Results and discussions We observed systemically elevated levels of Tregs prior to metastatic disease. These tumor-educated Tregs display a distinct phenotype and specifically accumulate in the lung and lymph node metastases that arise in our metastasis models, perhaps indicating their possible importance for metastasis formation and progression.

In addition to these systemic changes, within primary tumors and metastases a large population of PD1high Tregs is found. Preliminary data suggest that tumor-associated myeloid cells influence this population.

Conclusion We are currently setting out to dissect the mechanism behind this interplay of intra-tumoral immune cells and the role of distinct Tregs found prior to metastatic disease.

PO-389 THE ROLE OF IMMUNE MICROENVIRONMENT IN DETERMINING THE ORGAN-SPECIFIC HOMING OF METASTASES

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Introduction Metastasis to different organs or tissues may require distinct sets of regulators which may influence the homing and growth of tumour cells to specific secondary sites. Under the hypothesis that the immune microenvironment of the different niches may play an important role in this process, we have categorised metastatic samples from different primary tumours based on their immune profile.

Material and methods Gene expression data from metastatic samples with different primary tumour origin (n=342) were downloaded from open repository GEO. Samples were scored using different gene expression profiles and characterised on the basis of their immune and stromal infiltration and activation of immune response pathways (Immunophenoscore, MCPcounter, ESTIMATE; among others). Resultant scores were analysed for statistical differences with ANOVA test. Multivariate analysis was used for clustering the samples based in their immune-features.

Results and discussions As expected, significant differences were found between the immune profiles of samples metastasizing in distinct organs. For instance, breast cancer metastasis in lung showed a much higher immunogenic score than breast metastasis in brain (p=5e-4), suggesting a different immune microenvironment modulation. Also in breast, significant differences have been found in cell lineages infiltration, lung metastasis being the ones with the highest T cell component (p=0.002) and liver metastasis the ones with the lowest infiltration of endothelial cells (p=0.005). Moreover, in other cancer types like melanoma, samples showed differences among different metastatic locations. Interestingly, when comparing metastatic samples originating from different primary tumour, a high concordance among secondary tumours in immune scores were found; specifically in brain metastasis. These results suggest that cells needs to share similar molecular profiles to evade the immune surveillance and growth in a specific niche, independently of their origin.

Conclusion Metastases from the same primary tumour growing in different organs show differences in their immune profile. However, those samples from different primary origin but growing in the same secondary organ shared a characteristic immune profile. These results suggest that immune system plays a role in determining the organ-specific homing of metastasis.