mother father (homoplasmic)



All affected children (assuming complete penetrance)



Children may be affected or unaffected (depending on level of heteroplasmy, which can vary between children)



degradation of sperm mtDNA

- active elimination of sperm mtDNA in zygote
 - > ubiquitinated & targeted for distruction

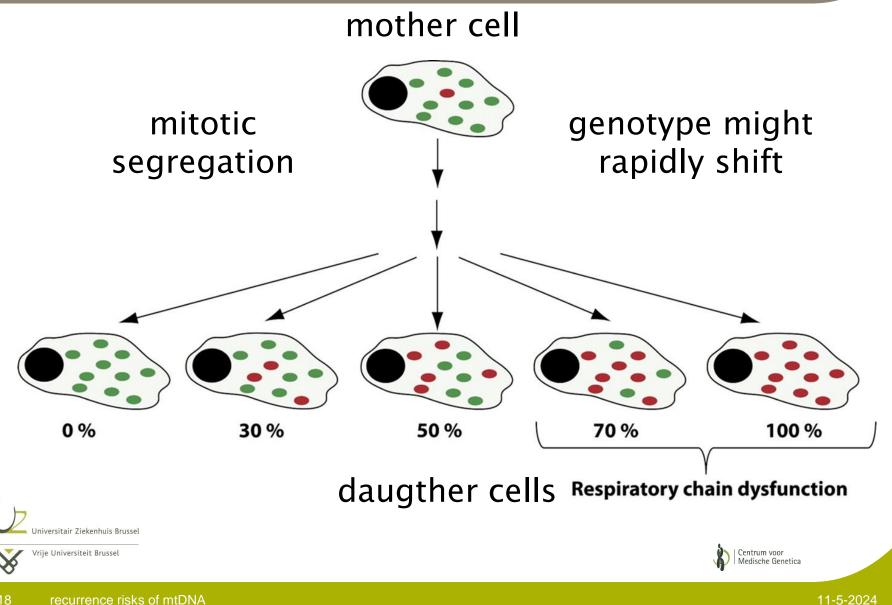
mitophagy

- paternal transmission
 - > extremely rare & results probably from defect
 > Schwartz & Vissing 2002
 - > Luo 2018





random distribution of mtDNA



unique characteristics of mtDNA

- polyploid genome
- homoplasmic/heteroplasmic
- maternal inheritance
- treshold level
- random mitotic segregation
- high mutation rate (polymorf)
- genetic bottleneck concept





genetic bottleneck concept (1)

- hypothesis to explain rapid shift in genotype in successive generations
- rapid intergenerational switch > no fit with random genetic drift model
- no exact mechanism in all details
 > 3 models were proposed





genetic bottleneck concept (2)

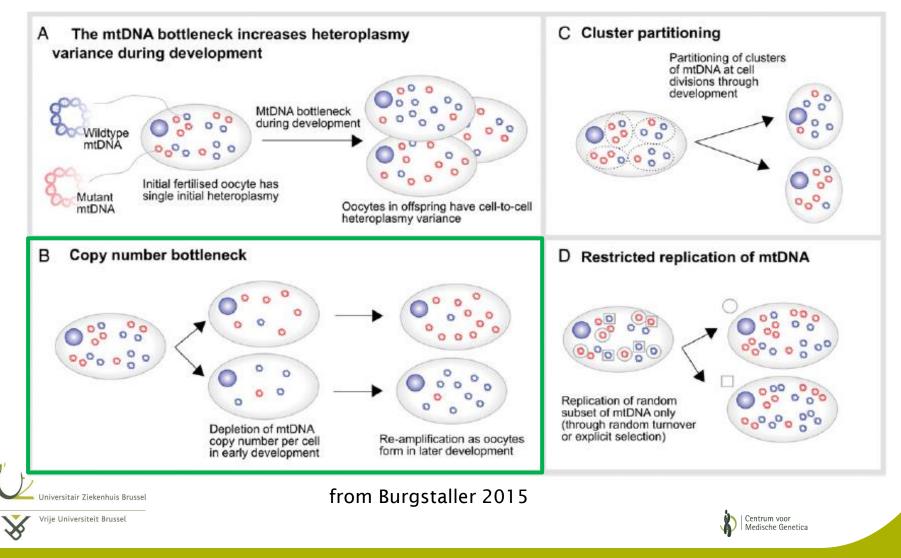
hypotheses:

- Cree et al. 2008: \$\frac{1}{2}\$ in \$\#\$ mtDNAs in oocytes \$+\$
 \$\phi\$ \$\phi\$ during early embryonic development
- Cao et al. 2007: no ↓ in # mtDNAs in oocytes
 random segregation of mtDNA clusters
- > Wai et al. 2008: no \downarrow in # mtDNAs
 - replication of subset of mtDNAs





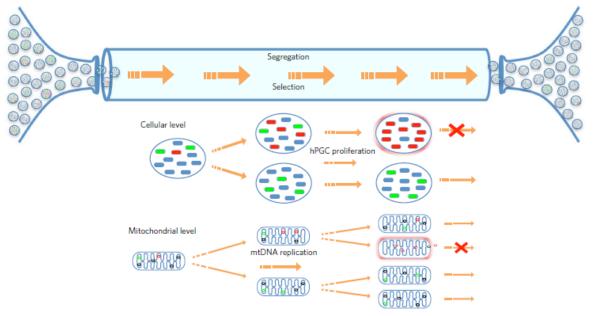
genetic bottleneck concept (3)



genetic bottleneck concept (4)

copy number bottleneck (Floros et al. 2018)

- > human embryos
- reduction > 5 mtDNA molecules / mitochondrion











mtDNA & disease

defects of mtDNA > (large scale) rearrangements deletions insertions or duplications (occasionaly) pathogenic point variants (>300) > scattered over the whole genome (protein coding and synthesizing genes)



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mtDNA & disease - recurrence risk

mtDNA inheritance no cure, limited therapy and no effective treatment

ſ

knowledge of risk assessment and reduction or prevention of transmission of mtDNA disease is **very important** for counseling of these families





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recurrence risk estimation

5 ≠ situations

- 1. *de novo* variant : single large deletions
- 2. homoplasmic variant : e.g. LHON
- 3. stable variant + predictable outcome : e.g.m.8993T>G for narp/LS.
- *unstable* variant + *unpredictable* outcome : e.g.m.3243A>G melas
- any private/family-specific variant + unknown outcome







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e.g. a single large mtDNA deletion nearly always sporadic ? ...<1% but ...??

- meta study of 226 families (7 UK centers) (Chinnery 2004)
- unaffected mothers > very unlikely to have another affected child (no case)
- 40 affected mothers > 3/73 children > recurrence risk of ≈ 4%



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recurrence risks of mtDNA



2. homoplasmic variant

e.g. LHON (<u>L</u>eber <u>H</u>ereditary <u>O</u>ptic <u>N</u>europathy)

- (sub)acute bilateral loss central vision
 > 15 35y (young male adults)
- degeneration retinal ganglion cells
- incidence > ≈12/100.000
- pathogenesis is not clear





Leber Hereditary Optic Neuropathy

• 3 frequent pathogenic variants (m.11778G>A (*MTND4*), m.3460G>A (*MTND1*), or

m.14484T>C (*MTND6*)) : \approx 95% of cases

- majority patients **homoplasmic**
- strong gender bias > 80% ♂ patients
- major incomplete penetrance (in a family)

secondary factors









Leber Hereditary Optic Neuropathy

homoplasmic variant

- all offspring will be homoplasmic
 > PND or PGT is not useful
- incomplete penetrance & gender bias
 > sex selection, an option ?
 > 9 embryos/fetuses
 > still residual risk



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- 3. stable variant + predictable outcome
- *4. unstable* variant + *unpredictable* outcome
- 5. private variant + unknown outcome

potential for **PND** ? > **criteria** defined



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criteria for 'mitochondrial' PND

- (i) close **correlation** between the level of variant load and disease severity
- (ii) uniform distribution of variant mtDNA in all tissues
- (iii) no change in variant load with time

Poulton & Turnbull 2000



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questions for PND ?

is variant load

- CV sample **representative** other villi ? all fetal tissue ?
- idem for amniotic cells ?
- constant during development, now (fetal) ?
- constant during development, later (adult) ?



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3. *stable* variant + *predictable* outcome

- e.g. m.8993 T>G mutation
- Narp (70-80% load)

<u>n</u>europathy, <u>a</u>taxia, <u>r</u>etinitis <u>p</u>igmentosa (with muscle weakness, seizures, MR, ...)

- common in Leigh syndrome (>90% load)
- 'rapid segregation' (only 1 generation)
- '*de novo*' families

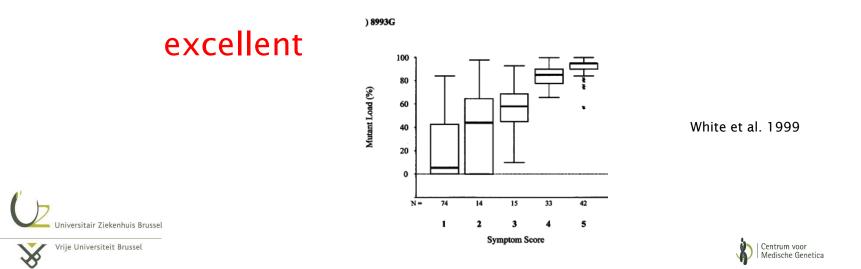




m.8993T>G mutation

check criteria ?

- tissue-dependent variation \downarrow
- age-dependent variation \downarrow
- genotype phenotype correlation



m.8993T>G mutation : PND ?

- affected fetuses 8 wk & 11 wk & 12 wk
- variety of fetal tissues: placenta, brain, muscle, limb, lung, heart, spinal cord, liver, kidney investigated

results: equal distribution of variant load & comparable to chorionic villi

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A.Harding

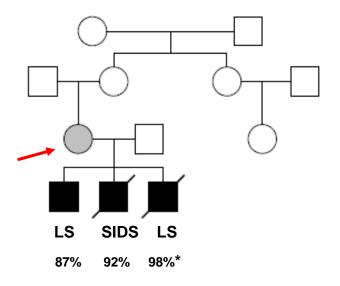
m.8993T>G mutation : oocytes ?

woman 50% m.8993T>G in leukocytes

study of oocytes

total of 8 oocytes

- 1 lost for analysis
- 6 load >95%
- I no mutation detected



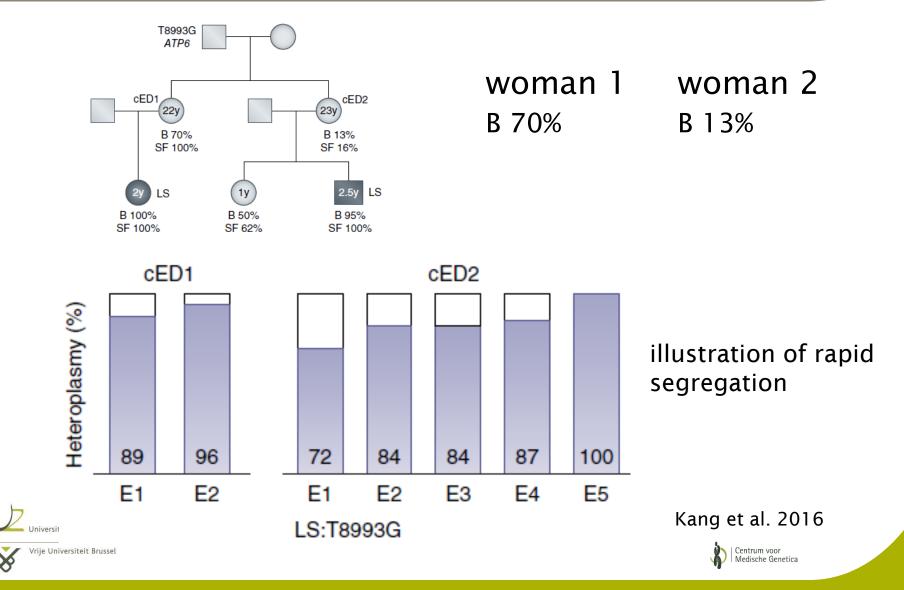
Blok et al. 1997



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m.8993T>G mutation : oocytes ?



4. *unstable* variant + *unpredictable*

e.g. m.3243A>G melas mutation check criteria ?

poor geno - phenotype correlation variant load differs among tissues variant load changes in time no good



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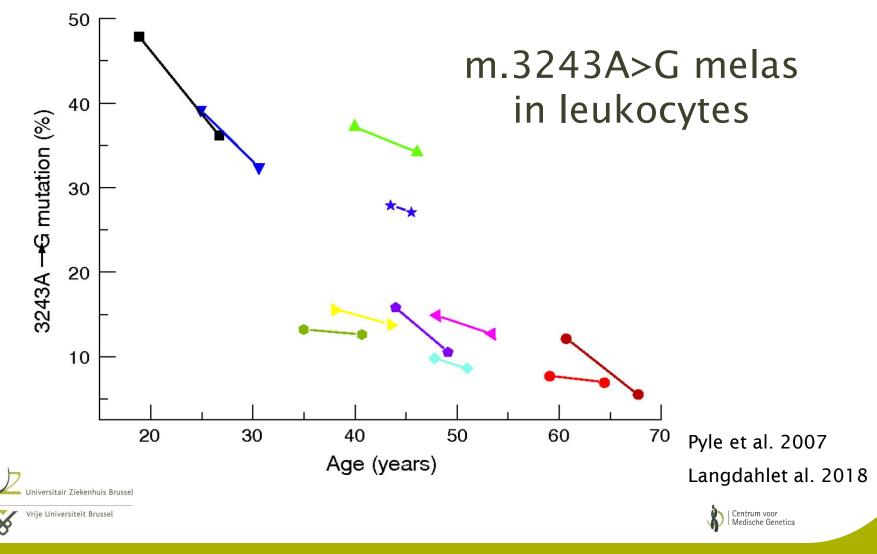
'unpredictability' of **m.3243A>G** is illustrated:

- load changes in leukocytes over time
- load variability in oocytes
- load variability in placenta samples
- transmission data:
 - > mother child
 - intersiblings

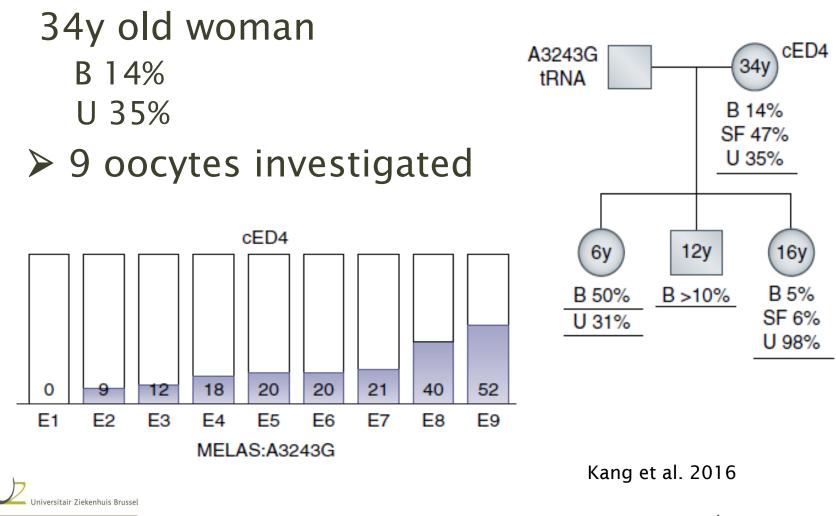




variant load declines with time



m.3243A>G melas : oocytes





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inheritance m.3243A>G variant

study of de Laat et al. 2012 analysis of urinary epithelial cells

• 56 mother-child relations

> 3 subgroups (0-5%; 5-25%; 25-50%)

• 63 intersibling relations

5 subgroups (0-5%; 5-25%; 25-50%; 50-75%; 75-100%)



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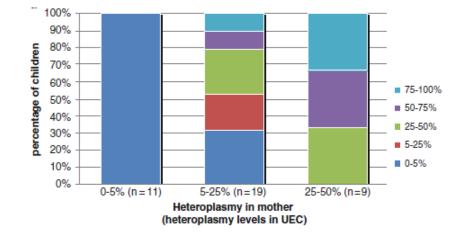
transmission between mother-child

- heteroplasmy <5%</p>
 - no detectable transmission
- heteroplasmy 5-25%
 - no detectable transmission in 30% offspring
- heteroplasmy >25%
 - transmission to all offspring



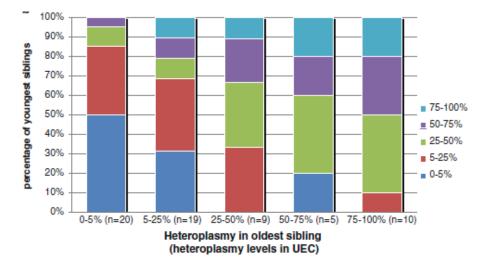


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transmission between **siblings**

- in oldest sibling no detectable level >5%
 - < 5% for 50% of youngest sibling
- in oldest sibling level >50%
 most siblings affected







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5. *unknown* outcome + 'private' variant

- unique/rare variants : few families
- no (or little) specific information
- genotype phenotype correlation ?
- treshold level ?
- identify potential healthy offspring ?

insufficient data for conclusion





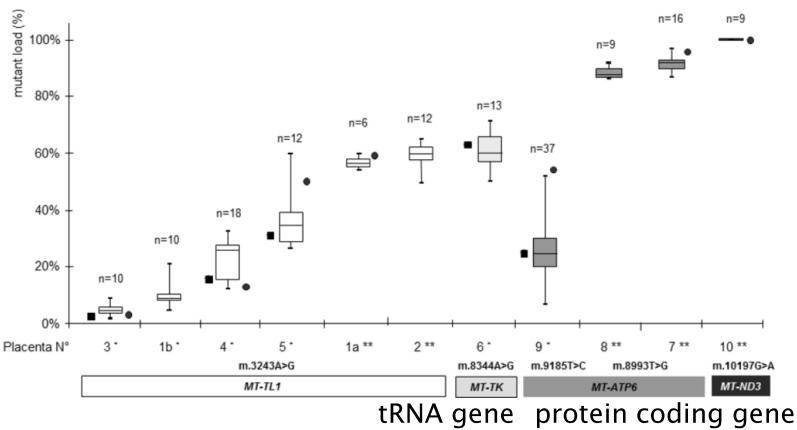


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placenta tissue (1)

11 placentas investigated







Vachin 2017



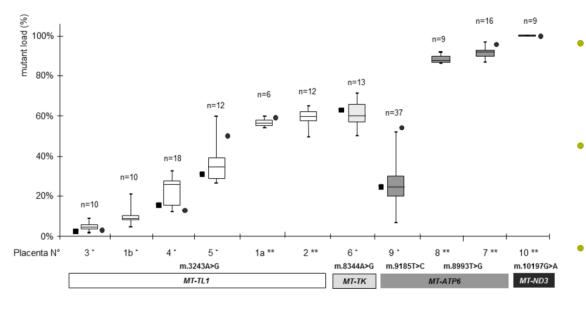
placenta tissue (2)

- 11 placentas investigated (Vachin 2017)
 6 full term / 5 > 12-18 weeks gestation
- multiple samples : (n=1 37) / placenta
 1 placenta homoplasmic (MT-ND3 gene)
 6/10: intraplacental variation limited to ≈ 10%
 4/10: large intraplacental variation
 up to 55% in 1 case





placenta tissue (3)



- 1 placenta homoplasmic (MT-ND3 gene)
- 6/10: intraplacental variation limited to ≈ 10%
 - 4/10: large intraplacental variation
 - > up to 55% in 1 case

CV sample not always appropriate tissue for PND



Vachin 2017



What about ART ?

Preimplantation Genetic Test or Mitochondrial Donation Therapy



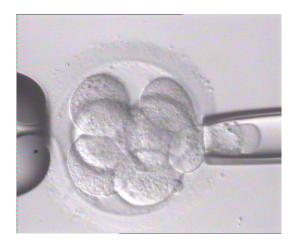






<u>**P</u>reimplantation** <u>**G**enetic</u> <u>**T**est ?</u></u>

solution ?



aim ?

selection of optimal ('healthy' or 'low risk') embryos to reduce the risk of mt disease transmission

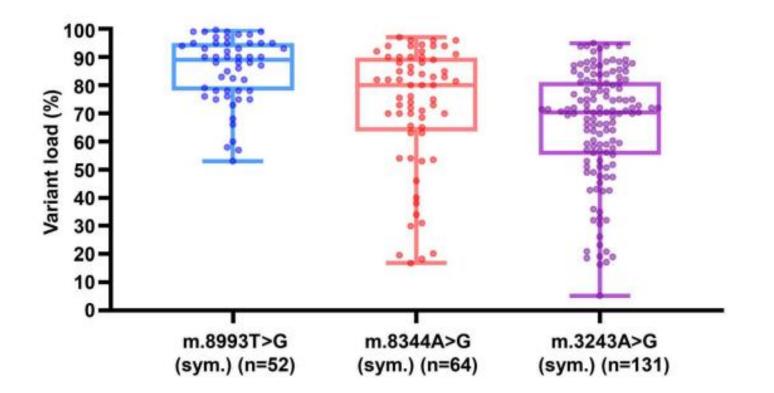








probability treshold for symptoms



meta analysis : distribution of variant load in 455 symptomatic individuals from 187 pedigrees (Ji 2023)



52 recurrence risks of mtDNA



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PGT procedure questions ?

- are results of 1 or 2 blastomeres representative for embryo ?
- which embryos are suitable for transfer ?
 - > save cut off point ?
 - > criteria ?
- results of one family representative for this variant in general ?



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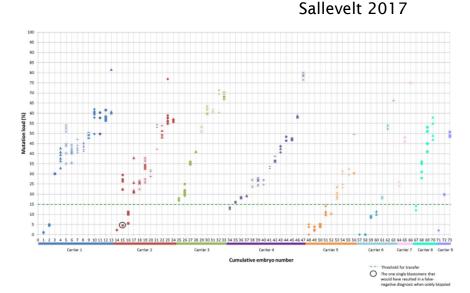
mtDNA load in PGT blastomeres

m.3243A>G variant load compared in single blastomeres from the same embryo

- 9 females
- 73 embryos
- 294 blastomeres

 $(n \ge 2 / embryo)$

• threshold 15%



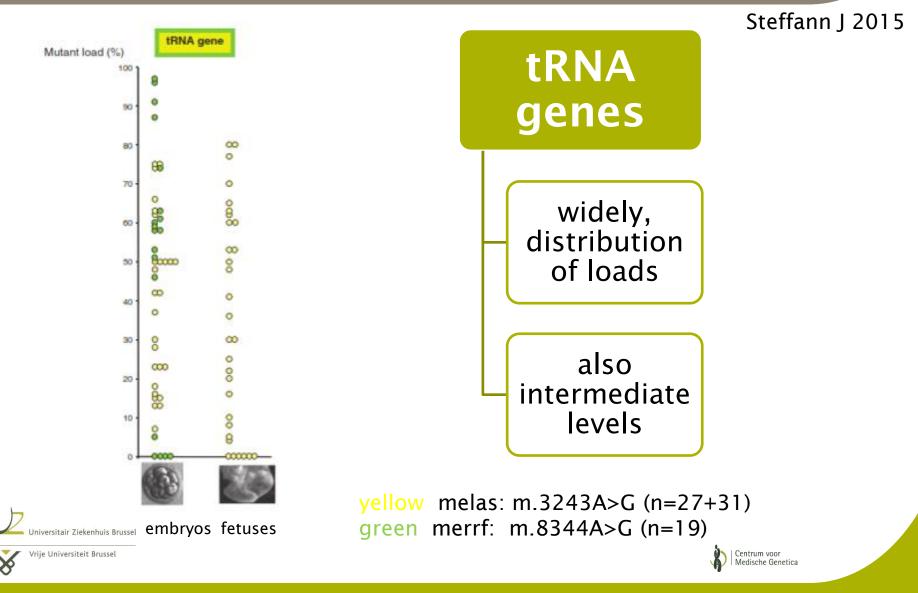
1 false-negative result (5% versus 22% & 30%)



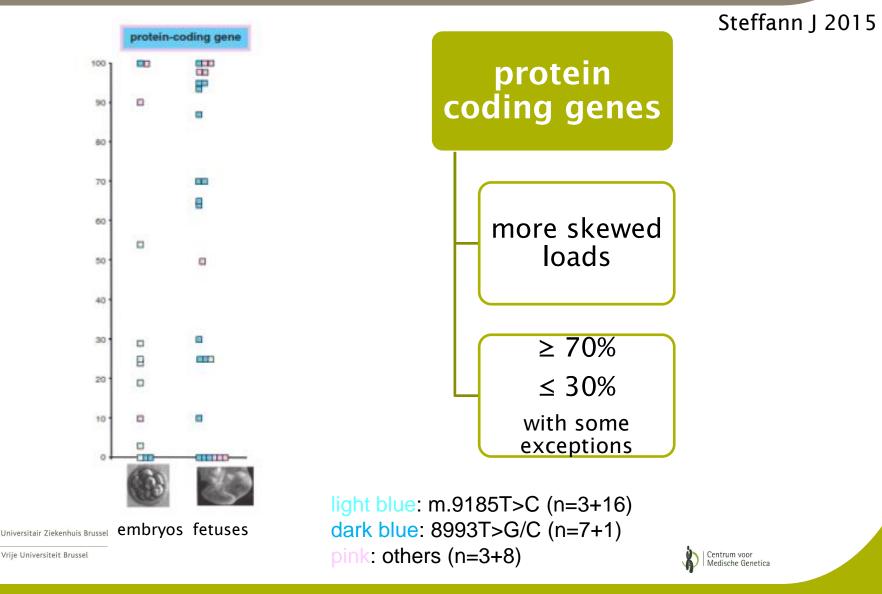




mtDNA load in PGT embryos & fetuses



mtDNA load in PGT embryos & fetuses



- variant-free embroys are scarcely produced
 - Selection of low risk embryos
 - stringent treshold level knowledge important
- robust correlation between blastomeres
 > study Monnot 2011; Sallevelt 2017
- results of TE biopsy migt be a problem
 heteroplasmy mosaicism risk (Hellebrekers 2023)





mutation burden @ biopsy does not always correspond with the one @ birth

Table 2 Mutation levels in live births following PGD for mitochondrial disease

Mutation At biopsy m.8993T > G 0% & 0%		At birth	Comments		
		0%	First report. Two embryos transferred		
m.8993T > G	2.5%	4%	3–5% cord blood & placenta; buccal cells 5% at age 4½ years		
m.3243A > G	5% & 13%	5%	Two embryos transferred; $15 \pm 5\%$ placenta, $5 \pm 1\%$ cord blood		
m.3243A > G	12%	15%	47% blood, 52% urine at 1½m; 46 & 42% at 18m		
m.8993T > G	0%	0%	'Healthy son', no further details		
m.8344A > G	53% & 59%	63% Two embryos transferred; no further details			
m.3243A > G	0%	0%	Male; measured in cord blood, urine, saliva		
m.36 ^b G > A	2%	7% Female, measured buccal and urine cells			
m.83 ^b A > G	48%	Not available	ailable Male; <60% generally asymptomatic		
m.130 ^b T > C	1%	0%	Male; undetectable in blood, buccal and urine cells		
m.101 ^b <i>T</i> > C	1%	1-2%	Male; cord blood		

^b characters hidden to respect confidentiality

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Greenfield et al. 2017



mutation burden @ biopsy does not always correspond with the one @ birth

Table 1. Clinical PGT cycles carried out for mtDNA disorders.

Reference	mtDNA mutation	Disorder	Number of patients	Mutation load of embryos	Mutation load difference	Mutation load of transferred embryo(s)	Mutation load of fetal/ neonatal tissues
(Steffann et al. 2006)	m.8993T→G	NARP/Leigh syndrome	1	0-100%	6% between two cleavage-stage blastomeres and the entire embryo	0%	0% in cord blood
(Sallevelt et al. 2013)	m.8993T→G	NARP/Leigh syndrome	1	30-100%	<10% between cleavage-stage blastomeres	0%	0% in cord blood
(Tajima et al. 2007)	m.8993T→G	NARP/Leigh syndrome	13	4-22%	2-11% between cleavage-stage blastomeres	NA	NA
(Spath et al. 2021b)	m.8993T→G	NARP/Leigh syndrome	2	0-88.7%	NA	0%	0% (not specified in which tissue)
(Sallevelt et al. 2013)	m.3243A→G	MELAS	3	1-70%	<10% (80% of embryos) and >15% (18% of embryos) between cleavage-stage blastomeres	NA	NA
(Monnot et al. 2011)	m.3243A→G	MELAS	2	5-77%	0-6% between cleavage-stage blastomeres 0-2% between cleavage-stage blastomeres and TE cells <7% between cleavage-stage blastomeres and the entire blastocyst	NA	NA
(Treff et al. 2012)	m.3243A→G	MELAS	1	7-90%	0.5-2.9% between cleavage-stage blastomeres2.1-5.0% between TE cells and inner cell mass	12%	0–15% in buccal cells, blood, and urine
(Heindryckx et al. 2014)	m.3243A→G	MELAS	1	0-65%	0-7% between TE cells	0%	0% in saliva, blood cells, and urine
(Spath et al. 2021a)	m.3243A→G	MELAS	1	3.1-29.2%	0-3.2% between halves of cleavage-stage embryos	NA	NA
(Sallevelt SC et al. 2017)	m.14487T→C	Leigh syndrome	1	6-100%	0–10% between cleavage-stage blastomeres	<18%	5% mutation load in cord blood
(Spath et al. 2021a)	m.10191T→G	Leigh syndrome	1	0%	0%	0%	0% in chorionic villi
(Ji et al. 2021)	m.3697G→A	Leigh syndrome	1	15.2%-100%	0–10.3% between cleavage-stage blastomeres	53.9%	47.7–49.7% in fetal tissues and amniotic fluid cells





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Lan et al. 2024



PGT m.3243A>G embryo

- trophoblast : 12%
- 30 days buccal cells : 15%
- 6 weeks
 - blood: 47%
 - > urine: 52%
- 18 months
 - blood: 46%
 - urine: 42%

Blastocyst preimplantation genetic diagnosis (PGD) of a mitochondrial DNA disorder

Nathan R. Treff, Ph.D., ^{a,b,c} Jessyca Campos, M.S., ^{a,b} Xin Tao, M.S., ^a Brynn Levy, Ph.D., ^d Kathleen M. Ferry, B.S., ^a and Richard T. Scott Jr., M.D.^{a,b}

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Limitations of Preimplantation Genetic Dionosis for Mitochondrial DNA Diseases

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other options ? now ? in the (near) future ?





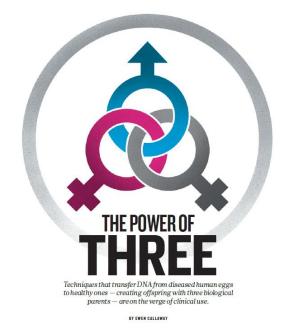
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replacement of mt genome of the **affected** woman with that of a **donor** woman

- applied *before* fertilisation
- > MST (maternal spindle transfer)
- > GVT (germinal vesicle transfer)
- > PBT (polar body transfer)
- applied after fertilisation
- > PNT (pronuclear transfer)



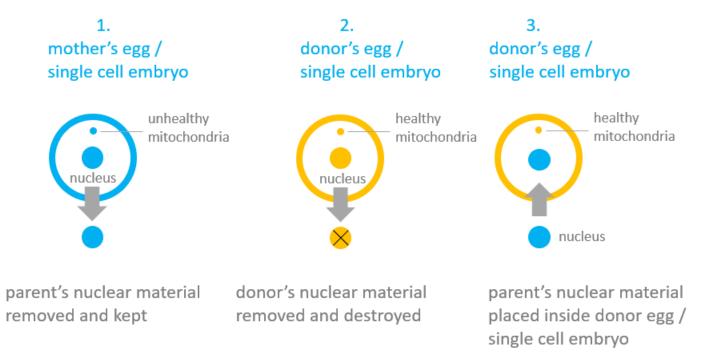
Herbert & Turnbull et al. 2018

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how to make a '3 persons' baby ?





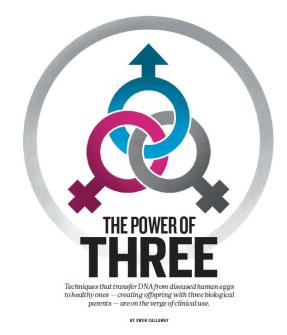


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replacement of mt genome of the **affected** woman with that of a **donor** woman

- applied *before* fertilisation
- MST (maternal spindle transfer)
- > GVT (germinal vesicle transfer)
- PBT (polar body transfer)
- applied after fertilisation
- > **PNT** (pronuclear transfer)



Herbert & Turnbull et al. 2018







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study of proof of principle demonstrated > safety > efficacy

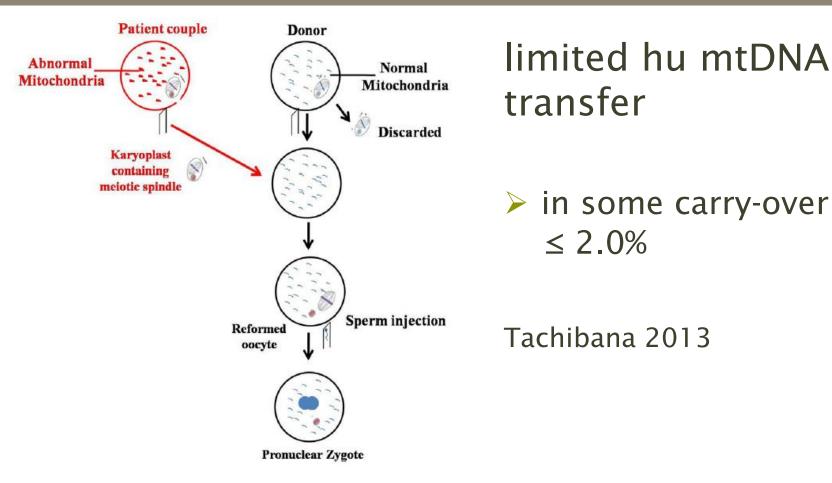
For different strategies & different teams in pilot studies





metafase II spindle transfer

 $\leq 2.0\%$



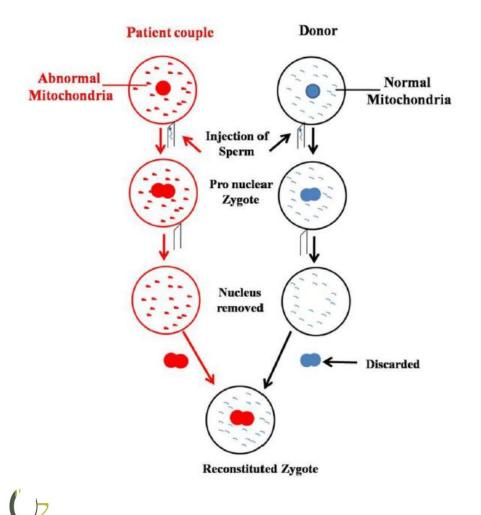




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pronuclear transfer



limited hu mtDNA transfer

carry-over ? in 4/9 embryos not detectable; in some 0,01 - 2%

Craven 2010

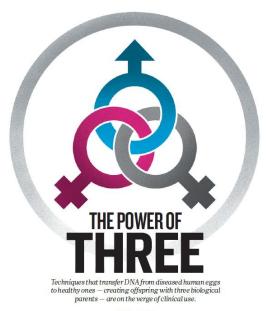


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mitochondrial donation therapy ?

promises & perils ?



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peril : reversion ? (1)

- 3 ES cell lines derived from MDT embryo
- in vitro reversion > original pathogenic LHON mtDNA variant m.14484T>C
- no haplogroup matching
 - is needed ?
 - (other) cause ?
 - what in vivo ?







peril : reversion ? (2)

uncertainties under debate / investigation

- << amounts mtDNA carry over ?</p>
- haplogroup differences ?
- > nuclear mtDNA interaction
 - haplogroup matching needed ?
- mtDNA mtDNA interaction
 - possible detrimental effect ?
- mtDNA segregation
 - genetic drift & mtDNA reversion ?



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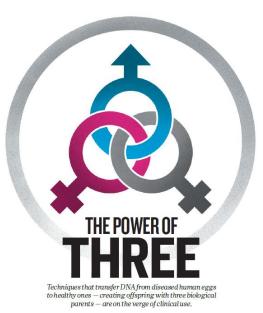


peril: reversion? (3)

uncertainties under debate

- << amounts mtDNA carry over ?</p>
 - limiting co-transfer = a technical chal
 - > genetic drift & mtDNA reversal ?

beneficial effects of MDT lost over time ? Greek pilot study



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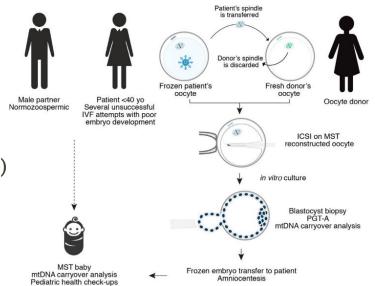
recurrence risks of mtDNA

72

<u>m</u>itochondrial <u>r</u>eplacement <u>t</u>herapy ?

Greek pilot study

- 25 infertile couples
- idiopathic infertility
- repeated IVF failure (n = 3-11)
- no mtDNA disease
- no haplogroup matching of donor
- 28 MST cycli



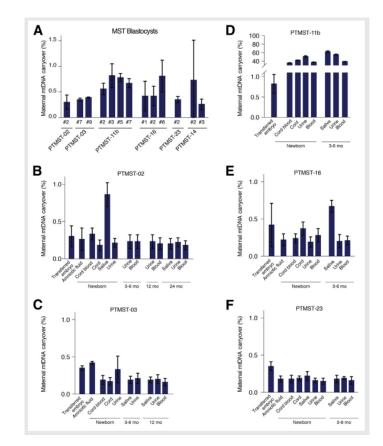


<u>m</u>itochondrial <u>r</u>eplacement <u>t</u>herapy ?

Greek pilot study

- 28 MST cycli
- 6 life births
- << at start amounts mtDNA carry over (<1%) in 5

> HOWEVER



Costa-Borges et al. 2023





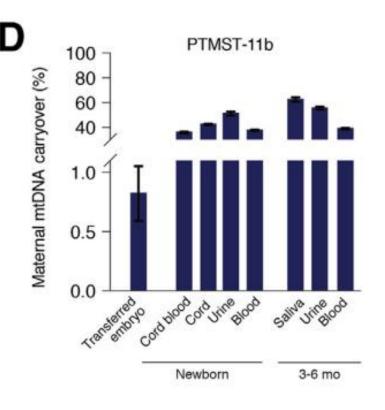


<u>m</u>itochondrial <u>r</u>eplacement <u>t</u>herapy ?

Greek pilot study

HOWEVER

> 1 baby with reversion of 30-60% of maternal mtDNA haplotype in ≠ tissues (cord blood, blood, urine & saliva) at birth







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promises ? reduce, not eliminate risk

- 2015 : licenced by UK parliament
- 2017 : HFEA licenced a fertility clinic
 - clinical trials have started in Newcastle Fertility Centre with PNT, on case-by-case basis
- 2023 baby's born (no further info yet)
- US : FDA ban on clinical trails of MDT

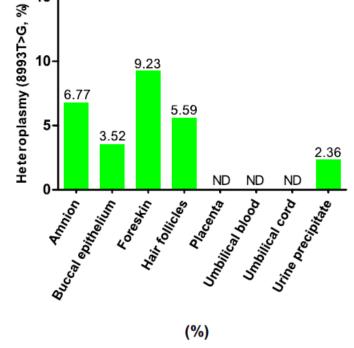




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a human baby was born in Mexico

- a 'spindle transfer baby' was born in Mexico (Zhang et al. 2017)
- m.8993T>G
 - 5,9% heteroplasmy blastocyst stage
 - 2,36 to 9,23% in various tissues at birth

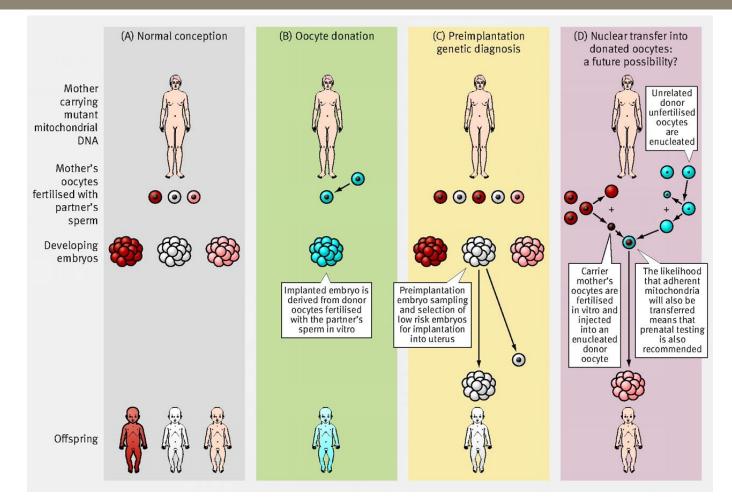






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transmitting mtDNA disease





option of oocyte or embryo donation which avoids all riks

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key points (1) summary

- mtDNA diseases are frequent in humans
- many different factors interfere in final risk determination
 - heteroplasmy
 - bottleneck
 - > variant
- counseling is complex





key points (2) summary

PNT can be an option

- Iow risk situations
- PGT can be an alternative
 - moderate risk situations
 - > analysis of oocytes might be directive
- interpretation of test results & 'grey zone' could be a problem (phenotypic threshold level ?)



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key points (3) summary

- oocyte / embryo donation option
- MDT is still experimental
 - > promising track in a near future
 - high risk situations & homoplasmic variants

NO one for all solution









THE END THANK YOU





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11-5-2024