Transcriptional changes induced by bevacizumab combination therapy in responding and non-responding recurrent glioblastoma patients - DTU Orbit (03/12/2018)

Transcriptional changes induced by bevacizumab combination therapy in responding and non-responding recurrent glioblastoma patients

Background: Bevacizumab combined with chemotherapy produces clinical durable response in 25-30% of recurrent glioblastoma patients. This group of patients has shown improved survival and quality of life. The aim of this study was to investigate changes in gene expression associated with response and resistance to bevacizumab combination therapy. Methods: Recurrent glioblastoma patients who had biomarker-accessible tumor tissue surgically removed both before bevacizumab treatment and at time of progression were included. Patients were grouped into responders (n = 7) and non-responders (n = 14). Gene expression profiling of formalin-fixed paraffin-embedded tumor tissue was performed using RNA-sequencing. Results: By comparing pretreatment samples of responders with those of non-responders no significant difference was observed. In a paired comparison analysis of pre- and posttreatment samples of non-responders 1 gene was significantly differentially expressed. In responders, this approach revealed 256 significantly differentially expressed genes (72 down and 184 up-regulated genes at the time of progression). Genes differentially expressed in responders revealed a shift towards a more proneural and less mesenchymal phenotype at the time of progression. Conclusions: Bevacizumab combination treatment demonstrated a significant impact on the transcriptional changes in responders; but only minimal changes in non-responders. This suggests that non-responding glioblastomas progress chaotically without following distinct gene expression changes while responding tumors adaptively respond or progress by means of the same transcriptional changes. In conclusion, we hypothesize that the identified gene expression changes of responding tumors are associated to bevacizumab response or resistance mechanisms.

General information
State: Published
Organisations: Department of Bio and Health Informatics, Genomic Epidemiology, Rigshospitalet, University of Copenhagen, Danish Cancer Society
Number of pages: 10
Publication date: 2017
Peer-reviewed: Yes

Publication information
Journal: B M C Cancer
Volume: 17
Article number: 278
ISSN (Print): 1471-2407
Ratings:
BFI (2018): BFI-level 1
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 1
Scopus rating (2017): CiteScore 3.49 SJR 1.464 SNIP 1.066
Web of Science (2017): Impact factor 3.288
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 1
Scopus rating (2016): CiteScore 3.56 SJR 1.488 SNIP 1.071
Web of Science (2016): Impact factor 3.288
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 1
Scopus rating (2015): CiteScore 3.72 SJR 1.652 SNIP 1.14
Web of Science (2015): Impact factor 3.265
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 1
Scopus rating (2014): CiteScore 3.73 SJR 1.719 SNIP 1.27
BFI (2013): BFI-level 1
Scopus rating (2013): CiteScore 3.84 SJR 1.694 SNIP 1.282
Web of Science (2013): Impact factor 3.319
ISI indexed (2013): ISI indexed yes
BFI (2012): BFI-level 1
Scopus rating (2012): CiteScore 3.79 SJR 1.654 SNIP 1.203
Web of Science (2012): Impact factor 3.333
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes
BFI (2011): BFI-level 1
Scopus rating (2011): CiteScore 3.55 SJR 1.541 SNIP 1.074
ISI indexed (2011): ISI indexed yes
BFI (2010): BFI-level 1
Scopus rating (2010): SJR 1.508 SNIP 1.123
Web of Science (2010): Indexed yes
BFI (2009): BFI-level 1
Scopus rating (2009): SJR 1.437 SNIP 1.069
Web of Science (2009): Indexed yes
BFI (2008): BFI-level 1
Scopus rating (2008): SJR 1.531 SNIP 0.956
Web of Science (2008): Indexed yes
Scopus rating (2007): SJR 1.274 SNIP 0.874
Scopus rating (2006): SJR 1.06 SNIP 0.729
Scopus rating (2005): SJR 1.082 SNIP 0.707
Scopus rating (2004): SJR 0.975 SNIP 0.824
Scopus rating (2003): SJR 0.664 SNIP 0.572
Scopus rating (2002): SJR 0.354 SNIP 0.596
Original language: English
Keywords: Anti-angiogenic, RNA-sequencing, Protein kinase C, Reverse mesenchymal transition, TGF-beta
Electronic versions:
art_3A10.1186_2Fs12885_017_3251_3.pdf
DOIs:
10.1186/s12885-017-3251-3

Bibliographical note
This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons license, and indicate if changes were made. The Creative Commons Public Domain Dedication waiver (http://creativecommons.org/publicdomain/zero/1.0/) applies to the data made available in this article, unless otherwise stated.
Source: FindIt
Source-ID: 2356856711
Research output: Research - peer-review › Journal article – Annual report year: 2017