**ABSTRACTS**

**LB1475**

**The immune-phenotype of small plaque psoriasis**

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Psoriasis is an inflammatory skin disease characterized by the uncontrolled proliferation of keratinocytes. There are various kinds of phenotype of psoriasis, including small plaque psoriasis (SPP), which usually develop multiple lesions and it is not clear whether advanced lesions (tumours) do or do not develop multiple lesions and it is not clear whether advanced lesions (tumours) do or do not develop multiple lesions and it is not clear whether advanced lesions (tumours) do or not.

**LB1476**

**Long-lived cells surviving myeloablative treatment provide proof for T cell tissue-residency in human skin**

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Due to lack of appropriate model systems, little is known about human T cell longevity and resistance to radiation. Myeloablative conditioning and subsequent allogeneic hematopoietic stem cell transplantation (HSCT) represent unique situations in the human body to studyresidency of skin T cells. Therefore, we profiled immune cell ablation and recovery dynamics in 45 patients in the process of HSCT. Skin biopsies and peripheral blood were taken at up to 5 time points before and after HSCT and analyzed for immune cell subtypes using flow cytometry, tissue immunofluorescence and low-input RNA sequencing. Upon myeloablative treatment (chemotherapy and total body irradiation), recirculating immune cells declined in skin and peripheral blood, while a subset of dermal T cells expressing residency markers and lacking expression of genes associated with tissue egress remained stable throughout all time points analyzed. This skin-resident subset displayed high proliferative potency after TCR stimulation and was enriched in patients who later developed acute graft-versus-host disease of the skin. Furthermore, chimerism analysis after transplantation revealed that, unlike in peripheral blood, skin-resident T cells of the recipient constituted a third of dermal T cells at time of full immunological recovery (14 weeks post-transplant) and coexisted with donor T cells years after engraftment. We have thus identified a long-lived and remarkably resistant population of dermal T cells in the skin of HSCT recipients, which is likely insufficiently targeted by current therapies for chronic inflammatory skin conditions.

**LB1477**

**IQGAP3 could be a promising target link for breaking the vicious circle of psoriasis**

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The IQGAP family is a group of scaffold proteins coordinating signaling by facilitating the physical interactions between the effector proteins and localizing them to specific areas of a cell. They seem to be promising therapeutic targets capable for altering of various signaling cascades without direct influence on the key regulators of the pathways. IQGAP proteins are involved in the regulation of the cell cycle, MAPK cascades, EGF cascades, farnesyltransferase signaling and other pathways important for psoriasis. IQGAP1 is present in all layers of the epidermis, whereas IQGAP3 accumulates in proliferating basal keratinocytes. We have carried out the analysis of the RNA-seq data from GEO database (GSE67785, GSE66311, GSE41745, 40 psoriatic biopsy pairs) and have identified only the IQGAP3 of the IQGAP family to be upregulated. The upregulated IQGAP3 expression was more common in the melanoma group, with 45 cases carrying at least one variant (62.5%), while only 18 controls (27.27%). Presence of MC1R variant conferred an increase of melanoma risk. The estimated OR for melanoma was 5.05 (95% CI: 1.68 - 15.21, P=0.004) and 11.55 (95% CI: 1.74 - 76.62, P=0.011) in individuals with one and two or more MC1R sequence variants, respectively. The risk of melanoma was not modified significantly by skin phenotype and hair color. Conclusions: Breaking a carrier of one MC1R variant is associated with an increase melanoma risk, if the individual has two or more, the risk is even higher. This predisposition is independent of phenotypic characteristics.

**LB1478**

**MC1R variants and cutaneous melanoma risk in the Southern Brazil population**

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Background: Melanocortin 1 receptor (MC1R) gene variants have been associated to fair skin and may independently cause an increase risk for the development of cutaneous melanoma. Objectives: To analyze the coding region of the MC1R gene in patients/with cutaneous melanoma and controls from Southern Brazil and the relationship of gene variants with melanoma risk factors. Methods: We evaluated 72 patients with melanoma and 66 controls. Genotyping of the MC1R coding region was performed by sequencing in all individuals. Results: The 138 patients studied, 63 (45.65%) carried at least one MC1R variant. Variants were more common in the melanoma group, with 45 cases carrying at least one variant (62.5%), while only 18 controls (27.27%). Presence of MC1R variant conferred an increase of melanoma risk. The estimated OR for melanoma was 5.05 (95% CI: 1.68 - 15.21, P=0.004) and 11.55 (95% CI: 1.74 - 76.62, P=0.011) in individuals with one and two or more MC1R sequence variants, respectively. The risk of melanoma was not modified significantly by skin phenotype and hair color. Conclusions: Breaking a carrier of one MC1R variant is associated with an increase melanoma risk, if the individual has two or more, the risk is even higher. This predisposition is independent of phenotypic characteristics.

**LB1479**

**Identifying intratumor heterogeneity in mycosis fungoides using high throughput DNA sequencing**

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Sequencing (WES) of MF tissue prepared by laser microdissection (LMD). Patients with MF were treated by chemotherapy, total body irradiation, and stem cell transplantation (HSCT). Heterogeneity at genomic level in MF.

**LB1480**

**Systemic platelet-activating factor-receptor agonist augments non-melanoma skin cancer growth**

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Platelet-activating factor-receptor (PAF-R) agonists are pleiotropic phospholipid mediators that influence multiple biological processes including the induction and resolution of inflammation as well as immunosuppression. Importantly, PAF-R agonists have been shown to modulate tumorigenesis and/or tumor growth in various cancer models by suppressing either cutaneous inflammation and/or anti-tumoral adaptive immunity. Notably, we have shown that systemic administration of a PAF-R agonist augments the growth of subcutaneously implanted melanoma tumors in a PAF-R-dependent manner. However, its topical applications suppressed tumor incidence/multiplicity and growth of non-melanoma skin cancer (NMSC) induced by the topical applications of two-stage chemical carcinogenesis (dimethylbenz[a]anthracene [DMBA] and phorbol 12-myristate 13-acetate [PMA]) model, in-part via exhibiting anti-inflammatory effects. These findings indicate the diverse effects of systemic versus topical PAF-R agonist in modulating cutaneous inflammation and carcinogenesis. The current pilot studies were sought to determine the systemic effects of a PAF-R agonist on a recently characterized model of 25 weeks of topical DMBA/PMA induced melanocytic nevus formation and their progression into malignant melanoma as well as NMSC. Our studies demonstrate that systemic administration of a PAF-R agonist for 30 weeks did not modulate melanocytic nevus formation, yet delayed tumor multiplicity, tumor growth, and may independently cause an increase risk for the development of cutaneous melanoma. Objectives: To analyze the coding region of the MC1R gene in patients/with cutaneous melanoma and controls from Southern Brazil and the relationship of gene variants with melanoma risk factors. Methods: We evaluated 72 patients with melanoma and 66 controls. Genotyping of the MC1R coding region was performed by sequencing in all individuals. Results: The 138 patients studied, 63 (45.65%) carried at least one MC1R variant. Variants were more common in the melanoma group, with 45 cases carrying at least one variant (62.5%), while only 18 controls (27.27%). Presence of MC1R variant conferred an increase of melanoma risk. The estimated OR for melanoma was 5.05 (95% CI: 1.68 - 15.21, P=0.004) and 11.55 (95% CI: 1.74 - 76.62, P=0.011) in individuals with one and two or more MC1R sequence variants, respectively. The risk of melanoma was not modified significantly by skin phenotype and hair color. Conclusions: Breaking a carrier of one MC1R variant is associated with an increase melanoma risk, if the individual has two or more, the risk is even higher. This predisposition is independent of phenotypic characteristics.