

## **Molecular profiling of neuroendocrine tumours to predict response and toxicity to peptide receptor radionuclide therapy**

Peptide receptor radionuclide therapy (PRRT) is a type of radiotherapy that targets peptide receptors and is typically used for neuroendocrine tumours (NETs). Some of the key challenges in its use are the prediction of efficacy and toxicity, patient selection, and response optimisation.

This review assesses current knowledge on the molecular profile of NETs and the strategies and tools used to predict, monitor, and assess the toxicity of PRRT. The few mutations in tumour genes that can be evaluated (eg, ATM and DAXX) are limited to pancreatic NETs and are most likely not informative. Assays that are transcriptomic or based on genes are effective in the prediction of radiotherapy response in other cancers. A blood-based assay for eight genes (the PRRT prediction quotient [PPQ]) has an overall accuracy of 95% for predicting responses to PRRT in NETs. No molecular markers exist that can predict the toxicity of PRRT. Candidate molecular targets include seven single nucleotide polymorphisms (SNPs) that are susceptible to radiation. Transcriptomic evaluations of blood and a combination of gene expression and specific SNPs, assessed by machine learning with algorithms that are tumour-specific, might yield molecular tools to enhance the efficacy and safety of PRRT.

<https://www.sciencedirect.com/science/article/pii/S1470204520303235?via%3Dihub>