



Whole genome duplication is an early event leading to aneuploidy in -wild type glioblastoma

Submitted by Beatrice Guillaumat on Tue, 01/08/2019 - 15:06

Titre	Whole genome duplication is an early event leading to aneuploidy in -wild type glioblastoma
Type de publication	Article de revue
Auteur	Boisselier, Blandine [1], Dugay, Frédéric [2], Belaud-Rotureau, Marc-Antoine [3], Coutolleau, Anne [4], Garcion, Emmanuel [5], Menei, Philippe [6], Guardiola, Philippe [7], Rousseau, Audrey [8]
Editeur	Impact Journals
Type	Article scientifique dans une revue à comité de lecture
Année	2018
Langue	Anglais
Date	13 Nov. 2018
Pagination	36017-36028
Volume	9
Titre de la revue	Oncotarget
ISSN	1949-2553
Mots-clés	aneuploidy [9], chromothripsis [10], Glioblastoma [11], SNP arrays [12], whole genome duplication [13]
Résumé en anglais	Glioblastoma, the most frequent and lethal form of glioma, displays chromosome instability and recurrent somatic copy number alterations (SCNA). Chromothripsis and whole genome duplication (WGD) have been recently identified in cancer. In the present study, we analyzed SCNA and determine the ploidy pattern in 123 -wild-type glioblastomas, using SNP array data. WGD and chromothripsis events were validated using, respectively, FISH and CTLPScanner. WGD was detected in 11.4% glioblastomas (14/123) and was associated with mutation ($= 0.0068$). It was an early event occurring after the recurrent SCNA observed in diffuse high-grade gliomas. Glioblastomas with WGD were more aneuploid compared to glioblastomas without WGD (< 0.0001). Chromothripsis occurred in 29.3% glioblastomas (36/123) and mostly affected chromosomes 7, 9 and 12, with amplification of oncogenes (EGFR, /), and homozygous deletion of tumor suppressor genes (/). There was a significant association between chromothripsis and gene rearrangement at a given locus. WGD is an early genetic event significantly associated to mutation and leading to chromosome instability and aneuploidy in -wild-type glioblastoma. Chromothripsis recurrently targets oncogenes and tumor suppressor genes that are key players in gliomagenesis and tumor progression. The occurrence of chromothripsis points to underlying gene rearrangements (including gene fusions), potential therapeutic targets in glioblastoma.
URL de la notice	http://okina.univ-angers.fr/publications/ua18541 [14]
DOI	10.18632/oncotarget.26330 [15]
Lien vers le document	http://www.oncotarget.com/index.php?journal=oncotarget&page=article&op=v... [16]

Autre titre Oncotarget

Identifiant

(ID) 30542515 [17]

PubMed

Liens

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- [15] <http://dx.doi.org/10.18632/oncotarget.26330>
- [16] [http://www.oncotarget.com/index.php?journal=oncotarget&page=article&op=view&path\[\]](http://www.oncotarget.com/index.php?journal=oncotarget&page=article&op=view&path[])
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Publié sur *Okina* (<http://okina.univ-angers.fr>)