GENOMIC SEQUENCING IN GLIOMAS: Case series

Yorio F.[1], Cardoso A.[1], Calabrese B.[1], Palomar N.[1], Cerrato S.[1], Muggeri A.[1], Diez B.[1]

Introduction

Cancer understanding and treatment strategies have dramatically changed based on genomic tumor analysis. Primary brain tumors classification has been modified upon molecular basis. However, its treatment and prognosis has not yet found a turning point with immunotherapies or targeted therapies. Genomic sequencing might be a key tool to select better treatments.

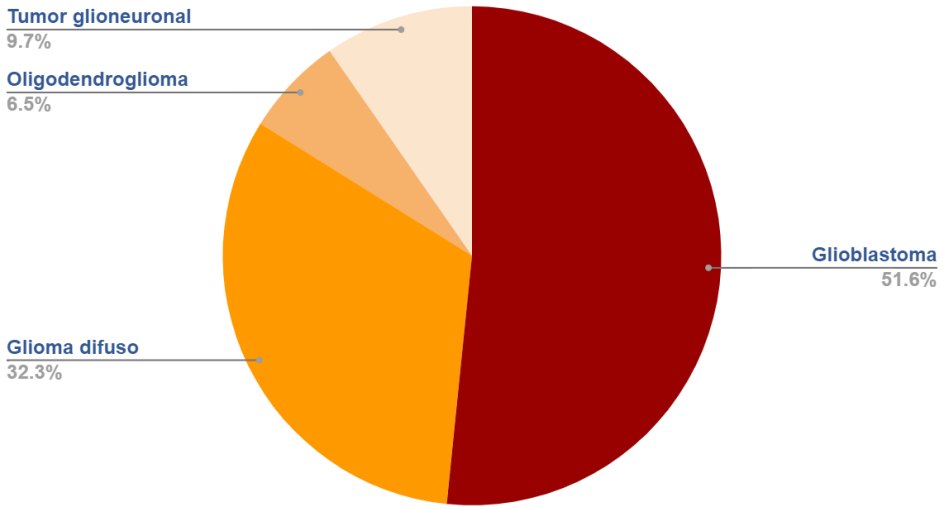
Objectives

The objective of this work is to analyze the frequency and type of genomic alterations found in genomic sequencing of glial tumors.

Materials and methods

Retrospective review of clinical records from patients with histopathologic diagnosis of glial tumors was assessed at a tertiary neurological center in Buenos Aires, Argentina. Those with further analysis of whole genome next generation sequencing (NGS) were selected. Only patients over 16 years of age were included.

Figure 1. Histological diagnosis



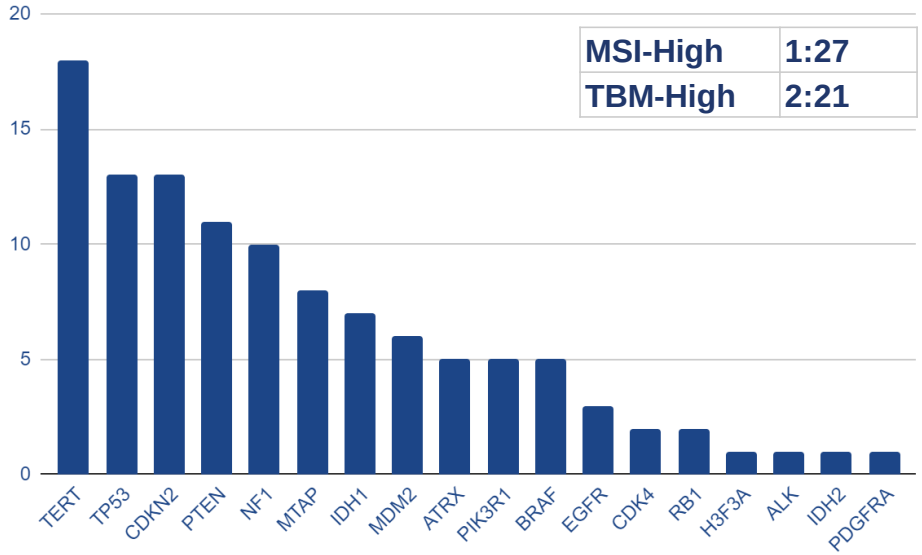


Figure 2. Frequency of genomic alterations in all samples

Table 1. Genomic alterations findings

	Number of genomic alterations (median)	Most frequent alterations
All tumors	5	See figure 2
Glioblastoma	5	TERT, TP53, PTEN, NF1, CDKN2
Diffuse glioma	4	ATRK, CDKN2, TP53
Glioneuronal tumor	4	IDH1
Oligodendroglioma	3	-

Conclusions

The most frequent genomic alteration in brain gliomas was found to be of the TERT gene. Microsatellite status is found to be stable in most brain primary tumors and tumoral mutational burden tends to be low with rare exceptions. Future analysis of large samples of brain tumor sequencing with NGS might clear up which are the most distinguishing features of genomic alterations in glial tumors.

1. Department of Neurooncology, FLENI. Buenos Aires, Argentina. **Authors disclosures:** authors have nothing to disclose.