Neurosurg Rev (2008) 31:247–248
DOI 10.1007/s10143-008-0125-9

ERRATUM

Candidate genes for the progression of malignant gliomas identified by microarray analysis

Negative results in the logarithmic M AstroIII/GBM quotient represents upregulation of the gene

Oliver Bozinov · Sylvia Köhler · Birgit Samans · Ludwig Benes · Dorothea Miller · Markus Ritter · Ulrich Sure · Helmut Bertalanffy

Published online: 27 February 2008

Erratum to: Neurosurg Rev (2008) 31:83-90
DOI 10.1007/s10143-007-0107-3

It was brought to our attention, that there is a misinterpretation of the data in the text of our article [2]. After comparing our data with the original ones, we found that the microarray data as shown in our *Table 1* [2] are correct. However, in the text the column indicating the direction of expression "down or up" has been mistaken: "down" in this table refers to a lower expression in anaplastic astrocytomas (AA) relative to glioblastomas (GBM).

This is consistent with the other values given in the Table. The median expression levels for both groups were calculated as mean log2-ratios. A negative result in the logarithmic M AstroIII/GBM quotient represents an upregulation of the gene inGBM. In this regard the direction of the expression level (FC) in column six can be misleading, but represents correctly the direction from GBM to AA and not vice versa, as we erroneously have used in the discussion [2].

Unfortunately, the real-time PCR results in the same (small) group of tumors did in fact falsely indorse the misinterpreted results. Recent further investigation in a larger group of tumors (34 samples) of the same histology has meanwhile put into perspective the results of IL-13Rα2 and *Olig2*. *Olig2* had an almost 4-fold higher expression in AA (0,1146) compared to GBM (0,0294) with statistical significance (p=0,025). IL-13Rα2 showed now a near equal expression (AA 2,5078, GBM 2,7831) with no statistical significance. Previous results [1, 5] showed significant decline of gene expression with tumor grade and lowest expression of *Olig2* in GBM, which is now consistent with our further analysis and correctly interpreted array results. The equal expression of *IL*-13Rα2 in our recent larger PCR series does not answer satisfactorily the question of expression differences between AA and GBM.

These differences in real-time PCR quantification compared to the array results make their confirmation insecure. In similar studies Hoelzinger et al. confirmed only 19 genes out of 21 by quantitative RT-PCR [3] and van den Boom et al. in 9 out of 12 cases [6]. According to Vandesompele

The online version of the original article can be found at http://dx.doi.org/10.1007/s10143-007-0107-3.

O. Bozinov (✉) · H. Bertalanffy
Department of Neurosurgery, University Hospital Zurich,
Frauenklinikstrasse 10,
8091 Zurich, Switzerland
e-mail: oliver.bozinov@usz.ch

S. Köhler · L. Benes · D. Miller · U. Sure
Department of Neurosurgery,
Philipps University Hospital Marburg,
Marburg, Germany

B. Samans
Institute of Molecular Biology and Tumor Research,
Philipps University Marburg,
Marburg, Germany

M. Ritter
Department of Oncology, Sindelfingen Hospital,
Sindelfingen, Germany

et al. normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes might be the solution and could open the possibility of studying the biological relevance of small expression differences [7]. However, small series, such as ours, seam to be at risk for false confirmation and even further studies in larger groups can be misleading. Additional tissue based investigation, such as immunohistochemistry or in situ hybridization may in future be more valuable to support the results from the PCR studies

It will be our obligation for the future, to provide profound data on a large amount of tissue samples and different quantification methods to clarify these uncertainties and initial microarray analysis, especially regarding IL-13Rα2, which plays a critical biologic role in IL-13 cytotoxin-mediated therapy for GBM [4]. Any possible beneficial role of this treatment regimen for GBM rather than for AA needs to be confirmed by a larger series. Accordingly, clinical trials addressing the prognostic relevance may highlight the functional significance. The conclusion of our article regarding the powerful approach of gene expression profiling to identify transcriptional differences of significance in gliomas remains [2], but its confirmation seems challenging and needs expansion to multiple quantification methods in order to avoid interpretation mistakes.

References

1. Bouvier C, Bartoli C, Guirre-Cruz L, Virard I, Colin C, Fernandez C et al (2003) Shared oligodendrocyte lineage gene expression in gliomas and oligodendrocyte progenitor cells. J Neurosurg 99:344–350
2. Bozinov O, Köhler S, Samans B, Benes L, Miller D, Ritter M, Sure U, Bertalanffy H (2008) Candidate genes for the progression of malignant gliomas identified by microarray analysis. Neurosurg Rev 31:83–90
3. Hoelzinger DB, Mariani L, Weis J, Woyke T, Berens TJ, McDonough WS et al (2005) Gene expression profile of glioblastoma multiforme invasive phenotype points to new therapeutic targets. Neoplasia 7:7–16
4. Kawakami K, Kawakami K, Taguchi J, Murata T, Puri RK (2005) Evidence that IL-13R alpha2 chain in human glioma cells is responsible for the antitumour activity mediated by receptor-directed cytotoxin therapy. J Immunother 28:193–202
5. Mokhtari K, Paris S, Guirre-Cruz L, Privat N, Criniere E, Marie Y et al (2005) Olig2 expression, GFAP, p53 and 1p loss analysis contribute to glioma subclassification. Neuropathol Appl Neurobiol 31:62–69
6. van den Boom J, Wolter M, Kuick R, Misek DE, Youkilis AS, Wechsler DS et al (2003) Characterization of gene expression profiles associated with glioma progression using oligonucleotide-based microarray analysis and real-time reverse transcription-polymerase chain reaction. Am J Pathol 163:1033–1043
7. Vandesompele J, De Preter K, Pattyn F, Poppe B, Van Roy N, De Paepe A et al (2002) Accurate normalization of real-time quantitative RT-PCR data by geometric averaging of multiple internal control genes. Genome Biol 18;3:RESEARCH0034