SUPPORTING INFORMATION

Characterization of non-olfactory GPCRs in human sperm with a focus on GPR18

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GPCR	Class	mEPKM	GPCR	Class	mEPKM	GPCR	Class	mEPKM
GPR137	Other	992.8	GPR68	Class A	0.7	CCR2	Class A	0.2
GPR135	Class A	204.6	EMR3	Adhesion	0.7	GPR116	Adhesion	0.2
GPR18	Class A	91.7	LPHN1	Adhesion	0.7	OXTR	Class A	0.2
S1PR2	Class A	78.7	F2RL1	Class A	0.7	MRGPRD	Class A	0.1
CCR6	Class A	38.3	GPR98	Class A Adhesion	0.7	P2RV8	Adnesion	0.1
CXCR4	Class A	29.5	P2RY13	Class A	0.7	GPR20	Class A Class A	0.1
ADORA3	Class A	25.6	BAI1	Adhesion	0.7	GPR146	Class A	0.1
PTH1R	Class B	21.0	GABBR1	Class C	0.6	MAS1	Class A	0.1
FPR1	Class A	17.8	P2RY6	Class A	0.6	ADORA2B	Class A	0.1
GPR153 GPR156	Class A	17.8	FZD3	Class A Frizzled	0.6	CCR4	Class A	0.1
OPRM1	Class A	11.2	LPAR2	Class A	0.6	FZD5	Frizzled	0.1
FPR2	Class A	10.3	LTB4R	Class A	0.6	SSTR4	Class A	0.1
LPAR6	Class A	9.9	HRH2	Class A	0.6	P2RY1	Class A	0.1
DRD2	Class A	9.8	CCR7	Class A	0.6	GPR61	Class A	0.1
HCAR3	Class A Class A	9.2	HTR2A	Class A	0.6	GRM6	Class A Class C	0.1
PROKR1	Class A	8.6	GPR25	Class A	0.6	GPR162	Class A	0.1
GPR56	Adhesion	7.6	GPR63	Class A	0.6	CCKBR	Class A	0.1
HCAR2	Class A	7.5	ADRA1A	Class A	0.6	GPR171	Class A	0.1
OPN3	Class A	7.3		Class B	0.6	FZD1	Frizzled	0.1
OPN5	Class C Class A	6.4	CHRM1	Class A	0.5	GPR157	Class A	0.1
MC1R	Class A	6.3	CELSR3	Adhesion	0.5	AVPR1A	Class A	0.1
P2RY2	Class A	5.8	CELSR1	Adhesion	0.5	GPR62	Class A	0.1
LPAR3	Class A	4.9	GPBAR1	Class A	0.5	NPBWR1	Class A	0.1
CHRM4	Class A	4.8	P2RY12	Class A	0.5	GPR33	Class A	0.1
FFAR2	Class C	4.0 4.8	PTGER2	Clase A	0.5	UPR3	Giass A	U. I
C3AR1	Class A	4.5	LPAR1	Class A	0.5			
MRGPRF	Class A	4.4	GPR35	Class A	0.5			
GPR97	Adhesion	4.4	F2R	Class A	0.5			
CCRL2	Class A	4.3	GPRC5A	Class C	0.5			
PTAFR	Clase A	4.3	EDNRR	Class A	0.5			
MTNR1A	Class A	4.0	GPR113	Adhesion	0.4			
GPR183	Class A	3.8	EMR4P	Adhesion	0.4			
GPR84	Class A	3.8	GPRC5C	Class C	0.4			
GRM5	Class C	3.4	TSHR	Class A	0.4			
GPR160 GPR85	Class A	3.4		Class A	0.4			
GPR65	Class A	3.1	GPR123	Adhesion	0.4			
CCR1	Class A	3.1	GALR3	Class A	0.4			
GPR182	Class A	3.0	GPR4	Class A	0.4			
HTR7	Class A	3.0	FZD7	Frizzled	0.4			
	Class A	2.9	NDEER1	Class A	0.4			
CELSR2	Adhesion	2.7	ADRB2	Class A	0.4			
GPRC5B	Class C	2.4	GRM2	Class C	0.4			
CXCR2	Class A	2.4	PTH2R	Class B	0.4			
SSTR2	Class A	2.2	UTS2R	Class A	0.3			
CHRM5	Class A	2.2	CMKLR1	Class C	0.3			
LGR6	Class A	2.1	MC5R	Class A	0.3			
GPR176	Class A	2.1	MC2R	Class A	0.3			
CXCR1	Class A	2.0	ADRA2A	Class A	0.3			
CD97	Adhesion	2.0	GPR132	Class A	0.3			
GPR107	Other	1.9	LTB4R2	Class A	0.3			
HCAR1	Class A	1.8	GPR161	Class A	0.3			
CHRM2	Class A	1.7	CASR	Class C	0.3			
DRD3	Class A	1.7	NPY1R	Class A	0.3			
GRM3	Class C	1.0	S1PR5	Class A	0.2			
FSHR	Class A	1.5	CXCR6	Class A	0.2			
EMR2	Adhesion	1.5	CCKAR	Class A	0.2			
GPR45	Class A	1.5	NMUR1	Class A	0.2			
LPAR5	Class A	1.5	NPV6P	Class A	0.2			
VIPR1	Class R	1.4	FFAR3	Class A	0.2			
BAI2	Adhesion	1.3	PTGFR	Class A	0.2			
TAS1R3	Class C	1.3	DARC	Class A	0.2			
GPR125	Adhesion	1.3	P2RY11	Class A	0.2			
INMBR BAI3	Class A	1.3	GRM4	Class B	0.2			
GABBR2	Class C	1.2	CCR3	Class A	0.2			
EMR1	Adhesion	1.2	CRHR2	Class B	0.2			
XCR1	Class A	1.1	GPR75	Class A	0.2			
MCHR2	Class A	1.1	P2RY10	Class A	0.2			
EPR3	Class A	1.0	MRGPRY3	Class A	0.2			
NPY5R	Class A	1.0	GPR143	Other	0.2			
TPRA1	Other	1.0	GPR141	Class A	0.2			
GPR133	Adhesion	1.0	GPR12	Class A	0.2			
GPR34	Class A	1.0	NPFFR2	Class A	0.2			
GPR158	Class C	0.9	CX3CP1	Class A	0.2			
P2RY14	Class A	0.9	GPR151	Class A	0.2			
GPRC5D	Class C	0.9	CCR9	Class A	0.2			
FZD6	Frizzled	0.9	GPR64	Adhesion	0.2			
FZD4	Frizzled	0.8	S1PR4	Class A	0.2			
GNRHR2	Class A	0.8	BDKRB1	Class A	0.2			
HTR1D	Class A	0.8	GPR22	Class A	0.2			
CHRM3	Class A	0.8	OXGR1	Class A	0.2			
CCR5	Class A	0.7	HRH1	Class A	0.2			

Figure S1. All detected non-olfactory GPCR transcripts in human sperm (mFPKM >0.1).

Gene		Primer Sequence (5' - 3')	Product length [bp]		
ADORA3	fwd	TCCTTCCAGTCATGTGGCTC	452		
ADORA3	rev	CTTGCGGACAACTTTGGGAG	402		
CRISP2	fwd	AGTTGCAAGTGCAAAGGGAG	360		
CRISP2	rev	CAATTCCACAGCCTACCTGG	300		
GPR137	fwd	CGTCTCAGCTATCAGACGGT	304		
GPR137	rev	AGATGACGAACAGGGAGTCG	594		
GPR18	fwd	GCCAAGCGTTACACTGGAAA	217/		
GPR18	rev	CAGCTTGTTGGTAGGCATGA	409		
GPR56	fwd	TCCTGAAGCATCCCCAGAAG	200		
GPR56	rev	GAGTCTCTTCTCAGCCTCCC	299		
LPAR6	fwd	TCTGCTATGGCTCTTCCTCAG	152		
LPAR6	rev	GAGGCCTTTTCCTCAGTTGC	152		
S1PR2	fwd	CCTGGGGACGCAGACG	259		
S1PR3	rev	AGGTTTTCCACCACAATGGC			

Figure S2. Primer sequences used for RT-PCR validation qPCR.



Figure S3. Expression of GPCR transcripts in comparison to housekeeping gene transcripts in human spermatozoa. Shown are the mFPKM values for the 20 most highly expressed GPCR in comparison to several housekeeping genes in spermatozoa. Transcripts are sorted by the mFPKM. Housekeeping genes are marked in red. RPL29: ribosomal protein L29, ACTB: β -actin; RPL13A: ribosomal protein L13A; GUSB: β -glucuronidase; TBP: TATA box binding protein.



Figure S4. Detection of GPR18 transcripts by RT-PCR. The sperm RNA of different donors and RNA from different tissues was investigated by real time RT-PCR basically as described [1] using intron-spanning primer pairs for GPR18 (Figure S2) and GAPDH (fw: ACCACAGTCCATGGCCATCAC, rv: TCCCACCACCCTGTTGCTGTA). The deltaCT values for the sperm samples (typically between -3 and - 5) point to a considerably higher relative transcript abundance in sperm compared to the control tissues.

[1] Flegel et al., PLoS One. 2015 Jun 12;10(6):e0128951



Figure S5. Detection of GPR18 transcripts by NGS. Recently, a comprehensive NGSbased study of RNA expression in sperm was conducted analyzing 72 samples (GEO dataset GSE65683) [1]. We reanalyzed the raw fastq data sets of 28 of these samples with the same parameters as used for our own NGS data sets and found a similar distribution of the FPKM values similar to our own generated data. GPR18 was expressed in these samples with a mean FPKM of 139 (min = 11, max = 573), not statistically different from the FPKM values calculated for our own sperm samples (mean FPKM of 86, min = 38, max = 173) (p > 0.05, Student's t-test). However, in both sperm data sets the FPKM values are significantly higher (p>0.0001) than in testis and in the 16 reference tissues of the Bodymap Project [2]. With the exception of one sample (white blood cells), in this reference data set all FPKM values are lower than the lowest FPKM found for GPR18 in sperm.

[1] Kravetz et al., Sci Transl Med. 2015 Jul 8;7(295):295re6

[2] Flegel et al., PLoS One. 2013;8(2):e55368



Figure S6. Secondary antibody control in human spermatozoa. As a negative control, staining was performed without primary antibody, showing no specific staining by the secondary antibody (Alexa Fluor 488 Goat Anti-Rabbit, (Control). Scale bar: 10 µm.



Figure S7. Cannabinoid-induced effects are mediated by GPR18 in human spermatozoa. Quantification of acrosomal exocytosis (categories III-IV) upon co-stimulation of THC and the selective GPR18-antagonists PSB-CB5 and PSB-CB27 (1:1, 1 μ M or 10 μ M) using PNA-FITC. Initial experiments showed that also the phytocannabinoid THC induced the acrosome reaction in human spermatozoa via GPR18. Stimulated cells (cannabinoid + antagonist) were compared to control cells (0.1 % DMSO). Three to five independent samples were analyzed with a sperm population ranging from 87 to 264 cells per single experimental condition. Values show the mean ± SEM (***p < 0.001, Student's t-test).



Figure S8. Cannabinoid receptor transcripts in human spermatozoa. Heatmap of known cannabinoid receptor transcripts.

Supporting Data

GPR18 antagonists

PSB-CB5, (*Z*)-2-(3-(4-Chlorobenzyloxy)benzylidene)-6,7-dihydro-2*H*-imidazo[2,1-*b*][1,3]-thiazin-3(5*H*)-one¹



PSB-CB27, (*Z*)-2-(3-(6-(4-Chlorophenoxy)hexyloxy)benzylidene)-6,7-dihydro-2*H*-imidazo-[2,1-b][1,3]thiazin-3(5*H*)-one



Table 1. Potencies of GPR18 inhibitors PSB-CB5 and PSB-CB27 for GPR18, GPR55, CB_1 and CB_2 receptors. All data result from three independent experiments, performed in duplicate. (For experimental details see below)¹

compound	Inhibition of a β-arrestin	agonist-induced recruitment	Radioligand binding vs. [³ H]CP55,940		
	human GPR18	human GPR55	human CB ₁	human CB ₂	
	$IC_{50} \pm S$	SEM (µM)	$K_i \pm SEM~(\mu M)$		
PSB-CB5 ¹	0.279 ± 0.111	>10 (0%)	>10 (0%)	4.03 ± 0.51	
PSB-CB27	0.650 ± 0.134	>10 (37%)	>10 (-14%)	>10 (12%)	

While PSB-CB5 showed incomplete inhibition of THC-induced GPR18 activation (58% maximal inhibition), PSB-CB27 led to a complete inhibition of GPR18-induced β -arrestin translocation.



Figure 1: Concentration-dependent inhibition of THC- $(10 \ \mu M)$ -induced GPR18 activation by the GPR18 antagonists PSB-CB5 and PSB-CB27.

Method

β-Arrestin recruitment assay

Recruitment of β -arrestin to the respective receptor was detected by using β -galactosidase enzyme fragment complementation technology (β-arrestin PathHunter[™] assay, DiscoverX, Fremont, CA, USA). CHO cells stably expressing the respective receptor were seeded in a volume of 90 µL into a 96-well plate and were incubated at a density of 20,000 cells/well in assay medium (Opti-MEM, 2 % FCS, 100 U/ml penicillin, 100 µg/ml Streptomycin, 800 µg/mL geneticin und 300 µg/mL hygromycin) for 24 h at 37°C. Then test compounds were diluted in PBS buffer containing 10 % DMSO and 0.1 % BSA and added to the cells in a volume of 10 µL, followed by an incubation for 90 min at 37° C. For determination of baseline luminescence PBS buffer (containing 10 % DMSO, 0.1 % BSA) in the absence of test compound was used. During the incubation period, the detection reagent was prepared. For determination of β -arrestin recruitment to GPR18 the provided detection reagent was used, according to the supplier's protocol. The composition of the detection reagent for GPR55 assays was changed: it was obtained by mixing the chemiluminescent substrate Galacton-StarR (2 mM), with the luminescence enhancer Emerald-II[™] and a lysis buffer (10 mM TRIS, 1 mM EDTA, 100 mM NaCl, 5 mM MgCl₂, 1 % Triton-X; pH 8) in a ratio of 1:5:19. After the addition of 50 µl/well of detection reagent to the cells, the plate was incubated for further 60 min at room temperature. Finally luminescence was determined in a luminometer (TopCount NXT, Packard / Perkin-Elmer).

Reference for supporting data

[1] Rempel, V.; Atzler, K.; Behrenswerth, A.; Karcz, T.; Schoeder, C.; Hinz, S.; Kaleta, M.; Thimm, D.; Kiec-Kononowicz, K.; Müller, C. E. Med. Chem. Comm. 2014, 5, 632.