

Influence of GSM and UMTS on the Blood Brain Barrier *in vitro* - additional results

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Dr. rer. nat. Helmut Franke Klinik und Poliklinik für Neurologie Universitätsklinikum Münster *In vitro*-Experiments on exposure to RF-fields of mobile telecommunication *C*. Blood brain barrier

- BBB in vitro (rat brain endothelial cell cultures)
- GSM 1800 exposure
- UMTS exposure
- differential gene expression (genechip arrays)
- selection of BBB related candidates
- verification of diff. gene expression (qRT-PCR)

goals

- Influence of RF-EMF on endothelial cells of the BBB ?
- reduction of BBB towards an in-vitro model
- investigations on cellular level
- identification of potential EMF-targets on molecular level
- <u>no</u> hypotheses on pathophysiological issues

overview: project parts

- establishment and characterization of RBEC cultures as BBB in-vitro model
- design of exposure unit
- exposure of RBEC and isolation of RNA
- gene expression analysis
- qRT-PCR verification of gene regulation

The Blood-Brain Barrier (BBB)

 maintenance homeostasis of the CNS

 essential for proper brain function

 control of substance flow between brain tissue and circulating blood

 controlled import of nutrients into the CNS

protection against toxins

Endothelial cells of the cerebral capillaries form the permeability barrier



Rat brain capillary endothelial cells (RBEC)



characterization of RBEC

- + squamous morphology
- + von-Willbrand-Factor-VIII
- + vimentin



- + tight junction proteins: ZO-1, occludin
- smooth muscle actin, GFAP, CD11b
- ---> minimal cell contamination





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assembly of radial waveguide



- 6 petridishes
- 40 cm diameter, 9 cm height
- sample holder centres petridishes
- temperature probe
- field probe





GSM-Exposure setup:

- amplifier
- signal generator
- wave guides
- fiberoptic temperature probes
- incubator



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biological replicates:

5+2 (38°C) 5+2 (40°C) Σ = 70 Chip Arrays

RNA isolation protocol

- lysis of RBEC immediately after termination of exposure (< 5 min.)
- RNA isolation from RBEC: *Qiagen RNeasy Micro-Kit* store samples @ -70°C
- quality control: Agilent Bioanalyzer
- RNA-conc: min. $1\mu g/\mu L$





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Affymetrix GeneChip® Rat Genome 230 2.0 Array



 data tables showing the signal intensities of the various probe sets

•28000 genes on the chip!
(=31099 probe sets)

31099 probe sets

source: http://privatewww.essex.ac.uk/~harry/images/affymetrix-genechip-hgu133p.gif

filtering of ,absent calls'

MAS 5.0 (Microarray Suite, Affymetrix)
normalization of signal levels
of 31099 probe sets on the chip, 18663 could be detected reliably ("present" calls in ≥ 3 of 5 chips per experimental group)



18,663

filtering of genes with fold-change < 1.4

•of 18663 present probe sets, 14287 showed at least 1.4x change in gene expression compared to sham exposed RBEC







Discriminatory Genes Analysis: SAM (Significance Analysis of Microarrays) 1W/kg vs. 3W/kg

GSM1800: of 11488 genes, 360 genes were identified by SAM as differentially expressed between 1 W/kg group and 3 W/kg
UMTS: 231 of 8900 genes
parameter: no false positives

360 GSM 231 UMTS



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Selection of genes for qRT-PCR validation

•SELECTION CRITERIA:

BBB-Genes: 2x regulation
SAM analysis 1W/kg vs. 3W/kg: 3x regulation
other genes: 5x regulation



68 genes GSM 61 genes UMTS

Selected genes for qRT-PCR validation

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available for TaqMan[®] Low Densitiy Arrays





selection of genes with BBB relevance (regulation to be validated)

- Agtr1a (angitensin II receptor; vasoconstriction)
- Col5a3 (procollagen Vα3; ECM)
- Sdc2 (syndecan 2; monocyte migrat. brain endot.)
- Slc33a1 (acetyl-CoA transporter)
- Abcc8 (ATP binding cassette transp.: MRP)
- Slc19a1 (folate & drug transporter)
- Cldn1 (claudin1, ZO-1 & Occl. associated TJ-prot.)
- Mmp2 (matrix metalloproteinase, involved in BBB regulation)

samples for qRT-PCR analysis



biological replicates for qRT-PCR: 5+5 GSM 5+5 UMTS

quantitative real time RT-PCR with TaqMan[®] Low Density Arrays

- reverse transcription of RNA to cDNA
- 200 ng cDNA in 100 µL per channel
- PCR reaction volume ~ 1 μ L
- 2x 47 genes (UMTS and GSM)
- comparative quantification: $\Delta \Delta C_{t}$ -method
- 7680 individual gRT-PCR reactions



amplification plot for 384 qRT-PCR reactions (one TLDA)



 $C_{\dagger}(\text{target gene}) - C_{\dagger}(\text{endogenous control}) = \Delta C_{\dagger}$ $\Delta C_{\dagger}(\text{exposed}) - \Delta C_{\dagger}(\text{sham}) = \Delta \Delta C_{\dagger}$ $RQ = 2^{-\Delta\Delta C_{\dagger}}$



\checkmark establishment of an isolation method for RBEC

- \checkmark characterazation of RBEC
- ✓ installation of exposure device and determination of field parameters
- ✓ exposure of RBEC
- ✓ RNA isolation
- ✓ chip-arrays for differential gene expression
- ✓ bioinformatic evaluation of gene-chip data
- ✓ qRT-PCR experiments / evaluation of PCR data
- identification of potential protein targets

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thank you