Metabolic pathways during the regulation of inflammation and immunity

**OP0006**

**ABNORMAL IRON METABOLISM AND MITOCHONDRIAL DYSFUNCTION: INVESTIGATING A NOVEL PATHOLOGICAL MECHANISM IN SYSTEMIC LUPUS ERYTHEMATOSUS**

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**Background:** Iron is vital for numerous essential physiological processes including erythropoiesis and energy metabolism (as iron is found in the mitochondrial electron transport chain, the central site of ATP production). Iron homeostasis is tightly controlled by a number of regulators including: 1. Hepcidin, which prevents iron release from stores (under the influence of IL6 and IL12); 2. Ferritin, an iron storage protein; 3. Lipocalin-2 (LCN2), which is released upon innate immune activation that induces iron sequestration; 4. Transferrin, which binds circulating iron and enables its transport to effector cell targets; 5. Haptoglobin, which binds free haemoglobin and assisting iron recycling; 6. Erythropoietin (EPO), which stimulates erythropoiesis as a result of hypoxia. Chronic inflammation may result in dysregulation of iron metabolism and in turn impair mitochondrial function yet little is known regarding how these processes change in systemic lupus erythematosus (SLE).

**Objectives:** In this study, we investigated how dysregulation of iron metabolism may occur in SLE and subsequently sought to identify how a lack of iron may ultimately induce abnormal mitochondrial function.

**Methods:** 1. Investigating abnormal iron metabolism in SLE. Serum samples from patients with SLE (n=39) and healthy controls (HC, n=17) were assessed hepcidin, IL-15, IL-6, ferritin, LCN2, EPO, haptoglobin and transferrin levels by ELISA. Hierarchical cluster analysis of normalised data (converted to Z-scores) was performed using MeV software in order to characterise patient groups based upon iron metabolism profile. Anti-dsDNA antibody titres, complement C3 levels and SLEDAI-2K were excluded to limit the influence of these variables on cluster analysis. Results were presented as a heatmap. 2. Studying mitochondrial function in iron deficiency and SLE. Peripheral blood mononuclear cells (PBMCs) from HC and patients with SLE were analysed using Seahorse Respirometry, which measures mitochondrial oxygen consumption rate (a measure of energy metabolism dependent upon oxidative phosphorylation). To assess differences between health, iron deficiency and SLE 3 groups were assessed; 1. PBMCs derived from HCs; 2. PBMCs from patients with SLE; 3. Healthy PBMCs cultured in iron deficient condition, in which cells were treated with the potent iron chelator, Diferiprone.

**Results:** Figure 1a demonstrates that basal mitochondrial respiration is significantly reduced in PBMCs derived from healthy controls when grown in iron deficiency conditions (following treatment with Deferiprone and is lower still in those with SLE. Figure 2b shows that PBMCs from patients with SLE have reduced maximal mitochondrial respiration capacity that is comparable to the levels seen in iron deficient healthy PBMCs.

**Conclusion:** Patients with SLE demonstrate abnormalities in iron metabolism that results in cellular iron deficiency as iron is not released from stores, nor adequately transported at the rate required to meet physiological demands. Furthermore, PBMCs derived from patients with SLE who impaired basal and maximal respiration that is comparable with healthy PBMCs treated potent iron chelation. This suggests that abnormal iron metabolism may in turn limit mitochondrial energy metabolism in SLE and represents a potential future therapeutic target.

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**Figure 2a** demonstrates that basal mitochondrial respiration is significantly reduced in PBMCs derived from healthy controls when grown in iron deficiency conditions (following treatment with Diferiprone and is lower still in those with SLE. Figure 2b shows that PBMCs from patients with SLE have reduced maximal mitochondrial respiration capacity that is comparable to the levels seen in iron deficient healthy PBMCs.