abstracts

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 0.25% was achieved. The images were interpreted by using the proposed 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
Norbert Gallicks, Diana Abdalla, Matthias Scheffler, Viola Schweinsberg, Max Schlaak, Nicole Kreuzberg, Jenny Landsberg, Philipp Lohmann, Garry Ceccon, Jan-Michael Werner, Eren Celik, Maximilian Rupp, Martin Kocher, Simone Marnitz, Gereon Fink, Karl-Josef Langen, Juergen Wolf, and Cornelia Mauch

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 (ICl) or targeted therapy (TT) may be challenging, especially when ICI or TT is applied in combination with radiotherapy (RT). Here, we assessed 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 melanoma (MM) and NSCLC. METHODS: With CE-MRI, MM and NSCLC patients with 74 BM (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 PtP 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-MRI 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. In 12 patients, populations to infer the utility 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 metastatic 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 >300x. Allele-specific copy number and clonal prevalence were established using AB-SOLUTION, and analyzed with ANNOVAR across primary and metastatic lesions to determine clonal architecture. Phylogenetic reconstruction identified ancestral clones with abundant driver mutations in RCC tumor suppressors (including VHL, SETD2, PBRM1, MTR) and independent subclonal populations 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 metastases, and performed deep sequencing and statistical inference of metastases can identify distinct tumor types for which there are FDA approved targeted medications. Improving diagnostic precision with the 92-gene assay helps identify a subset of therapy-responsive metastatic brain tumors, thus improving therapy and possibly providing better outcomes and survival.

OTHR-15. PATIENTS WITH LIMITED STAGE SMALL CELL LUNG CANCER THAT RECUR WITH ISOLATED BRAIN METASTASES HAVE PROLONGED SURVIVAL
Bryan Bonder, Fatemeh Ardeshir Larjani, Ashvin Dowlatsh, and Lisa Rogers

INTRODUCTION: Small cell lung cancer (SCLC) frequently metastasizes to the brain. In patients with limited-stage disease (disease confined to one radiation portal), the incidence of brain metastasis after 3 years is 50–60%. We reviewed patients with SCLC and hypothesized that isolated brain metastases may add valuable information for treatment monitoring in individual BM patients undergoing RT in combination with ICI or TT.

OTHR-16. MOLECULAR PROFILING USING THE 92-GENE ASSAY FOR TUMOR CLASSIFICATION OF BRAIN METASTASES
Andrew Brenner, Raul Collazo, Catherine Schnabel, and Anthony Greco

BACKGROUND: Nearly 200,000 patients are diagnosed with brain metastases in the US annually. Advances in targeted therapies make definitive diagnosis of the primary tumor type important but can be challenging in many cases. The 92-gene assay is a validated genetic algorithm for 50 tumor types for patients with uncertain tissue of origin diagnoses. Results from a clinical series of brain biopsies and potential impact on treatment were evaluated. METHODS: An IRB approved, de-identified database of clinical and molecular information from biopsies (N=486) was queried for testing with the 92-gene assay (CancerTYPE ID, Biotheranostics, Inc.) as part of routine care were reviewed. Descriptive analysis included patient demographics and molecular diagnoses. RESULTS: Analysis included 464 brain biopsies. A molecular diagnosis was provided in 433 (93.3%) tested (<5% assay failure rate). Twenty-four different tumor types made up the majority (67.4%) with almost one-third of the molecular predictions being Lung (31.2%), followed by Neuroendocrine (NET) (9.9%), Sarcoma (7.9%), Skin (6.4%), Gastroesophageal (6.2%), and Urinary bladder (5.8%). All of these 6 tumor types, for which activity in the CNS has been documented, have immune checkpoint inhibitors or other targeted therapies approved in selected cases by the US Federal Drug Administration (FDA). CONCLUSIONS: Molecular classification of brain metastases can identify distinct tumor types for which there are FDA approved targeted medications. Improving diagnostic precision with the 92-gene assay helps identify a subset of therapy-responsive metastatic brain tumors, thus improving therapy and possibly providing better outcomes and survival.

OTHR-17. PHYLGENETIC RESOLUTION OF TISSUE-SPECIFIC METASTASISogenous CLONES IN RENAL CELL CARCINOMA
Nelson Moss, Samuel Berman, Salvatore Piscigallo, Charlotte Ng, Pier Selenica, Rahul Kumar, Jorge Reis Filho and Cameron Brennan

Genomic factors predictive of organ-specific tropism have been established in several cancers. 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 metastases, and performed deep sequencing and statistical inference of metastases can identify distinct tumor types for which there are FDA approved targeted medications. Improving diagnostic precision with the 92-gene assay helps identify a subset of therapy-responsive metastatic brain tumors, thus improving therapy and possibly providing better outcomes and survival.

RADIATION

RADJ-01. PROGNOSTIC FACTORS OF SHORT SURVIVAL FOR BRAIN METASTASES TREATED WITH SRS WITHOUT WBRT
Maciej Harat, Maciej Blok, Roman Marekewicz, and Krzysztof Rosekowski

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 analyses were treated with WBRT or combination of WBRT and SRS. No data regarding limited brain metastases were included due to 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 can be used very short tumors, 1 to 5.

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