Growth Factor Receptor Fusions Predict Therapeutic Sensitivity

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Dysregulated growth factor pathways promote tumor growth in many cancers, but receptor-targeting strategies frequently offer limited benefit despite activation by receptor overexpression or amplification. In contrast, tumors harboring growth factor receptor fusions display exquisite dependence on receptor activity, providing predictive markers for patient response to inform precise oncology treatment. Clin Cancer Res; 21(14); 3105–7. ©2015 AACR.

See related article by Di Stefano et al., p. 3307

In this issue of Clinical Cancer Research, Di Stefano and colleagues (1) discuss the use of RT-PCR-sequencing as a sensitive and specific method to identify FGFR–TACC fusion genes in patients with grade 2–4 gliomas. In their study, FGFR3–TACC3-positive patients treated with a FGFR inhibitor derive clinical benefit.

Theodor Boveri proposed that acquired chromosomal abnormalities have an important role in the initiation of carcinogenesis a century ago (2). Growth factors promote a myriad of potentially oncogenic activities; therefore, it is not surprising that growth factor receptors and downstream effectors are commonly altered in cancers through transcriptional upregulation, gene amplification, activating mutation, and genomic fusion events. Fusion genes are generated when two previously separate genes rearrange and fuse together, resulting in a hybrid gene. The first fusion gene described in cancer cells was the Philadelphia chromosome in chronic myeloid leukemia (CML) discovered in 1960 as a result of the work of Nowell and Hungerford (3). Four decades later, the extraordinary activity of imatinib against CML harboring the BCR–ABL1 fusion exemplified precision targeting of genetic targets as an effective therapeutic approach in oncology (4). In solid tumors, the EML4–ALK fusion reported in 4% to 7% of lung cancers has been successfully targeted with a FGFR inhibitor resulting in prolonged survival of mice harboring intracranial FGFR3–TACC3-initiated glioma. Hence, a subset of glioblastoma patients that harbor the FGFR–TACC fusions could derive benefit from targeted FGFR kinase inhibition. FGFR inhibitors for FGFR3–TACC3-positive glioblastomas may have large therapeutic indices due to the relatively low levels of wild-type FGFR3 within the brain. FGFR3 inhibitors would presumably target only the neoplastic compartment expressing FGFR3–TACC3, while sparing normal healthy tissues.

The precise application of FGFR targeting for patients with the relevant fusions will require rapid and accurate detection of these fusion events. Selection of methods utilized to diagnose the fusion genes is informed by the type of fusion. Fusion genes resulting from translocations are usually diagnosed by fluorescence in situ hybridization (FISH), detecting abnormal chromosomes within the cell, e.g., BCR–ABL1 fusions in chronic CML. Microarray techniques are also used to diagnose fusion genes that arise as a result of overexpression of one of the fusion partners, e.g., TMPRSS2–ERG fusions in prostate cancer (11). Next-generation whole transcriptome sequencing aids in diagnosis of fusions genes by analyzing the different reads from fusion gene as compared with normal tissue. Polymerase chain reaction (PCR) with primers flanking the fusion junction followed by sequencing informs the diagnosis of fusion gene if both fusion partner genes are present on analysis. In the current issue, Di Stefano and colleagues describe the detection, characterization, and inhibition of FGFR–TACC fusions in glioma with wild-type isocitrate dehydrogenase 1 (IDH1). Due to the close proximity of FGFR3 and TACC3 on chromosome 4p16.3, FISH detection of FGFR3–TACC3 rearrangements is not optimal using currently available methods.

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available methods. The authors developed an RT-PCR assay to identify the known and possibly novel variants of FGFR1–TACC1 and FGFR3–TACC3 fusions that retain the mRNA sequences coding for the key FGFR–TK and TACC domains required for the oncogenic activity of the fusion protein. Critically, confirmation of the in-frame breakpoint was performed by Sanger sequencing.

Three of 85 wild-type IDH1/2 grade 2–3 gliomas (3.5%) harbored FGFR3–TACC3 fusions; however, none of 126 IDH1/2–mutant tumor samples demonstrated evidence of FGFR3–TACC3 fusions. Seventeen of the 584 glioblastoma (2.9%) harbored FGFR–TACC rearrangements. These findings are consistent with the 3% incidence of FGFR–TACC rearrangements in glioblastoma described earlier (10). IDH wild-type grade 2–3 gliomas (diffuse glioma and anaplastic glioma) have similar prevalence of FGFR–TACC3 fusions to that of glioblastoma, suggesting an early mutation consistent with a tumor driver. The authors report 6 new fusion transcripts that have not been reported before. Collectively, these results suggest that FGFR fusions may serve as early tumor drivers in the absence of IDH1 mutations and that the direct contribution TACC to oncogenic function may be modest.

Recent work from the comprehensive analysis of 293 grade 2 and 3 gliomas using multiple genomic and proteomic platforms from The Cancer Genome Atlas reported three superclusters of these tumors (12). Group 1 tumors are wild-type for IDH1/IDH2; group 2 tumors are IDH1/IDH2 mutant with chromosome 1p/19q intact; and group 3 harbors IDH1/IDH2 mutations with codeletion of chromosome 1p/19q. The IDH wild-type group of grade 2 or 3 gliomas have a glioblastoma-like phenotype: focal gains of EGFR, CDK4, and MDM4, mutations in NF1, EGFR, and PTEN, and a poor median survival, compared with those who harbor IDH1/IDH2 mutations. Di Stefano and colleagues also report that FGFR–TACC rearrangements are mutually exclusive with IDH1/2 mutations and EGFR amplification whereas co-occur with CDK4 amplification and MDM2 to a lesser extent. In this era of precision medicine and targeted therapy, knowledge of these molecular characteristics will help enrich the future trials with patients who harbor appropriate mutations and that are likely to derive benefit from agents targeting the mutation.

Di Stefano and colleagues further describe the clinical benefit they observed when they used INJ-42756493, an inhibitor of FGFR1–4, in the treatment of 2 patients whose tumors harbored the fusion gene FGFR3–TACC3. This preliminary clinical activity supports further evaluation of FGFR inhibition in FGFR–TACC-positive patients. Previous trials of FGFR inhibitors, such as nine-tinib (13) or dottinib (14), in unselected recurrent glioblastoma did not demonstrate meaningful clinical activity. However, an ongoing phase II study of BC2198 in recurrent glioblastoma enriches patients that harbor amplification, translocation, or activating mutation in FGFR1, 2, 3, or 4 (NCT01975701) and may address the clinical utility of these agents in this patient population. Whether the success in targeting BCR–ABL1 in leukemia and in the EMLA–ALK fusion in lung cancer will be replicated for the FGFR inhibitors in gliomas with FGFR3 fusions remains to be determined, but new hope for targeted therapies against growth factor pathways is emerging for these tumors.
Disclosure of Potential Conflicts of Interest

M.S. Ahluwalia reports receiving commercial research grants, through his institution, from Boehringer Ingelheim, Eli Lilly/ImClone Systems, Novartis, Spectrum Pharmaceuticals, and TRACON Pharmaceuticals; speakers bureau honoraria from Sigma-Tau Pharmaceuticals; and is a consultant/advisory board member for Caris Life Sciences, Genentech/Roche, and Incyte. No potential conflicts of interest were disclosed by the other author.

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Development of methodology: M.S. Ahluwalia
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): M.S. Ahluwalia
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): M.S. Ahluwalia
Writing, review, and/or revision of the manuscript: M.S. Ahluwalia, J.N. Rich
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): M.S. Ahluwalia
Study supervision: M.S. Ahluwalia

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