Investigation of the factors involved in the activation of ERK1/2 and AKT in chondrosarcoma and analysis of their role in cell proliferation and migration

Mohamed Ouzaïne
Centre National de la Recherche Scientifique, France

Chondrosarcomas are heterogeneous tumors characterized by production of a cartilaginous matrix. They are the second most common primary bone tumors with currently no effective therapies when unresectable or metastasized. Conventional chondrosarcoma does not respond to existing chemo and radiotherapy modalities, thus development of distal metastases are almost invariably fatal events. Thus, there is a clear need to develop new targeted therapies with high impact on this disease. Deregulated kinase pathways are of growing interest in the field of cancer and have been suggested to have a role in chondrosarcoma. Several investigators have shown that the PI3K/AKT is the most active pathway in chondrosarcoma followed by MEK/ERK pathway. These pathways are crucial to many aspects of cell growth and survival, proliferation, drug resistance, terminal differentiation and apoptosis. Therefore, therapeutic strategies that suppress one or both pathways may prove effective. In this study, we investigated the signaling pathways leading to activation of PI3K/AKT and MEK/ERK in chondrosarcoma and determined the consequences of their inhibition on cell proliferation and survival as well as on tumor growth in xenograft models.

Establishment of the recurrence prediction model of colorectal cancer using nCounter analysis system

Xiaohan Shen
Clinical Pathology Diagnosis Center, China

Background: As one of the most common malignancy, colorectal cancer (CRC) poses a serious threat to human health. Both CRC incidence and mortality rates continue to increase worldwide. The establishment of recurrence prediction model of CRC has a very important practical significance.

Methods: 37 gene mRNA expression levels in 473 CRC tissues were detected using nCounter analysis system. Differentially expressed genes were screened out between the recurrent group and the non-recurrent group. The recurrence prediction model of CRC was established by using the binary Logistic regression analysis.

Results: A 37 gene prediction model was generated by using the binary logistic regression analysis. The univariate analysis (Log-Rank) indicated that DFS was significantly worse in the recurrent group than in the non-recurrent group both in training group and testing group (P<0.05). The univariate analysis also indicated that DEPDC1 mRNA expression were significantly higher in non-recurrent group than those in recurrent group (P<0.05). DEPDC1 and TNM stage had significant correlation with DFS (P<0.05). The Cox proportional hazards regression indicated that DEPDC1 mRNA expression was an independent factor for CRC patients.

Conclusion: In this part, we have validated the expression of differentially expressed genes and established the recurrence prediction model of CRC using nCounter analysis system which is a high-throughput platform, further study will be done to verify and optimize the prediction model in the future.