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The prognostic utility of pre-treatment 18F-FDG-PET for salvage re-irradiation in head and neck cancer patients

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Aim: Statistical image features of tumor metabolism from pretreatment 18F-FDG-PET/CT scans were studied for their potential to predict clinical outcome of salvage re-irradiation with intensity modulated radiotherapy (IMRT) for recurrent squamous cell carcinoma of head and neck (HNSCC).

Materials & Methods: Pretreatment PET/CT scans and after treatment PET/CT scans of patients who underwent IMRT re-irradiation for recurrent HNSCC, were retrospectively evaluated. Metabolic response was assessed using PET response criteria for solid tumors (PERCIST). Multiple statistical image features related to the standard uptake value (SUV) were computed: Metabolic tumor volume, maximum SUV, mean SUV, total lesion glycolysis (TLG). The correlation between the image features and local control and overall survival was calculated.

Results: Complete tumor metabolic response (CMR) was achieved in 5 patients (45.5%). Six patients failed to achieve CMR: Progressive metabolic disease was in 4 patients (36.4%); stable metabolic disease in one patient (9.1%); one patient had partial metabolic response (9.1%). The median follow-up time was 18.2 months. Out of the calculated image features, only pre-treatment tumor TLG (individual tumor volume multiplied by its mean SUV) correlated with tumor metabolic response in the early PET/CT follow-up. Also dividing the patient population based on the median tumor TLG showed a split of the Kaplan-Meier survival curves.

Conclusions: The tumor TLG of pre-treatment PET/CT scans has important information on the failure risk to achieve CMR in recurrent HNSCC patients. It is necessary to obtain additional patients data to validate these results.

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Implication of methylene-tetrahydrofolate reductase gene polymorphisms in chronic myeloid leukemia occurrence

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Methylenetetrahydrofolate reductase (MTHFR) is a key enzyme of folate metabolism. Few studies were reported about its relationship with chronic myeloid leukemia (CML). We conducted a case-control study analyzing the prevalence of the polymorphisms MTHFR C677T and MTHFR A1298C in Algerian CML patients. Using TaqMan[®] allelic discrimination assay, we investigated MTHFR C677T and A1298C polymorphism distribution in 90 cases of CML and 100 healthy subjects. The frequencies of 677T alleles and genotypes 677TT and 677CT were significantly higher in cases than in control ($P=1E-6$; $OR=6.77$ [4.22-10.86]) and ($P=1E-6$; $OR=10.38$ [4.56-23.6]) respectively. Also, the frequencies of 1298C alleles and genotypes 1298CC and 1298AC were higher in cases ($P=9E-6$; $OR=2.65$ [1.71-4.10]) and ($P=0.008$; $OR=2.22$ [1.21-4.06]) respectively. We report also the higher significance of the haplotype 677T/1298A and 677T/1298C in cases ($P=0.007$; $OR=2.57$ [1.26-5.24]) and ($P=5E-6$, $OR=6.91$ [2.7646-17.2899]) respectively. Our results demonstrate that 677T and 1298C alleles are both associated with an increased risk of CML in Algeria.

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