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Genitourinárne malignity

Chovanec M, Albany C, **Mego M**, Montironi R, Cimadamore A, Cheng L.
Emerging Prognostic Biomarkers in Testicular Germ Cell Tumors: Looking Beyond Established Practice.
Front Oncol. 2018 Nov 28;8:571. doi: 10.3389/fonc.2018.00571. eCollection 2018.

Testicular germ cell tumors are unique among solid cancers. Historically, this disease was deadly if progressed beyond the stage I. The implementation of cisplatin-based chemotherapy regimens has drastically changed the clinical outcome of metastatic testicular cancer. Several biomarkers were established to refine the prognosis by International Germ Cell Collaborative Group in 1997.

Among these, the most significant were primary tumor site; metastatic sites, such as non-pulmonary visceral metastases; and the amplitude of serum tumor markers α-fetoprotein, β-chorionic gonadotropin, and lactate dehydrogenase. Since then, oncology has experienced discoveries of various molecular biomarkers to further refine the prognosis and treatment of malignancies. However, the ability to predict the prognosis and treatment response in germ cell tumors did not improve for many years. Clinical trials with novel targeting agents that were conducted in refractory germ cell tumor patients have proven to have negative outcomes.

With the recent advances and developments, novel biomarkers emerge in the field of germ cell tumor oncology. This review article aims to summarize the current knowledge in the research of novel prognostic biomarkers in testicular germ cell tumors.

Schmidtova S, **Kalavska K**, Kucerova L.
Molecular Mechanisms of Cisplatin Chemoresistance and Its Circumventing in Testicular Germ Cell Tumors.
Curr Oncol Rep. 2018 Sep 26;20(11):88.

Purpose of review: Testicular germ cell tumors (TGCTs) represent the most common solid tumors affecting young men. Majority of TGCTs respond well to cisplatin-based chemotherapy. However, patients with refractory disease have limited treatment modalities associated with poor prognosis. Here, we discuss the main molecular mechanisms associated with acquired cisplatin resistance in TGCTs and how their understanding might help in the development of new approaches to tackle this clinically relevant problem. We also discuss recent data on the strategies of circumventing the cisplatin resistance from different tumor types potentially efficient also in TGCTs.

Recent findings: Recent data regarding deregulation of various signaling pathways as well as genetic and epigenetic mechanisms in cisplatin-resistant TGCTs have contributed to understanding of the mechanisms related to the resistance to cisplatin-based chemotherapy in these tumors. Understanding of these mechanisms enabled explaining why majority but not all TGCTs patients are curable with cisplatin-based chemotherapy. Moreover, it could lead to the development of more effective treatment of refractory TGCTs and potentially other solid tumors resistant to platinum-based chemotherapy. This review provides additional insights into mechanisms associated with cisplatin resistance in TGCTs, which is a complex phenomenon, and there is a need for novel modalities to overcome it.

Chovanec M, Cheng L.
Molecular characterization of testicular germ cell tumors: chasing the underlying pathways. Editorial.
Future Oncol. 2019 Jan;15(3):227-229.

Podporná liečba

Ricna D, Lengerova M, Bezdicek M, Kocmanova I, **Drgona L,** Weinbergerova B, Mayer J, Racil Z.
Detection and identification of fungi in bronchoalveolar lavage fluid from immunocompromised patients using panfungal PCR.
Folia Microbiol (Praha). 2018 Dec 8.

Rapid diagnostics of fungal pneumonia and initiation of appropriate therapy are still challenging. In this study, we used two panfungal assays to test bronchoalveolar lavage fluid (BALF) samples to prove their ability to confirm invasive fungal disease diagnosis and identify causative agents. Two methods targeting different fungal rDNA regions were used, and the obtained PCR products were sequenced directly or after cloning. In total, 106 BALF samples from 104 patients were tested. After sequencing, we obtained 578 sequences. Four hundred thirty-seven sequences were excluded from further analysis due to duplication (n = 335) or similarity with sequences detected in the extraction control sample (n = 102); 141 unique sequences were analyzed. Altogether, 23/141 (16%) of the fungi detected belonged to pathogenic species, and 63/141 (45%) were identified as various yeasts; a variety of environmental or very rare fungal human pathogens represented 29/141 (21%) of the total and 26/141 (18%) were described as uncultured fungus. Panfungal PCR detected fungal species that would be missed by specific methods in only one case (probable cryptococcosis). Panfungal PCR followed by sequencing has limited use for testing BALF samples due to frequent commensal or environmental fungal species pickup.

Abstrakty príspevkov zo zahraničných konferencií

Mego M, Karaba M, Minarik G, Benca J, Jurisova S, Sedlackova T, Manasova D, Kalavska K, Pindak D, Cristofanilli M, Reuben JM, Mardiak J.
Circulating tumor cells (CTCs) with epithelial to mesenchymal transition (EMT) phenotypes are associated with inferior outcomes in primary breast cancer.
San Antonio Breast Cancer Symposium, 4-8.12.2018 San Antonio, TX, USA