Greater understanding about the role of a long non-coding RNA in the development of cutaneous squamous cell carcinoma

Cutaneous squamous cell carcinoma (cSCC) is one of the most frequently diagnosed cancers worldwide, particularly affecting White populations. The incidence of cSCC is on the rise. In the USA, cSCC is the second most common form of cancer, with an estimated 1 million cases reported every year among the Medicare population. Most cSCCs can be surgically removed and patients have a favourable outcome. However, the 5-year survival rate drops dramatically (to less than 30%) for patients with advanced cSCCs with metastases (where the cancer has spread to other parts of the body), making cSCC the second leading cause of skin cancer-related death after melanoma.

Long non-coding RNAs (lncRNAs) are a group of RNA molecules that have limited protein-coding potential and are more than 200 nucleotides long. Mounting evidence suggests that lncRNAs are crucial regulators of gene expression and exert a large amount of control over biological and pathological processes. Our study found increased expression of the lncRNA called plasmacytoma variant translocation 1 (PVT1) in cSCC versus normal skin and actinic keratosis (a pre-cancerous lesion of cSCC).

Our findings indicate that PVT1 may play a role in the invasive phenotype (the observable characteristics) of cSCC. In cSCC, the expression of PVT1 is regulated by the MYC gene. PVT1 also plays a role in cSCC by suppressing cell ageing and deterioration by inhibiting the expression of a protein called CDKN1A and preventing cell cycle arrest. The PVT1 gene locus encodes more than 35 similar proteins and our study demonstrates that transcripts containing the part of the gene called exon 2 contribute to the oncogenic role of PVT1 in cSCC. Therefore, PVT1 may serve as a potential malignant transformation biomarker and therapeutic target for cSCC.