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Cancer Diagnostics Conference & Expo

June 13-15, 2016 Rome, Italy

A functional approach for searching biomarkers of glioma

Kopylov A^{1, 3}, Pasynkova K³, Pustogarov N^{2, 3}, Revishchin A^{2, 3} and Pavlova G^{2, 3}
¹Lomonosov Moscow State University, Russia
²Institute of Gene Biology-RAS, Russia
³Apto-Pharm Ltd, Russia

Trends in developing biomarker for tumors, including gliomas are bifurcated into following directions. Firstly, studying differential expression of genes in tumors versus corresponding normal tissues is done. Secondly, expert studying of expression of particular genes selected according to presumed function in glioblastoma multiform (GBM) development and malignancy. Neural cancer stem cells (CSCs) or neural/glial cancer progenitor cells (CPCs) are developing into different glioma grades: Diffuse astrocytoma (II), anaplastic astrocytoma (III), primary and secondary glioblastomas (IV). Series of surgical specimens with different clinical cases were analyzed by RT-qPCR. GBM is built by hierarchies developed by tumorigenic GSCs, which are controlled by Notch, Wnt, BMP, TGFb, RTK pathways. We have studied expression of some of these genes in progression of astrocytomas and GBM; in particular, growth factor receptors EGFR, PDGFR, FGFR, Notch; members of signaling pathways, including cytoplasmic and nuclear intermediates (MELK, MAP, TUBB3, GFAP and CDK4, CDK6, MDM2,GAPDH); and transcription factors (OLIG2, SOX2, OCT4, NANOG). Some marker of SCs and neural differentiation were also included (CD133). The level of expression of EGFR was increased in the majority of GBM compared to other grades. The rate of expression level of transcription factors (sox2, oct4, nanog) involved in maintenance of stemness was increased in all samples, suggesting relationship between stemness and GBM progression.

Biography

Kopylov A has completed his PhD from Chemistry Department, Lomonosov Moscow State University and Doctor of Chemistry from the same University. He was Post-Doc at University of California Santa Cruz and Invited Professor at University of Massachusetts, USA. He is the Lecturer and the Group Leader at the University and Science Director of Apto-Pharm start-up. He has published about 70 papers in reputed journals.

kopylov.alex@gmail.com

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