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Men: 439 Women: 572



Men: 257 Women: 261 Men: 1172 Women: 1989

Cair



Men: 189 Women: 544

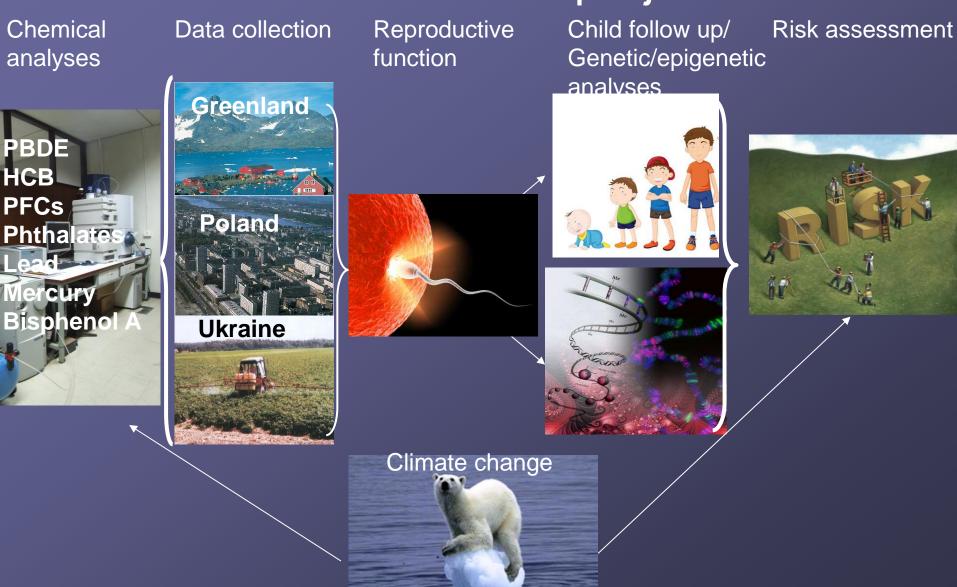


Men: 287 Women: 612



INUENDO

The CLEAR project



Modeling effects of climate change on contaminant distribution

 The influence of realistic GCC scenarios on chemical fate and transport were modeled to be relatively low, with model outputs from the GCC scenarios generally within a factor of two (typically ±30%) of the baseline.

- Dietary transitions are expected to have a large effect on human exposure

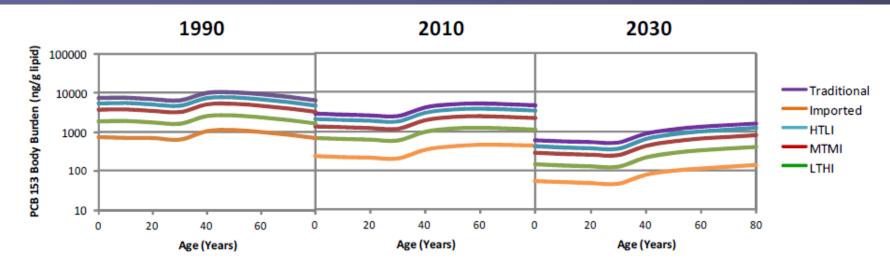
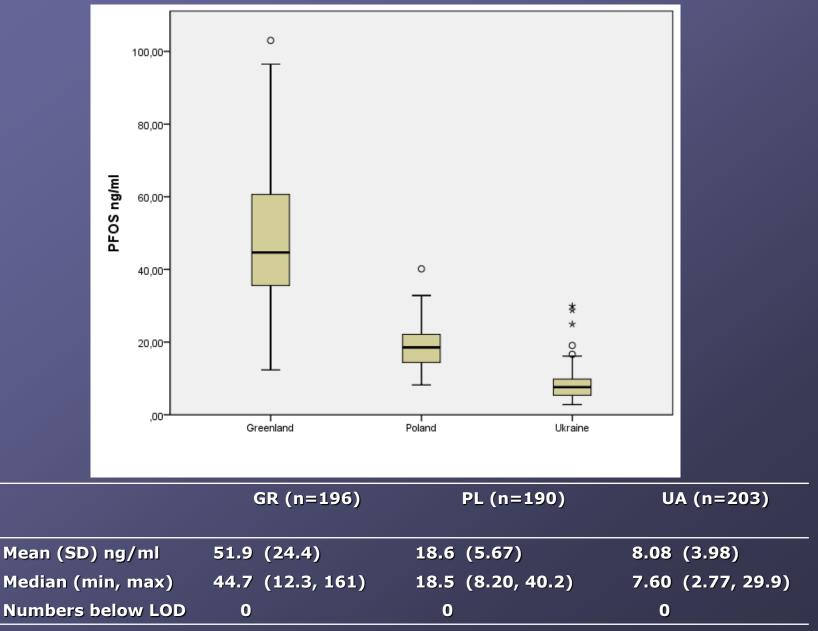


Figure 7: Comparison of ACC-Human generated cross-sectional body burden age trends for PCB-153 for cross-sectional biomonitoring studies conducted in 1990, 2010, and 2030 and assuming five different diet types: traditional only (purple), HTLI (blue), MTMI (red), LTHI (green), and imported only (orange).

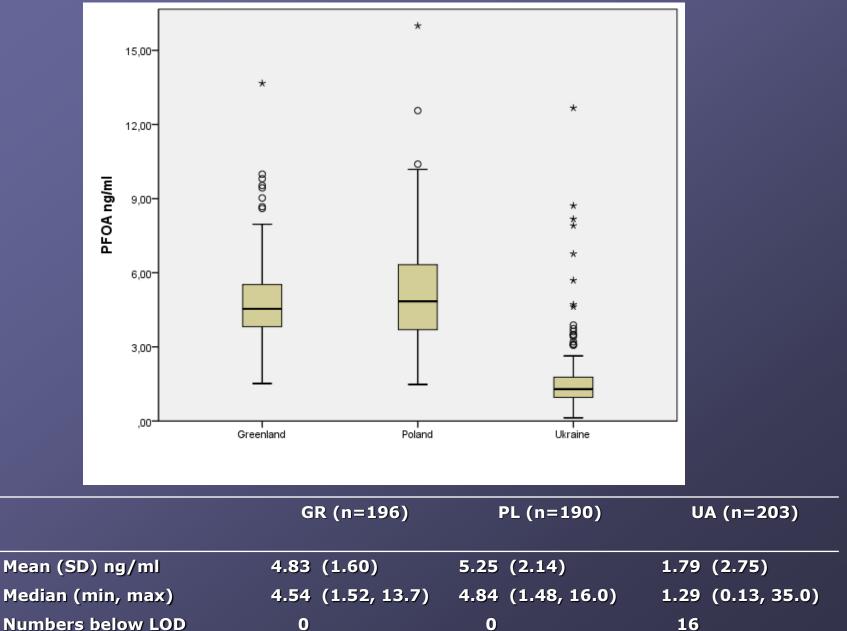
Contaminant assessment

- Phthalate metabolites, perfluorinated chemicals, bisphenol A, hexachlorobenzene, cotinine, lead, cadmium and mercury have been measured in the blood of 602 males.
- Phthalate metabolites, perfluorinated chemicals, bisphenol A and cotinine have been measured in sera from 1441 women
- HCB, lead, cadmium and mercury have been measured in 400 women

PFOS (male)



PFOA (male)



Determinants for PFOS exposure

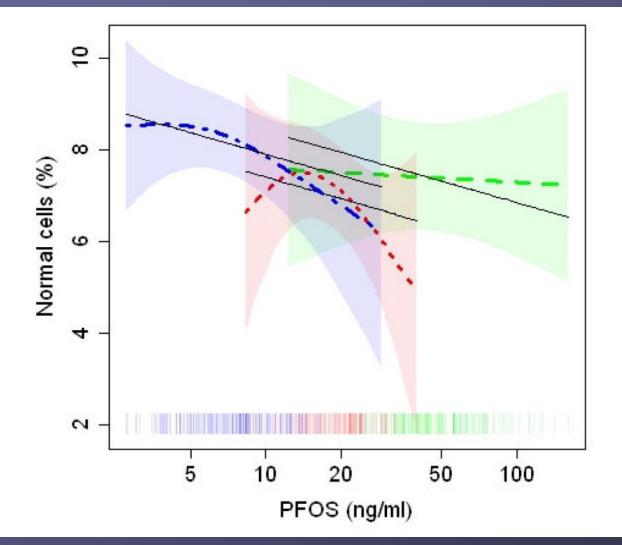
Determinants	Multivariate ß 95% CI adjus	st R ²
Greenland		
PFOS	0.19	
Seafood (days/week)	2.0 (0.46, 3.6)	
Age (years)	0.86 (0.37, 1.3)	
Tea (cups/day)	2.1 (0.31, 3.9)	
Area (Nuuk = reference)	-	
West	2.3 (0.62, 3.8)	
East/Nord	2.3 (0.62, 3.8)	

PFC and sperm quality

PFOS and PFOA not associations with:

- Sperm concentration and total sperm count
- Sperm Volume
- Reproductive hormone levels
- Measures of sperm DNA integrity

PFOS og sperm cell morphology



Blue= Ukraine, **Red**=Poland, **Green** = Greenland

Adjusted for adjusted for age, abstinence time, spillage, smoking; urogenital infections and BMI

Child growth and development

Weight, height, behavioral development (SDQ), motoric development (DCDQ) and developmental milestones were collected on 1234 children (6-9 years).

Gene-environment interaction

On 582 male (fathers) blood sample polymorphisms determined in:

Gene		rs_id	chr	allele	location
Androgen receptor	AR	rs5902610	X	[CAG]n	exon_1
Androgen receptor	AR	rs3138869	Х	[GGN]n	exon_1
Arylhydrocarbon receptor	AHR	rs2066853	7p15	G>A	exon_10
AhR repressor	AHRR	rs2292596	5	C>G	exon_6
5α-reductase type II	SRD5A2	rs9282858	2p23	G>A	exon_1
5α-reductase type II	SRD5A2	rs523349	2p23	C>G	exon_1
Estrogen receptor α	ESR1	rs2207396	6	G>A	Intron_6
Estrogen receptor β	ESR2	rs1256049	14	G>A	exon_7

Offspring genotyping

On salvia samples from children in the cohort the polymorphisms will be evaluated of:

- steroid hormone receptor (androgen receptor and estrogen receptor)

- steroidogenesis enzymes (5α-reductase and aromatase)

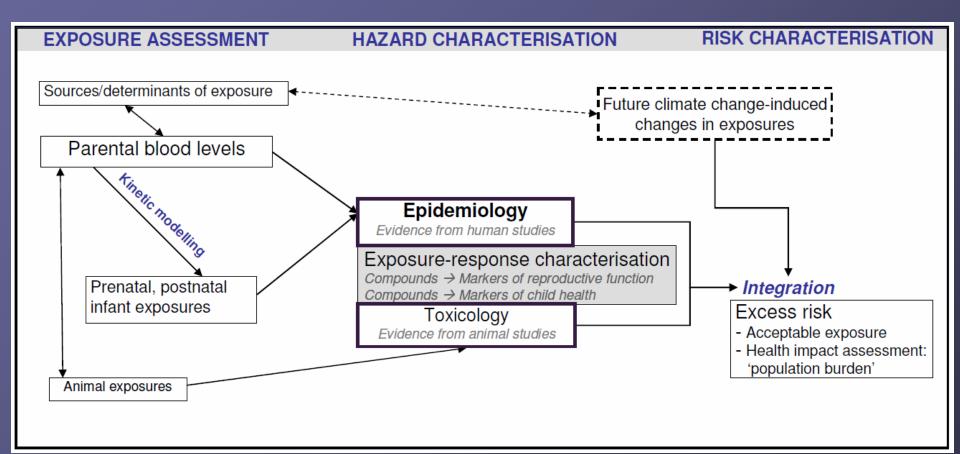
- detoxification enzymes (aryl hydrocarbon receptor with its cofactors and cytochrome P 1a1)

- genes involved in early growth

Global methylation of sperm cells

A method has been developed and flow cytometric assessment of DNA methylation has been performed on sperm samples from 269 men

Risk assessment



Overview of the risk assessment process for the CLEAR project

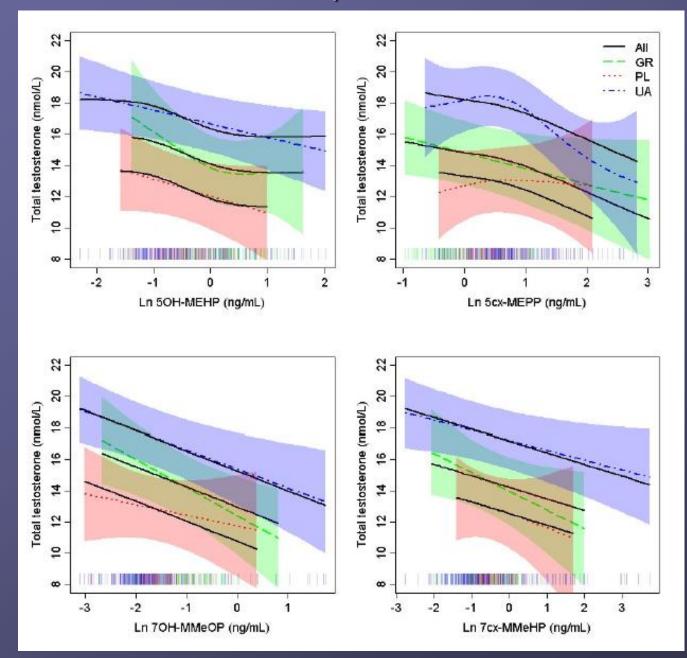
Global screening for noteworthy associations

Using PLSR regression techniques all measured male exposures and all measured outcomes have been evaluated

- This identified only a few noteworthy (strong and independent) associations

 The most clear signal was seen in relation to testosterone level and phthalate exposure

Testosterone and phthalate metabolites



Conclusions

The final conclusions from the project are not available yet but:

- We will most likely conclude that the direct physical effects of climate change on human contamination level is likely to be minimal compared to lifestyle changes and changes in food webs

- Furthermore, environmental chemicals at the present exposure levels are likely to have only limited effects on male reproductive function

- Possible effects on female reproductive function, childhood growth and development and geneenvironment interactions are not fully evaluated yet