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RNASeq of Pituitary Adenomas reveals dysfunctional metabolic, secretory and differentiation molecular pathways

Robert Formosa & Josanne Vassallo

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Pituitary adenomas consist of a group of highly heterogeneous intracranial tumours with variable presentation, clinical prognosis and management. High throughput sequencing was used in order to try and identify common de-regulated pathways and characterize tumours according to specific molecular behaviour. RNA sequencing (RNAseq) was chosen since it provides not only information regarding the expression profile but also the mutational load of each specific tumour analysed. 58 locally resected tumours (36 non-functional tumours; 17 growth hormone-secreting; 3 prolactin-secreting; 2 Cushing's) were stored in RNAlater (Qiagen, US) and RNA was extracted to purified. RNAseq was performed on all samples plus a control on the BGI-Seq500 platform (Beijing Genomics Ind., China). Bioinformatic analyses was also performed by BGI with additional analyses still being carried out. Preliminary data reveals a number of known and novel de-regulated pathways which characteristically differentiate between different tumour types such as hormone signalling and production pathways. However, novel metabolic pathways also appear to differ significantly, not only between controls and tumours but also between different tumour types with changes in lipid transport and glucose metabolism being observed. Additionally various hormone receptor signalling pathways were also found to be altered. Verification and additional bioinformatic analyses will be required to further delve into the vast data that is generated by this technique which has provided a wealth of information.

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