



Epigenetics in glioma

_

MGMT, ABCB1 and ABCG2 methylation in glioma

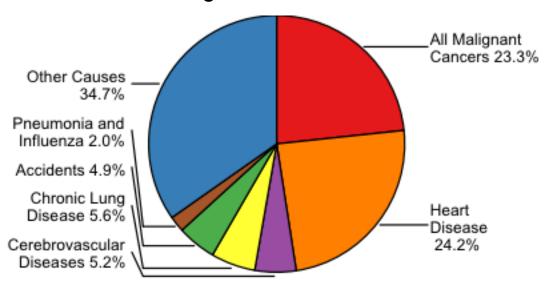
Moritz C. Oberstadt, PhD



Tumor diseases



One of the leading death causes



US Mortality Files, National Center for Health Statistics, Centers for Disease control and Prevention

High maligne tumors with low 5 years overall survival (OS):

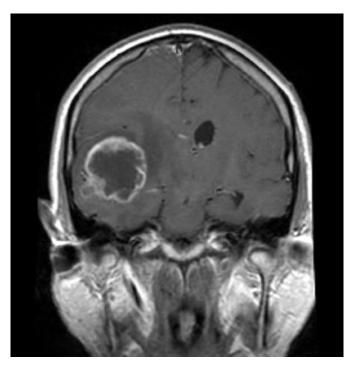
- Brain tumors (13%/15%)
 - Stomach- (12%/13%) and Oesophaguscarcinoma (7%/8%)
 - Lung carcinoma (6%/6%)
 - Pancreas carcinoma (3%/2%)

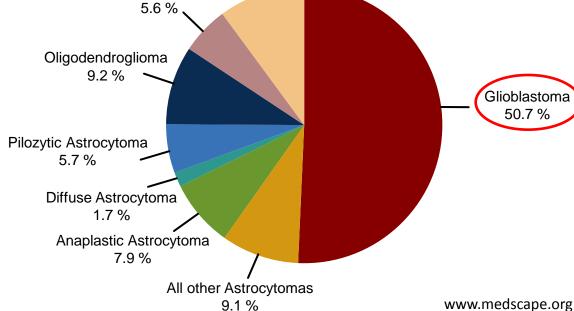


Glioblastoma multiforme



- Glioblastoma multiforme is the most frequent and aggressive primary brain tumor in adults
- Referring to WHO cassification of brain tumors: Grade IV





All other Gliomas 10.1 %

Ependymoma

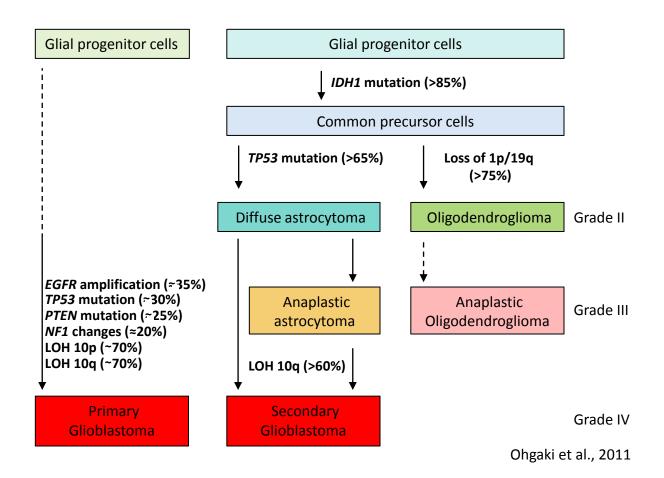
www.radiopaedia.org



Glioblastoma multiforme



- Multimodal therapy with resection, radiotherapy and chemotherapy with temozolomide leads to a median OS of 14.6 months
- 2 year OS rate of patients with glioblastoma just 26,5%

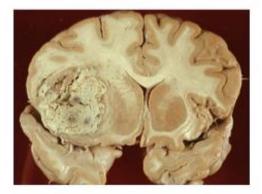




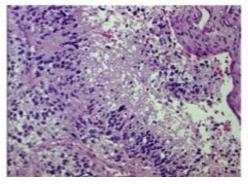
Glioblastoma multiforme



 Markers: High cellular proliferation rate, diffuse infiltration, necrosis, angiogenesis, apoptosis resistence and genomic instability.



D.P. Agamanolis



PD Dr. Vogelgesang, Greifswald

 Necrotic centers typically surrounded by hypercellular zones: pseudopallisades

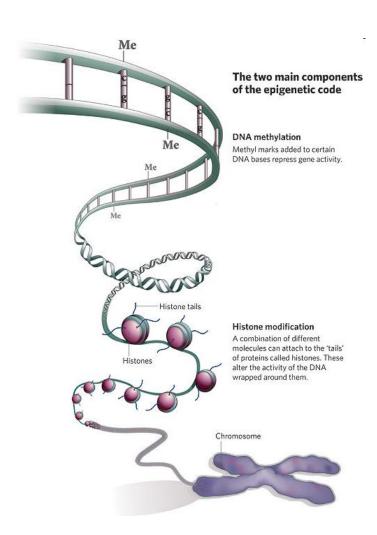


Epigenetic mechanisms



DNA-Methylation

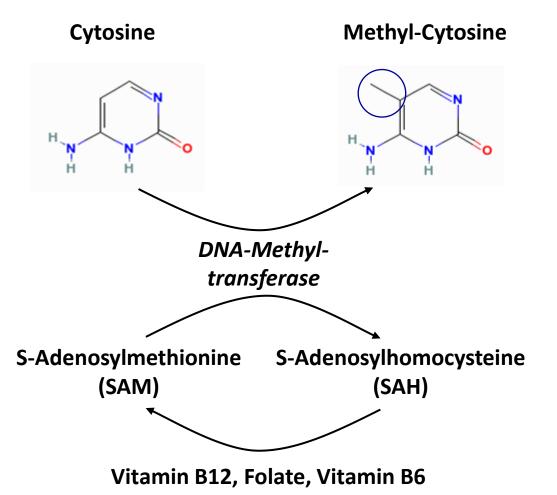
Histone modification





DNA methylation



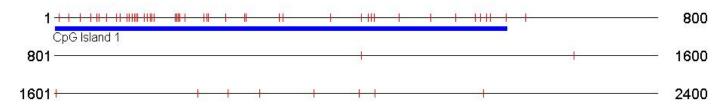




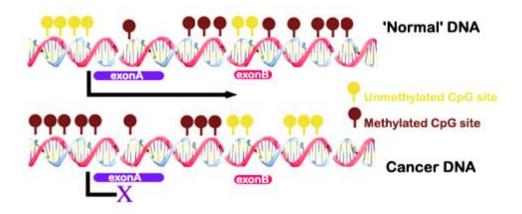
DNA methylation



Clusters of CpG sites: CpG islands



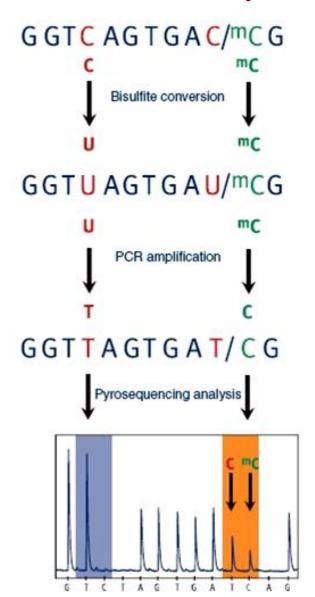
- CpG islands in promoters of about 60% of all human genes
- Loss of methylation throughout the genome in cancer cells



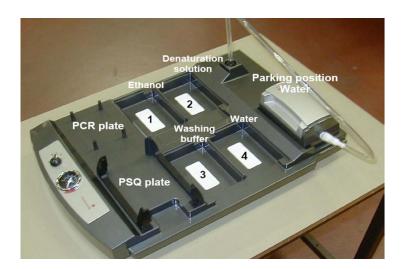


Analysis of methylation Pyrosequencing





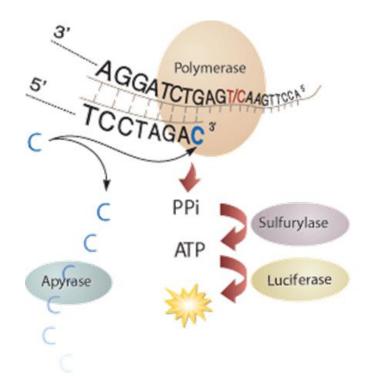
Pyrosequencing after Bisulfite treatment

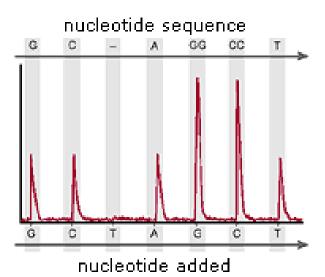


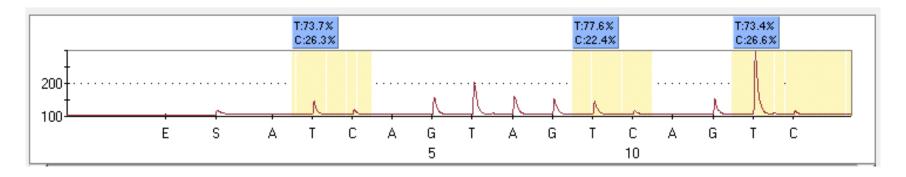


Analysis of methylation Pyrosequencing











Genes to analyze



- MGMT (O6 methylguanine methyltransferase)
- ABCB1 (P-gp)
- ABCG2 (BCRP)



Genes to analyze



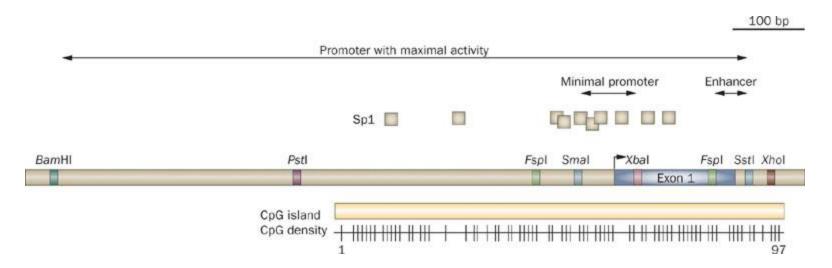
- MGMT (O6 methylguanine methyltransferase)
- ABCB1 (P-gp)
- ABCG2 (BCRP)



MGMT



- DNA repair enzyme, removing mutagenic adducts from the O6 position of guanine
- MGMT causes resistance to alkylating drugs
- Survival of patients with gliomas is significantly better in previous publications, if the promoter of MGMT is methylated





Genes to analyze

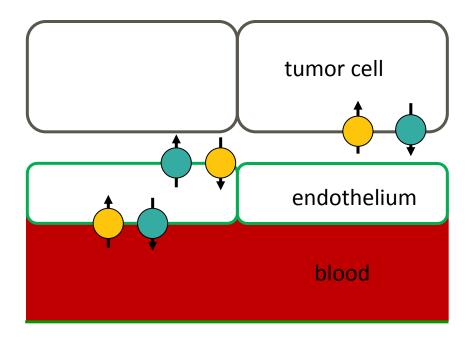


- MGMT (O6 methylguanine methyltransferase)
- ABCB1 (P-gp)
- ABCG2 (BCRP)



Transport proteins











Clinical characteristics

Cillical Characteristics			
Characteristic	Age [Years]		
Median age at diagnosis	61.6		
Range [MinMax.]	40.2 - 79.9		
Patients with temozolomide therapy			
Median age at diagnosis	59.2		
Patients without temozolomide therapy			
Median age at diagnosis	64.0		
Characteristic	Number of	% of	
	patients	patients	
Age classes			
<50 years	11	17.2	
50 - 60 years	18	28.1	
60 - 70 years	20	31.3	
>70 years	15	23.4	
Sex			
Male	39	60.9	
Female	25	39.1	
Pathohistology			
Glioblastoma multiforme	64		
Relapses of primary glioblastoma multiforme	17		
Therapy			
Only Radiotherapy	11	17.2	
Radiotherapy and temozolomide	45	70.3	
No adjuvant therapy	6	9.4	
No therapy data applicable	2	3.1	
Overall survival (OS)			
Median [Days]	459		
Range [MinMax.]	34 - 1954		
1-year survival	38	59.4	
2-year survival	9	14.1	
OS of patients with temozolomide therapy			
Median [Days]	515		
Range [MinMax.]	95 - 1954		
OS of patients without temozolomide therapy			
Median [Days]	87		
Range [MinMax.]	34 - 701		
Vital status at study end (30.06.2009)	l		
Dead	47	73.4	

Alive

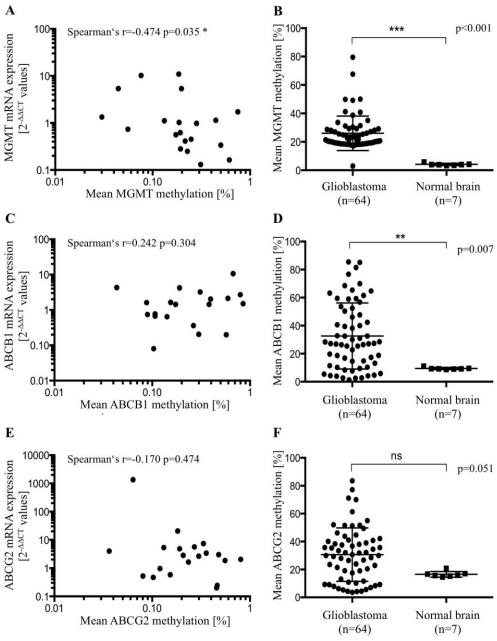
26.6





Methylation and expression







MGMT methylation and OS



Variable	Haz. Ratio	p-value	[95% Conf. Interval]	
Sex				
male	1.488	0.238	0.769	2.876
(ref. female)	1.259	0.602	0.530	2.992
	1.724	0.393	0.494	6.024
Age				
50-<60 years	1.734	0.299	0.613	4.903
(ref. <50 years)	1.648	0.394	0.523	5.192
	1.183	0.916	0.053	26.577
Age				
60-<70 years	2.567	0.057	0.972	6.780
(ref. <50 years)	3.242	0.039	1.061	9.901
,	1.417	0.757	0.156	12.826
Age				
≥70 years	6.427	0.001	2.194	18.824
(ref. <50 years)	10.700	0.000	2.998	38.191
,	2.442	0.445	0.247	24.152
Mean methylation				
level (continuous)	0.988	0.315	0.964	1.012
	0.975	0.121	0.945	1.007
	1.023	0.403	0.970	1.078



ABCB1 methylation and OS



Variable	Haz. Ratio	p-value	[95% Conf. Interval]	
C				
Sex	1			• 0.66
male	1.457	0.276	0.740	2.866
(ref. female)	1.130	0.793	0.454	2.813
	4.222	0.043	1.045	17.060
Age				
50-<60 years	1.793	0.282	0.619	5.191
(ref. <50 years)	1.500	0.490	0.474	4.742
	5.358	0.234	0.338	84.863
Age				
60-<70 years	2.474	0.066	0.942	6.499
(ref. <50 years)	2.235	0.140	0.768	6.507
,	3.596	0.290	0.336	38.441
Age				
≥70 years	6.069	0.001	2.107	17.479
(ref. <50 years)	9.872	0.000	2.786	34.988
	5.112	0.167	0.505	51.721
Mean methylation				
level (continuous)	0.995	0.461	0.981	1.009
	1.002	0.864	0.984	1.020
	0.973	0.032	0.950	0.998



ABCG2 methylation and OS

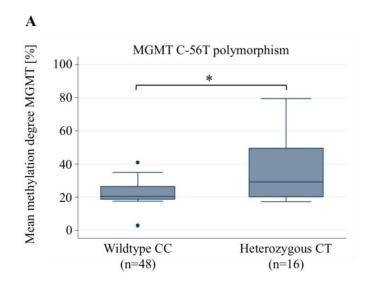


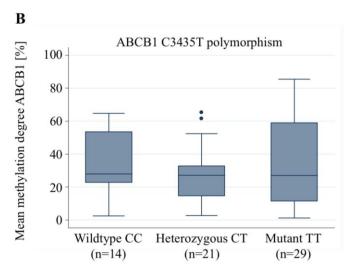
Variable	Haz. Ratio	p-value	[95% Conf. Interval]	
Sex				
male	1.463	0.271	0.743	2.879
(ref. female)	1.092	0.842	0.459	2.600
	2.489	0.211	0.596	10.389
Age				
50-<60 years	1.745	0.317	0.586	5.195
(ref. <50 years)	1.454	0.545	0.433	4.882
•	1.552	0.760	0.092	26.033
Age				
60-<70 years	2.270	0.085	0.892	5.778
(ref. <50 years)	2.271	0.118	0.811	6.358
,	1.068	0.957	0.102	11.210
Age				
≥70 years	6.112	0.001	2.087	17.903
(ref. <50 years)	9.923	0.000	2.808	35.062
	2.774	0.376	0.290	26.572
Mean methylation				
level (Continuous)	1.003	0.736	0.986	1.021
	0.998	0.836	0.977	1.019
	1.018	0.430	0.974	1.065

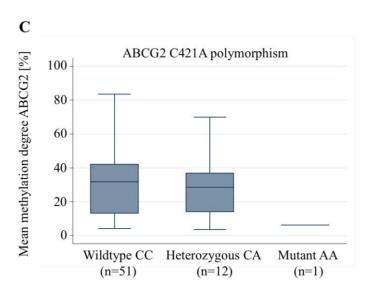


Methylation and Polymorphisms





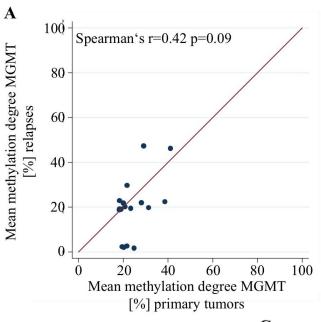


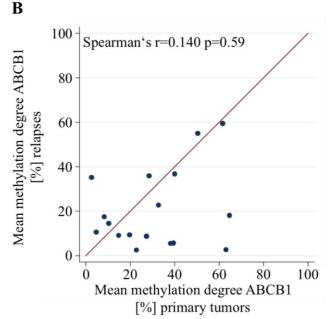


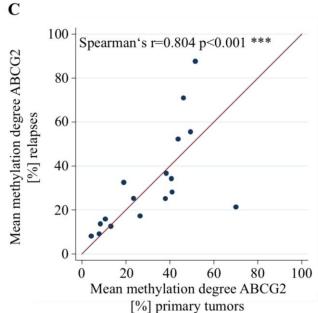


Methylation in relapses











Conclusions



- Methylation of MGMT, ABCB1 and ABCG2 have no prognostic impact for OS in glioblastoma multiforme
- Significant negative correlation between MGMT methylation and expression
- Markedly elevated MGMT and ABCB1 methylation in glioblastoma specimens
- Significant correlation between MGMT methylation and MGMT C-56T polymorphism
- Significant correlation of ABCG2 methylation in primary tumors and relapses

Acknowledgements



- Heyo K. Kroemer, PhD
- S. Bien-Möller, PhD
- S. Herzog
- M. Ricker and all members of the Kroemer Lab





- Eric C. Holland, MD, PhD
- E. Bazzoli, MD
- M. Squatrito, PhD
- N. Schultz
- B. Wee Trent and all members of the Holland Lab
- Henry W. S. Schroeder, MD
- PD Dr. Vogelgesang

Acknowledgements for the financial support by

- Gerhard-Domagk-Program of the University medicine Greifswald, Germany
- Rottendorf Foundation, Ennigerloh, Germany



