random under sampling boost (RUSBoost) classification method to reduce the false positive metastases, RESULTS: The computational pipeline was tested on real brain images. A sensitivity of 97.28% and false positive rate of 2.25% were achieved when the images were preprocessed using this method. CONCLUSION: Our results demonstrated the deep learning-based method can detect metastases in very challenging cases and can serve as CAD tool to help radiologists interpret brain MRIs in a time-constrained environment.

OTHR-14. TREATMENT MONITORING OF IMMUNOTHERAPY AND TARGETED THERAPY USING FET PET IN PATIENTS WITH MELANOMA AND LUNG CANCER BRAIN METASTASES: INITIAL EXPERIENCES
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BACKGROUND: Due to the lack of specificity of contrast-enhanced (CE) MRI, both the response assessment and differentiation of progression from pseudoprogression (PP) following immunotherapy using checkpoint inhibitors (ICIs) or targeted therapy (TT) may be challenging, especially when ICI or TT is used in combination with radiotherapy (RT). Here, we present the value of amino acid PET using O-2-[18F]fluoroethyl-L-tyrosine (FET) as a problem-solving tool in comparison to CE-MRI in patients with brain metastases (BM) secondary to malignant melanoma (MM) and NSCLC. METHODS: We retrospectively identified 44 patients (74 BM) with MM (n=20 with 42 BM) and NSCLC (n=11 with 32 BM) who underwent 52 FET-PET scans during the course of disease. All patients had RT prior to ICI or TT initiation (61%) or RT concurrent to ICI or TT (39%). In 13 patients, FET-PET was performed for treatment response assessment of ICI or TT using baseline and follow-up scans (median time between scans, 4.2 months). In the remaining 18 patients, FET-PET was used for the differentiation of progression from PP related to RT plus ICI or TT. In all BM, metabolic activity on FET-PET was evaluated by calculation of tumor/brain ratios. FET-PET imaging findings were compared to CE-MM and correlated to the clinical follow-up or neuropathological findings after neurosurgery. RESULTS: In 4 of 13 patients (31%), FET-PET provided additional information for treatment response evaluation. Patients with populations to inflammatory and essential genetic features acquired prior to systemic dissemination and site-specific colonization. Exome capture and deep sequencing were performed on tissues from 3 patients with postmetastatic RCC (including 12 metastases, multiple regions of primary tumors, and paired germline tissue) to a mean depth of 250x. Somatic point mutations were called with MuTect, and insertions and deletions with Strelka and VarScan. Validation was performed with a custom NimbleGen panel hybridized to a custom sequence library and sequenced to a mean depth of >500x. Allelic-specific copy number and clonal prevalence were evaluated using ABSOLUTE, and analyzed with pyclone across primary and metastatic lesions to determine clonal architecture. Phylogenetic reconstruction identified ancestral clones, with attendant driver mutations in RCC tumor suppressors (including VHL, MET2D, PBRM1, MTO1) and independent subclonal populations in metastases of all 3 patients. In index case with multiple metastases separated spatially and temporally, bone and soft tissue metastases demonstrate apparent independent ancestors. Convergent loss of known tumor suppressors was also noted in all cases, and in several cases found in conjunction with de novo mutations in known RCC driver genes acquired late in tumor development. In this demonstration of subclonal and evolutionary analysis of multiple paired multi-organ RCC metastases, we identified subclonal populations characterized by alteration of several tumor suppressors which subsequently exhibited organ-specific patterns of metastasis.

OTHR-17. PHYLOGENETIC RESOLUTION OF TISSUE-SPECIFIC METASTATIC CLONES IN RENAL CELL CARCINOMA
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Genomic predictors of organ-specific tropism have been established in several cancer subtypes. However, the evolutionary dynamics at work in metastatic carcinoma have yet to be characterized in detail. We identified a cohort of clear cell renal cell carcinoma (RCC) patients who also had multiple metastasectomies, and performed deep sequencing and statistical inference of subclonal populations to infer evolutionary and essential genetic features acquired prior to systemic dissemination and site-specific colonization. Exome capture and deep sequencing were performed on tissues from 3 patients with postmetastatic RCC (including 12 metastases, multiple regions of primary tumors, and paired germline tissue) to a mean depth of 250x. Somatic point mutations were called with MuTect, and insertions and deletions with Strelka and VarScan. Validation was performed with a custom NimbleGen panel hybridized to a custom sequence library and sequenced to a mean depth of >500x. Allelic-specific copy number and clonal prevalence were evaluated using ABSOLUTE, and analyzed with pyclone across primary and metastatic lesions to determine clonal architecture. Phylogenetic reconstruction identified ancestral clones, with attendant driver mutations in RCC tumor suppressors (including VHL, MET2D, PBRM1, MTO1) and independent subclonal populations in metastases of all 3 patients. In index case with multiple metastases separated spatially and temporally, bone and soft tissue metastases demonstrate apparent independent ancestors. Convergent loss of known tumor suppressors was also noted in all cases, and in several cases found in conjunction with de novo mutations in known RCC driver genes acquired late in tumor development. In this demonstration of subclonal and evolutionary analysis of multiple paired multi-organ RCC metastases, we identified subclonal populations characterized by alteration of several tumor suppressors which subsequently exhibited organ-specific patterns of metastasis.

RADIATION

RAD1-01. PROGNOSTIC FACTORS OF SHORT SURVIVAL FOR BRAIN METASTASES TREATED WITH SRS WITHOUT WBRT
Maciej Harat, Maciej Blok, Roman Makarewicz, and Krzysztof Roszkowski

Nowadays multiple brain metastases (up to 10–15 tumors) are treated with SRS alone. The most common diagnosis-specific Graded Prognostic Assessment and Score for Radiosurgery indices are based on data regarding limited brain metastases (1–4). Moreover, many of patients included in that basis were treated with WBRT. There is also a lack of data in cases where some relevant data were not included due to a retrospective analysis of large datasets. SRS may increase intracranial control of disease, however, treatment of patients with a prognosis of fewer than 3 months survival after SRS may not be clinically reliable. Therefore we conducted an analysis of prospective registry to find the factors that could be used very short term, i.e. after SRS.