

SCIENTIFIC PROGRAMME & BOOK OF ABSTRACTS



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expression and functional program, and while the individual signaling pathways are well understood, little is known about the global changes in the proteome pattern in freshly isolated Treg and Tconv and during their *in vitro*-expansion, a condition that can deeply modulate the switch in fuel utilization, thus affecting metabolic/functional responses.

Here we identified a detailed map of individual protein alterations in human Treg and Tconv cells, unveiling distinct and specific metabolic assets of these two cellular subsets, both *ex vivo* and during *in vitro* culture conditions. We show that freshly isolated Treg are highly glycolytic, whereas Tconv use lipid beta-oxidation for fuel energy. In contrast, an early down-modulation of glucose metabolism and its subsequent increase, together with the induction of beta-oxidation are required to sustain *in vitro* Treg cell proliferation, whereas only glycolysis is necessary for Tconv cells proliferation to occur. Taken together, these data should help to better understand the mechanisms underlying Treg/Tconv cell functions, and provide the clear evidence that modulation of energy metabolism may represent a useful tool for manipulation of Treg/Tconv cells *in vivo* and *in vitro*.

49 - GUT FLORA SPECIFIC IMMUNE RESPONSES IN MULTIPLE SCLEROSIS

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the FoxP3 expression and the activity of regulatory T cells in MS patients. All these data should help the comprehension of mechanisms that control the immune system function and its alteration during autoimmune diseases.

38 - PROTEOMIC LANDSCAPE REVEALS DISTINCT AND SPECIFIC METABOLIC PROGRAMS IN HUMAN TCONV AND TREG CELLS

- Claudio Procaccini** ⁽¹⁾ - **Fortunata Carbone** ⁽¹⁾ **Veronica De Rosa** ⁽²⁾ - **Mario Galgani** ⁽¹⁾ **Vincenzo Gigantino** ⁽³⁾ - **Derigio Faicchia** ⁽¹⁾ **Valentina Pucino** ⁽⁴⁾ - **Pier Luigi Mauri** ⁽⁵⁾ **Giuseppe Matarese** ⁽⁶⁾ **Istituto di Endocrinologia e Oncologia Sperimentale, Consiglio Nazionale delle Ricerche (IEOS-CNR), Napoli, Italy** ⁽¹⁾ - **Istituto di Endocrinologia e Oncologia Sperimentale (IEOS-CNR) and Unità di Neuroimmunologia, IRCCS Fondazione Santa Lucia, Consiglio Nazionale delle Ricerche, Napoli, Italy** ⁽²⁾ - **Unità di Patologia, Istituto Nazionale Tumori "Pascali", Napoli, Italy** ⁽³⁾ - **Dipartimento di Scienze Mediche Traslazionali, Università di Napoli "Federico II", Napoli, Italy** ⁽⁴⁾ - **Istituto for Biomedical Technologies (ITB-CNR), Consiglio Nazionale delle Ricerche, Segrate (Milano), Italy** ⁽⁵⁾ - **Dipartimento di Medicina e Chirurgia, Università di Salerno and IRCCS MultiMedica, Milano, Università di Salerno, Baronissi (Salerno), Italy** ⁽⁶⁾

The different CD4⁺ T cells subsets are characterized by specific phenotypic and functional features associated with the expression of multiple lineage-specific transcription factors. Regulatory T cells (Tregs) are a specific subpopulation of T cells which modulate the immune system, maintaining tolerance to self-antigens by suppressing proliferation and functions of several immune cells, such as conventional T cells (Tconv). Recent evidence has indicated that Treg and Tconv display a specific and different gene