Germinomas are 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.


Podporná liečba


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 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