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“EVALUATION OF THE NUTRITIONAL EFFECT ON THE IMMUNE PROFILE IN OBESE INDIVIDUALS”

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1. ABSTRACT

Obesity is an emerging nutritional problem associated with low level chronic inflammation and deregulated immunity. Adipocytes that increase in number and size under obese condition are responsible for the production of an array of cytokines (adipokines) that trigger the inflammatory response and modify circulating immune cell numbers. Weight loss has a direct effect upon inflammation and can be achieved through personalized nutrition that is based on each person's characteristics. 34 obese volunteers (BMI= 34.45 ± 1.08 kg/m²) undergoing a weight loss program [personalized intervention group following a genotype- based diet ($7.30 \pm 5.5\%$ weight loss, n=4), conventional diet group following conventional low- calorie diet ($8.76 \pm 3.82\%$ weight loss, n=7)] and 15 lean volunteers (BMI= 22.64 ± 0.52 kg/m²) were recruited. PBMCs were isolated by density gradient centrifugation and leukocyte subpopulations were assessed before and after a 3-month intervention by flow cytometry. Statistical analysis was performed using the unpaired Mann- Whitney t- test (two- tailed) (differences in cell absolute counts and percentages between obese and lean participants) and two- way analysis of variance (ANOVA) (differences in PBMCs subtypes levels between genotype-based and conventional diet following the 3- month intervention). Our data demonstrate that obesity is associated with a significant increase in circulating PBMCs and memory T cells confirming the proinflammatory status of obese individuals. Moreover, a trend towards an increase in total leukocytes, neutrophils, CD3⁺ cells, B lymphocytes, CD4⁺ T cells, naïve and terminally differentiated effector memory (TEMRA) T cells, CD45RO⁺CXCR3⁺ T cells, T regulatory cells, as well as non- classical, intermediate and CD14^{low}CD16⁺ monocytes was reported in obese participants. Conversely, a trend towards a reduction in basophils, eosinophils, classical monocytes, lymphocytes, natural killer (NK) cells, CD8⁺ and CD45RA⁺CXCR3⁺ T cells was reported in the obese group. Furthermore, the genotype- based type of intervention induced a statistical significant reduction in naïve T cells and a statistical significant increase in TEMRA cells indicating that weight loss is in line with a more differentiated status of CD4⁺ T cells. Thus, further studies are needed in order to confirm this trend in the intermediate stages, i.e. central and effector memory T cells.

1. ΠΕΡΙΛΗΨΗ

Η παχυσαρκία αποτελεί ένα διαρκώς αναπτυσσόμενο πρόβλημα και σχετίζεται με χαμηλού βαθμού χρόνια φλεγμονή. Στην παχυσαρκία, τα κύτταρα του λιπώδους ιστού αυξάνονται σε αριθμό και μέγεθος και παράγουν μεγάλο αριθμό κυτταροκινών οι οποίες ενεργοποιούν την φλεγμονώδη απόκριση και τροποποιούν τα επίπεδα των περιφερικών κυττάρων του ανοσοποιητικού συστήματος. Η απώλεια βάρους επηρεάζει άμεσα τη φλεγμονή και μπορεί να επιτευχθεί, μεταξύ άλλων, μέσω της εξατομικευμένης διατροφής. 34 παχύσαρκοι εθελοντές (BMI= 34.45±1.08 kg/m²) οι οποίοι συμμετείχαν σε πρόγραμμα απώλειας βάρους [εξατομικευμένη διατροφή (7.30±5.5% απώλεια βάρους, n=4), κλασική υποθερμιδική δίαιτα (8.76±3.82% απώλεια βάρους, n=7)] και 15 νορμοβαρείς εθελοντές (BMI= 22.64±0.52 kg/m²) συμπεριλήφθηκαν στη μελέτη. Για την απομόνωση των μονοπύρηνων κυττάρων του περιφερικού αίματος (PBMCs) χρησιμοποιήθηκε φυγοκέντρηση σε κλίση πυκνότητας και οι υποπληθυσμοί των λευκών αιμοσφαιρίων αξιολογήθηκαν πριν και μετά την τρίμηνη παρέμβαση με κυτταρομετρία ροής. Η στατιστική επεξεργασία των αποτελεσμάτων πραγματοποιήθηκε με Mann-Whitney t- test για την ανάδειξη των διαφορών στους απόλυτους αριθμούς και τα ποσοστά μεταξύ παχύσαρκων και νορμοβαρών εθελοντών και με ανάλυση διασποράς (ANOVA) για τις διαφορές στα επίπεδα των PBMCs στο τέλος της παρέμβασης μεταξύ των ατόμων που ακολούθησαν εξατομικευμένη και κλασική υποθερμιδική δίαιτα. Βάσει των αποτελεσμάτων μας, η παχυσαρκία σχετίζεται με μία στατιστικά σημαντική αύξηση στα επίπεδα των κυκλοφορούντων PBMCs και των T κυττάρων μνήμης επιβεβαιώνοντας με τον τρόπο αυτό την προ-φλεγμονώδη κατάσταση που χαρακτηρίζει τα παχύσαρκα άτομα. Επιπλέον, μία τάση για αυξημένη συχνότητα των λευκών αιμοσφαιρίων, ουδετερόφιλων, CD3⁺ κυττάρων, B λεμφοκυττάρων, CD4⁺ T κυττάρων, αδιαφοροποίητων και τελικώς διαφοροποιημένων (TEMRA) T κυττάρων μνήμης, CD45RO⁺CXCR3⁺ T κυττάρων, T ρυθμιστικών κυττάρων, όπως επίσης και των μη-κλασικών, ενδιάμεσων και CD14^{low}CD16⁺ μονοκυττάρων παρατηρήθηκε στους παχύσαρκους εθελοντές. Στην ίδια ομάδα εθελοντών καταγράφηκε μία τάση για μείωση στα επίπεδα των κυκλοφορούντων βασεόφιλων, ηωσινόφιλων, κλασικών μονοκυττάρων, λεμφοκυττάρων, φυσικών φονικών κυττάρων (NK), CD8⁺ και CD45RA⁺CXCR3⁺ T κυττάρων. Επιπρόσθετα, η απώλεια βάρους χάρη στην εξατομικευμένη δίαιτα οδήγησε σε μία στατιστικά σημαντική μείωση στα επίπεδα των κυκλοφορούντων αδιαφοροποίητων T κυττάρων και σε αύξηση στα TEMRA κύτταρα υποδηλώνοντας ότι η απώλεια βάρους είναι συνυφασμένη με μία περισσότερο διαφοροποιημένη κατάσταση των T κυττάρων. Συνεπώς, περαιτέρω μελέτη απαιτείται για να επιβεβαιωθεί αυτή η τάση και για τα ενδιάμεσα στάδια των T κυττάρων μνήμης.

2. INTRODUCTION

2.1 Obesity

The worldwide epidemic of obesity is an emerging nutritional problem that, along with its related disease cluster represents a global public health challenge. Based on the criteria published by the US National Institutes of Health and the World Health Organization (WHO), individuals with a body mass index (BMI) 25-30 kg/m² are considered overweight, those with a BMI 30-40 kg/m² are considered obese and a BMI >40 kg/m² is considered morbid obesity, whereas normal weight individuals are those with a BMI 20-25 kg/m². Although BMI serves as a useful tool for the evaluation of obesity, the characterization of obesity state using BMI is not always effective because it usually underestimates fat mass in females and overestimates the total amount of fat in muscular individuals [1, 2].

According to the WHO, at least one billion adults are overweight, 300 million are obese, and an increase in those numbers is expected in the future without intervention [3]. Based on the latest statistics, overweight affects 30-70% and obesity affects 10-30% of the adult population in Europe [4], whereas in the United States, obesity is prevalent in 34.9% of adults [5]. Obesity is related to 4 million deaths and 120 million disability-adjusted life-years [6] and it is estimated to cost \$147 billion dollars to the healthcare system annually [7].

It is now evident that obesity not only affects developed countries but also low-income countries where poverty and malnutrition are most widespread [8]. Both obesity/overweight and childhood malnutrition/underweight are among the top 10 causes of global mortality and disease [9-11]. The most worrying fact about obesity is that its prevalence has tripled in the past thirty years driving the occurrence of serious health problems that will affect their adult life [12].

2.1.1 Cause of obesity

Increased energy intake and decreased energy expenditure is the leading cause of obesity resulting in increased number (hyperplasia) and size (hypertrophy) of adipocytes [13]. Those metabolic cells are responsible for the emergence of metabolic signals that trigger the inflammatory responses and the disruption of metabolic homeostasis. Physical activity, food consumption, and the dissipation of energy as

heat via inducible thermogenesis in beige adipocytes of white adipose tissue (WAT) and via constitutive thermogenesis in brown adipocytes of brown adipose tissue (BAT) regulate energy balance. Several factors including the sympathetic nervous system and mechanisms within the cells affect thermogenesis that is triggered in response to diet, exercise or cold exposure [14].

Lipid uptake and storage, as well as fatty acid mobilization in response to increased energetic requirements are the main responsibilities of WAT. Despite the storing role of this tissue, adipocytes also possess an endocrine role producing cytokines (adipokines), peptides and hormones and consequently affecting immunity and energy balance [15]. Adipokine production, including leptin, adiponectin, resistin and visfatin, contributes to the preservation of the inflammatory mechanism that modulates several physiopathological processes [16] (Figure 1).

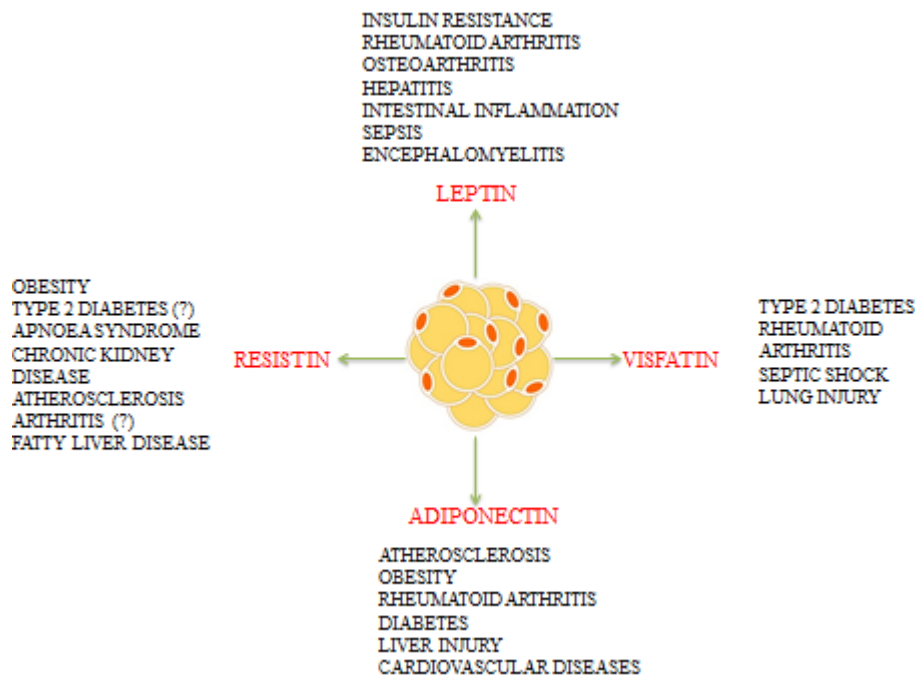


Figure 1. The effect of the production of major adipokines (adiponectin, leptin, resistin, visfatin) by adipocytes on the development of several inflammatory diseases [16].

During weight gain, an increase in adipocyte size takes place due to excess lipid storage leading to the disruption of normal cellular function. Since adipocytes are not

able to store excess lipids any more, the latter are redirected to the liver enhancing dyslipidemia along with plasma free fatty acids, low-density lipoprotein (LDL), and triglycerides increase, and a diminution in high-density lipoprotein (HDL) levels. Additionally, increased lipolysis of triglycerides in large adipocytes results in the formation of glycerol and free fatty acids, the latter of which contribute to the increase of their plasma levels and liver triglyceride synthesis [17].

In case of obesity, several proinflammatory factors including leptin, tumor necrosis factor alpha (TNF- α) and interleukin-6 (IL-6), are produced by adipocytes and are released into the circulation whereas the production of anti-inflammatory molecules such as adiponectin, is decreased compared to lean adipose tissue (AT) [18] (Figure 2). Interestingly, the circulating levels of the anti-inflammatory cytokine interleukin-10 (IL-10) have been found elevated during obesity [16]. Elevated numbers of M1-polarized proinflammatory macrophages and CD8⁺ T cells which are thought to stimulate the development of insulin resistance derive from the excessive energy storage in obese AT [19].

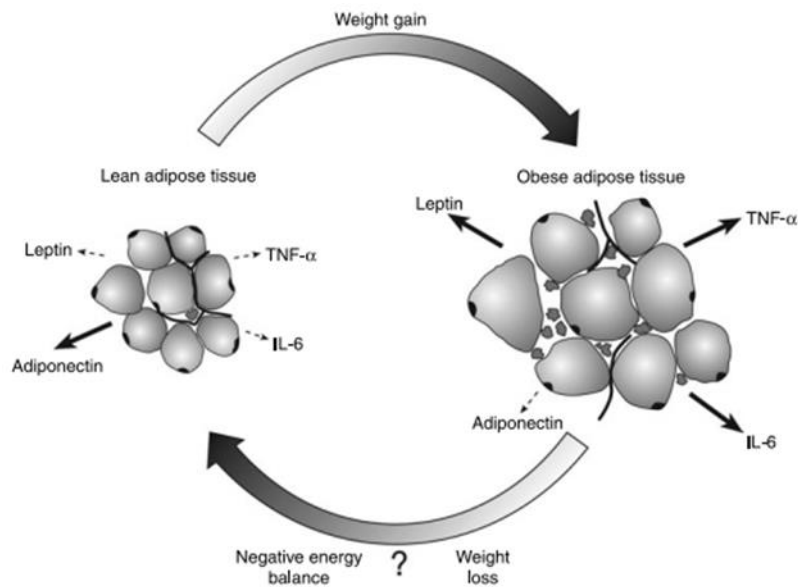


Figure 2. In obesity, adipocytes increase in size (hypertrophy) and they are responsible for the increased production of proinflammatory agents (including TNF- α , IL-6, and leptin) and the decreased production of the anti-inflammatory factor, adiponectin. This inflammatory condition can be reversed in case of weight loss most probably due to a negative energy balance period [18].

Insulin resistance is the state during which an increase in insulin levels does not cause increased uptake of glucose by liver and muscle, leading to increased insulin production by pancreatic beta cells. Increased abundance of circulating free fatty acids in obesity might lead to β - cell malfunction and type 2 diabetes (T2D) occurrence [17]. Obesity- induced inflammation might contribute to a variety of effects on several tissues, including dysbiosis and intestinal permeability (gut), elevated food intake (central nervous system), insulin insensitivity (liver, muscle, AT), and decreased insulin secretion from pancreatic islets [20] (Figure 3). Obesity- driven liver inflammation, leads to the development of non- alcoholic fatty liver disease (NAFLD), non- alcoholic steatohepatitis (NASH) and cirrhosis [19].

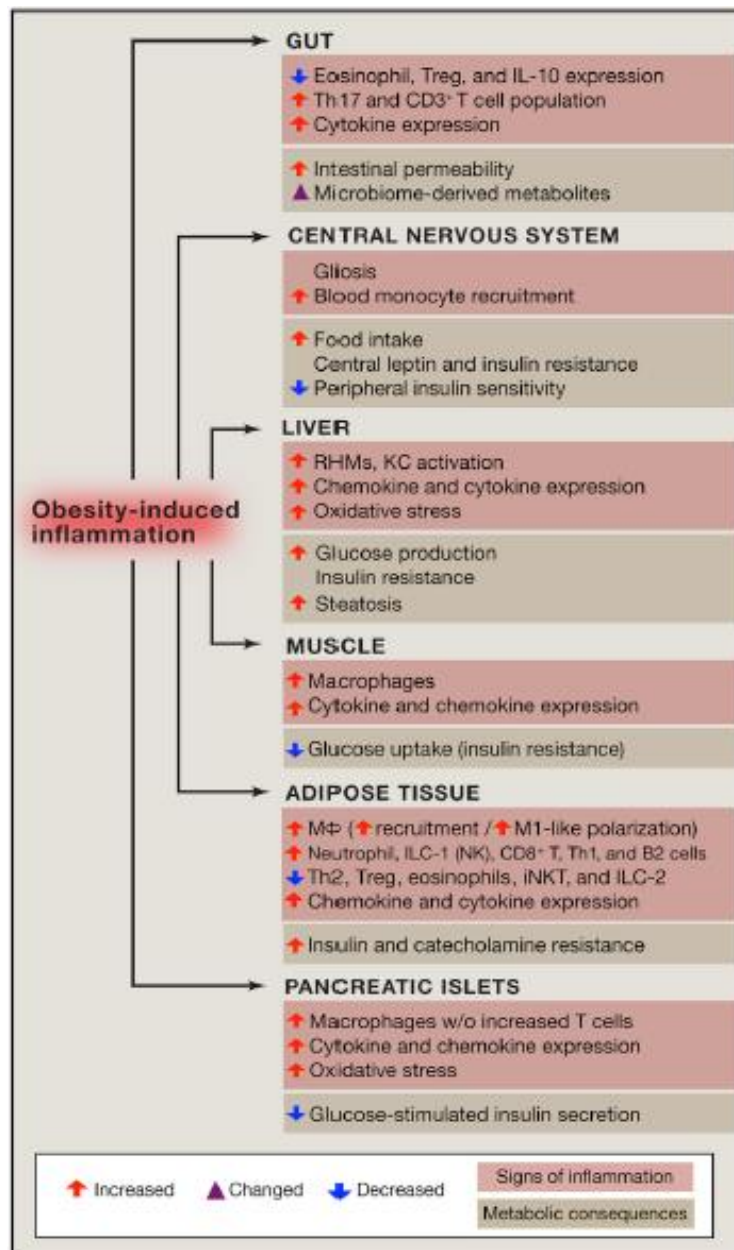


Figure 3. The immunomodulatory and metabolic effect of obesity- induced inflammation on several tissues (Treg: T regulatory cells, Th17: T helper 17 cells, RHMs: recruited hepatic macrophages, KC: Kupffer cells, MΦ: macrophages, ILC-1: innate lymphoid type 1 cells, Th1: T helper 1 cells, Th2: T helper 2 cells, iNKT: invariant natural killer cells, ILC-2: innate lymphoid type 2 cells) [20]

AT dysfunction under the state of excess body weight is further supported by the hypoxic environment of the tissue and the activation of the endoplasmic reticulum (ER) stress response [19]. Those events might affect several tissues and might act upon parenchymal cells to secrete an array of chemokines. The latter trigger chemotaxis and migration of several immune cells including macrophages into the inflamed tissue. Macrophages secrete a variety of proinflammatory factors that result in development of insulin resistance in liver, muscle and AT, as well as in decreased insulin secretion from β cells [20].

The increase in obesity- related inflammatory markers contributes to the orchestration of a state called chronic or low-grade systemic inflammation [18] in which inflamed vascular endothelium and activated immune cells are involved; both of them are potentially affected by nutrient excess, dyslipidemia, hyperglycemia or oxidative stress [21]. A more recent term used to describe the metabolically triggered inflammation that is characterized by the elevated levels of inflammatory factors observed in obesity is “meta-inflammation” (i.e. inflammation in metabolic tissues) [22]. The latter represents the absence of clinical manifestations of inflammation and a modest increase in circulating proinflammatory agents [23]. It is also noteworthy that dietary intake behavior has a direct effect on the composition of gut microbiota along with considerable consequences on immune response [24].

2.1.2 Inflammation & obesity- historical facts

The association between inflammation and metabolic perturbations, including obesity and insulin resistance, was first discussed in 1993, when Hotamisligil et al. [25] demonstrated the constitutive expression of the proinflammatory cytokine TNF- α by adipocytes and its increased expression in adipocytes of obese animals (ob/ob mouse lacking leptin secretion, db/db mouse lacking leptin receptor, and fa/fa Zucker rat).

This inflammatory phenotype was reversed when neutralization of TNF- α by soluble TNF- α receptor took place leading to an improvement in insulin resistance. These data were the first to reveal a potential link between the increased levels of a proinflammatory cytokine and insulin resistance. Further, TNF- α production is known to orchestrate glucose and lipid metabolism, inflammatory processes and immune response [26].

Later on, increased expression of TNF- α in human AT, as well as elevated plasma TNF- α levels in obese individuals were observed. Those levels decreased following weight loss indicating the association between TNF- α expression and BMI [27-29]. Obesity is also characterized by elevated levels of TNF receptor [30, 31]. However, infusions of TNF- α antibody were not effective against the reduction of TNF- α activity and amelioration of insulin resistance in human obesity [32].

The discovery of leptin, a 16-kDa non-glycosylated anorexia peptide, and its production by adipocytes in 1994 by Zhang et. al [33] shed light into the active endocrine role of AT, as it could no longer be regarded as an organ that solely stores fat. The levels of circulating leptin directly correlate with the amount of body fat stored and with adipocyte size [34]. This proportion can be attributed to the induction of energy expenditure and to the suppression of food intake triggered by overproduction of leptin in obesity that directly affects hypothalamic cell populations [35-38]. Upregulated metabolic rate and decreased food intake along with weight reduction are observed in lean or leptin deficient ob/ob mice that were administered with leptin [39]. From an immunological point of view, leptin enhances proliferation and inhibits apoptosis in several immune cell types, such as Th1 CD4⁺ cells, as well as this peptide triggers the secretion of proinflammatory agents including TNF- α (early), IL-6 (late) and interleukin-1 (IL-1) by macrophages [40, 41].

Leptin production, at lower levels, is conducted by other tissues as well such as the bone marrow, skeletal mass, stomach, and placenta [42] and can be induced by inflammatory cytokines, including TNF- α , leukemia inhibitory factor and IL-1 [43]. Leptin receptors are broadly distributed in fat, muscle, brain, small intestine and colon, and their continuous stimulation by high leptin concentration during chronic obesity may lead to leptin resistance [44, 45]. Given the expression of the isoform of leptin receptor, obRb, involved in leptin signaling by nearly all cells of the innate

observed. Thus, leptin might play an active role in lymphopoiesis [39]. Moreover, leptin and leptin receptor deficiency are related to resistance in autoimmune manifestations, including multiple sclerosis, type 1 diabetes (T1D), and experimental colitis in mice, but also increased susceptibility to infections [50].

Several other proinflammatory factors are also elevated in the plasma of obese individuals, including plasminogen activator inhibitor-1 (PAI-1) [51], serum amyloid A (SAA), interleukin-8 (IL-8), C-C chemokine ligand 2 (CCL2)/ monocyte chemoattractant protein 1 (MCP-1), CCL5/ regulated on activation, normal T cell expressed and secreted (RANTES) [21, 22, 52], IL-6 [53], and C- reactive protein (CRP) [1, 54-56], contributing to obesity- induced inflammation.

CRP belongs to the pentraxin family of proteins and its secretion by the liver is induced by IL-6 production in inflammatory states such as trauma and sepsis [57-59]. Its levels follow the trigger or resolution of inflammation and stimulate the production of pro- or anti- inflammatory cytokines through its interaction with immune cells. TNF- α stimulates the production of IL-6 which in turn induces CRP synthesis in the liver [54]. The levels of CRP have been observed to increase progressively with increasing BMI [60] and to decrease following weight loss regardless of the intervention used to induce body weight reduction [56, 61-64].

Mature adipocytes of WAT are responsible for the production of the anti-inflammatory peptide hormone adiponectin. The gene that codes for this hormone is located at a susceptibility locus for cardiovascular disease and diabetes [65]. Visceral obesity and insulin resistance are associated with decreased levels of adiponectin [66, 67] whereas this proportion could be reversed in case of weight loss and with the use of thiazolidinediones that promote insulin sensitivity [68]. Further, adiponectin treatment has been reported to improve insulin resistance [69]. This hormone could be also produced by non fat cells, such as endothelial cells, skeletal muscle cells and cardiac myocytes [70].

Adiponectin affects natural killer (NK) cell cytotoxicity [71] and stimulates the synthesis of anti- inflammatory cytokines [72] such as IL-1RA (receptor antagonist) and IL-10 by human dendritic cells, macrophages and monocytes [70]. Conversely, adiponectin inhibits the production of proinflammatory cytokines, including TNF- α

and interferon- γ (IFN- γ) [70], whereas the secretion of adiponectin is inhibited by proinflammatory cytokines including TNF- α [70, 73] and IL-6 [70, 74].

Weight loss has a direct effect upon inflammation. In that case, the levels of inflammatory markers, such as CRP, TNF- α , IL-6 and leptin, seem to decrease whereas the levels of the anti-inflammatory marker adiponectin increase. Forsythe et al. [18] concluded that the most outstanding improvements in inflammation were observed only when at least 10% weight loss was achieved and when weight loss was a result of low-calorie diet (with or without lifestyle changes) and gastric bypass surgery.

2.1.3 Co-morbidities

Obesity-related co-morbidities are subsequently linked to reduced life expectancy and premature death. Among them are hyperlipidemia, hypertension, as well as insulin resistance that leads to T2D, all being part of the metabolic syndrome [9, 75]. This association is further supported by a parallel increase in the prevalence of both obesity and diabetes during the last 20 years [76]. The rise in human obesity is closely related to an increase in several other diseases including cardiovascular disease, hepatic steatosis, neurodegeneration, airway disease, and biliary disease [22, 77] (Figure 5).

Moreover, obese individuals are at high risk of multiple forms of autoimmunity, including T1D, multiple sclerosis and thyroid autoimmunity [78-82]. Obesity has also been associated with various types of cancer (Figure 5), including thyroid, colorectal, gallbladder, pancreatic, esophageal, kidney, breast and endometrial, leukaemia, non-Hodgkin's lymphoma and multiple myeloma [83-86].

The link between obesity and increased susceptibility to several infectious diseases (Figure 5), such as Hepatitis C, pneumonia [87] and influenza [46, 88, 89] with respiratory, periodontal, nosocomial, surgical or post-operative nature [71] can be attributed to impaired host defense during obesity. Further, obese individuals seem to respond differently to vaccination and several drugs, including antibiotics [71].

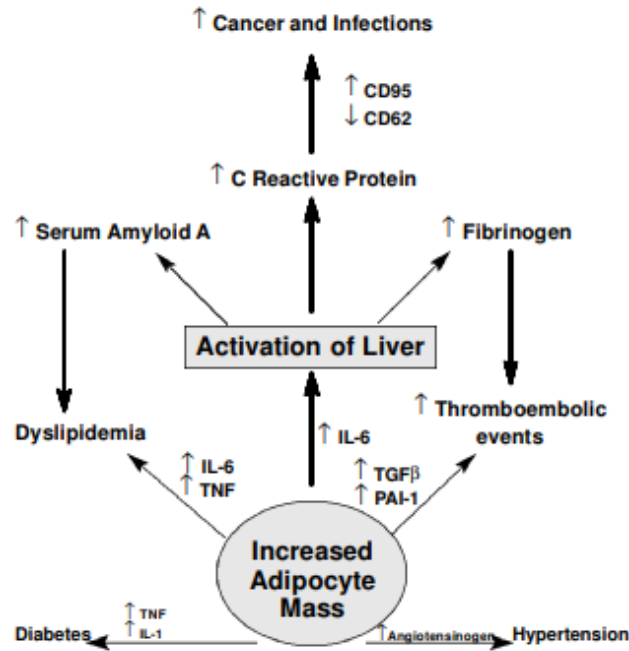


Figure 5. The association between increased adipocyte mass and possible existing co-morbidities, including diabetes, hypertension, dyslipidemia, thrombotic events, cancer and infections, under obese condition [90].

2.2 Immune response (peripheral blood leukocyte subclasses)

The active role of AT in the preservation of obesity- induced inflammation impacts on immune cell numbers that are recruited and on their circulating numbers. Both innate and adaptive immunity cooperate during the inflammatory process involved in obesity.

Several studies report elevated leukocyte numbers in obese children and adults [91] and a positive correlation between the number of total white blood cells and BMI [92].

2.2.1 Innate immunity

2.2.1.1 Polymorphonuclear leukocytes

Neutrophils

Neutrophils are the first cells recruited to site of infection where they trigger strong inflammatory reactions through the production of several cytokines and chemokines including IL-1 β , IL-8, TNF- α and MIP-1a [69]. There, they combat invading

pathogens either by phagocytosis or by degranulation of their antimicrobial factors [93]. The recruitment of cells participating in innate and adaptive immunity, such as dendritic cells, macrophages and lymphocytes, is regulated by neutrophils [94]. Although neutrophils only express the short form of leptin receptor [95], leptin signaling is enough to promote chemotaxis, the expression of CD11b, the production of reactive oxygen species (ROS) and neutrophil survival [15, 16, 71].

Obesity is associated with elevated neutrophil counts (i.e. neutrophilia) [96], increased AT infiltration by those cells [97] and greater activation of their status in plasma [98]. Their numbers are found elevated in response to high fat diet [24] and increase more rapidly than macrophages [99] that dominate in more chronic conditions [97]. Body weight loss results in decreased neutrophil levels regardless of the type of intervention [100]. The correlation between neutrophil levels and BMI has even been observed in children [101], while they are also related to an increase in inflammatory and insulin resistance markers [100]. Further, neutrophil inhibition results in amelioration of liver and AT inflammation, as well as in improvement in insulin resistance induced by obesity [102].

Eosinophils

Eosinophils are among the less abundant circulating granulocytes (Figure 6) and they play a vital role in allergic inflammation. They control AT inflammation by creating an anti-inflammatory environment through the secretion of IL-4 and IL-13 and adipose tissue macrophages (ATM) maintenance in M2 state [103]. Eosinophil's survival and function were shown to be induced by leptin action [100] that promotes the chemokinesis of eosinophils and triggers the production of inflammatory cytokines, such as IL-1 β and IL-6, and chemokines, including IL-8, MCP-1 and growth-related oncogene-alpha. Leptin also stimulates the expression of the adhesion molecules ICAM-1 and CD18 on neutrophils cell surface, but inhibits L-selectin and ICAM-3 [15].

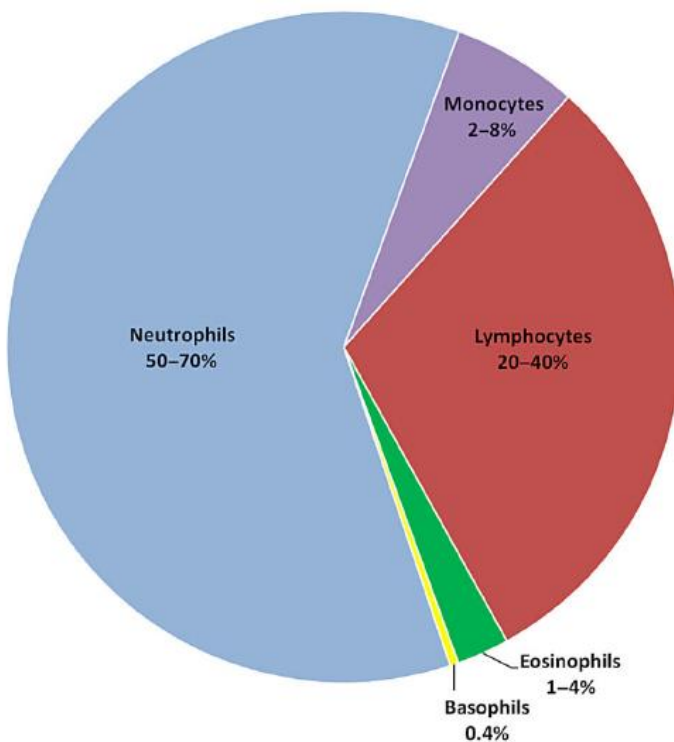
Data concerning eosinophils number during human obesity are inconsistent. No association between eosinophils levels (absolute count or percentage) and BMI/metabolic syndrome has been reported by several studies [100]; conversely, eosinophil percentage of total leukocytes was elevated in a group of morbidly obese individuals with several comorbidities compared to the healthy lean group and this

percentage did not follow weight loss after Roux-en-Y gastric bypass (RYGB) surgery [104]. Moreover, eosinophils were decreased in number in VAT of obese mice [105] and mice that lack eosinophils are characterized by insulin resistance and increased inflammation [106].

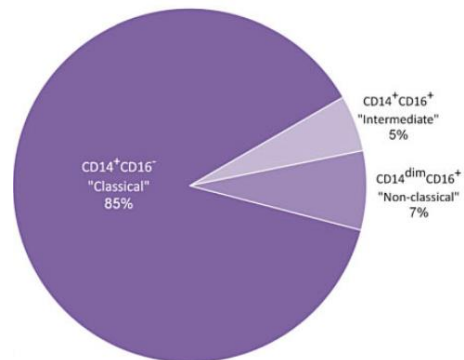
Basophils

Basophils constitute the vast minority among granulocytes and all classes of total circulating leukocytes (Figure 6). They stimulate hypersensitivity inflammatory reactions by binding antigen-specific immunoglobulin E (IgE) that triggers the production of several factors involved in allergic reactions including histamine [100]. Leptin receptor expression on basophil's cell surface has been implicated in prolonged survival, activation, cytokine production, degranulation and migration [107]. The correlation between BMI/metabolic syndrome and basophils circulating levels has been found positive, negative or absent [100], indicating the lack of information concerning the role of basophils in obesity-induced inflammation.

(a) Circulating leucocyte classes



(b) Monocyte subclasses



(c) Lymphocyte classes and subclasses

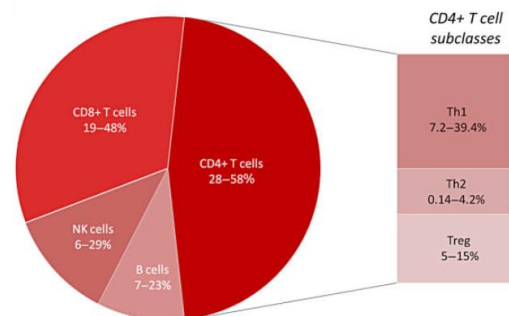


Figure 6. Percentages of the major leukocyte classes (a), monocyte subtypes based on the expression of the surface markers CD14 and CD16 (b), as well as lymphocytes classes and CD4⁺ T cell subclasses (c) in the periphery [100].

2.2.1.2 Natural killer (NK) cells

NK cells that belong to CD3⁻ lymphocytes are implicated in exerting quick responses against virus- infected cells and tumor formation [108]. They comprise 10% of peripheral blood mononuclear cells (PBMCs) [109] and 6-29% of human lymphocytes [100] (Figure 6). Despite their presence in the circulation, NK cells are also encountered in several peripheral tissues and most importantly in the liver and uterus where they constitute up to 30 and 45%, respectively, of total lymphocytes [110, 111]. NK cells are involved in both innate and adaptive immunity [108]. NK cell contribution to adaptive immunity might be reflected on the production of chemokines and cytokines including TNF- α and IFN- γ that participate in macrophage recruitment and insulin resistance induction [112]. In mouse AT, NK cell frequency was lower in the epididymal fat pad of mice fed with a high- fat diet (HFD) [113].

Short and long form of leptin receptor is constitutively expressed by human NK cells [15]. It has been demonstrated that leptin levels are associated with NK cell activity [114]. Further, NK cells are directly affected by leptin administration that modulates NK cell maturation, proliferation, differentiation, activation, and cytotoxicity through the phosphorylation of signal transducer and activator of transcription-3 (STAT-3) and elevated expression at the transcription level of perforin and interleukin- 2 (IL-2) [115] (Figure 7). Leptin induces IL-12 and inhibits IL-15 expression in NK cells [116] whereas leptin has an indirect effect on NK function via regulation of the TNF- α , IL-1 β and IL-6 production by monocytes and macrophages [117]. In a study including 8 normal weight (BMI=22.2 \pm 0.6 kg/m²) and 12 obese (BMI=38.5 \pm 0.8 kg/m²) participants, NK cells from the first group produced higher levels of IFN- γ compared to those from obese individuals following in vitro administration with leptin [118]. Moreover, impaired NK cell function has been observed in db/db mice [116, 119].

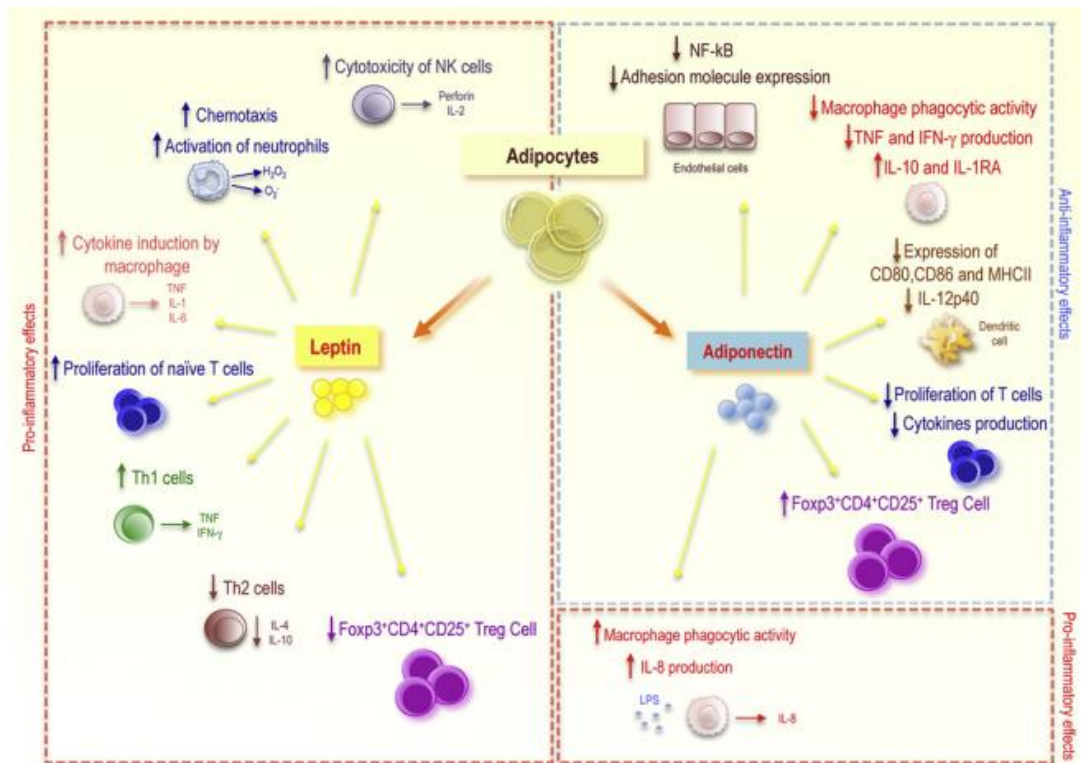


Figure 7. The effect of leptin and adiponectin production by adipocytes on survival, proliferation, activation and function of cells belonging to both innate and adaptive immunity [70].

In case of obesity, NK cells exhibit impaired functionality [120-124] and their numbers are found decreased in the circulation of obese individuals compared to lean controls [121, 125] (Figure 8). Similar reductions in NK cell levels have been reported in childhood obesity as well [126]. When an obese group was stratified into 26 metabolically healthy (MHO) and 26 age-, sex- and BMI matched metabolically unhealthy obese (MUO) individuals, the latter had 50% less circulating NK cells independent of BMI; their activation status was higher though [125]. In another study that included 116 obese and 41 lean women, no statistically significant difference was found in NK cells' frequency between the two groups [127]. Furthermore, NK cells' levels did not change significantly following weight loss regardless of the intervention type (diet, diet plus exercise, bariatric surgery) [128, 129] even when total leukocytes and specific subsets were decreased [128].

NK cells can be categorized into 3 subtypes based on the expression of CD56 and CD16 markers: CD56^{bright}CD16⁻, CD56^{dim}CD16⁻, and CD56⁺CD16⁺. CD56 or neural adhesion molecules are expressed on the surface of glia, neurons, skeletal muscle and NK cells. They mediate in the migration to areas of infection or inflammation and in cell- cell adhesion. Further, CD56⁺ lymphocytes possess a critical role in the immune response against intracellular pathogens and tumor formation. CD16 molecules are expressed on various cells, including monocytes, macrophages, neutrophils, NK and NKT cells, and are implicated in cytotoxic responses [130]. CD56⁺CD16⁺ cells are the predominant subpopulation of NK cells in peripheral blood with important cytotoxic function [131, 132] which actively takes part in antibody- dependent cell-mediated cytotoxicity (ADCC) [133]. Conversely, CD56^{+/}CD16⁻ cells dominate lymphoid tissues and possess a significant immunoregulatory role via the secretion of anti- inflammatory cytokines and the regulation of T cell proliferation [134-137].

Increased counts of CD56⁺CD16⁺ NK cells in obese (4×10^5 cells) compared to control (0.8×10^5 cells) individuals were reported in a study examining the effect of polyphenols in PBMCs responses *in vitro* [138]. Conversely, no statistical difference in CD3⁻CD56⁺CD16⁺ cells between obese and control women was detected in whole blood preparations by others [127, 139], whereas a negative correlation between the expression of NK cell marker CD3⁻CD16⁺CD56⁺ and BMI was reported in another study [1140].

It is widely accepted that NK cell activity is modulated by several factors including metabolites and nutrients [100]. Based on *ex vivo* experiments, NK cells from MUO individuals had impaired cytotoxic capacity [121] and this obesity-related defective function was reversed six months after RYGB surgery reaching the activity level of control group. The last fact could be attributed to an increase in cytokines controlling NK cytotoxic function including IFN- γ , IL-12 and interleukin- 18 (IL-18) [129]. Moreover, in another study evaluating the expression of the early activation marker CD69 on NK cells, they found decreased time- dependent expression 12 months after weight- loss surgery [141]. Similar reduction in NK cytotoxicity was observed in obese women following an 8- week hypo- caloric diet [128]. As a result, it has been proposed that obesity- associated inflammation leads to NK functional impairment and activation- stimulated cell death [108]. Overall, taking published data into

account, NK cell counts/ capacity are found decreased in morbidly obese patients revealing a picture possibly not encountered in mildly obese subjects [100].

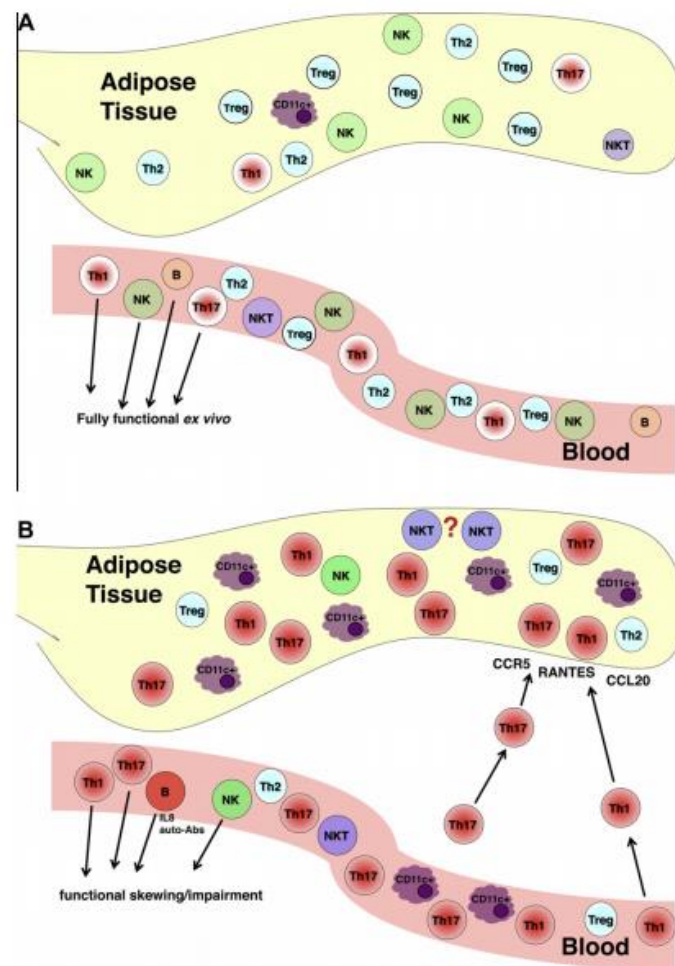


Figure 8. Differences in immune cell counts in adipose tissue and circulation under lean (A) and obese (B) state (NK: natural killer cells, NKT: natural killer T cells, Th1: T helper 1 cells, Th2: T helper 2 cells, Th17: T helper 17 cells, Treg: T regulatory cells, B: B lymphocytes, CD11c⁺: antigen presenting cells, CCR5: C-C chemokine receptor type 5, RANTES: regulated on activation, normal T Cell expressed and secreted, CCL20: chemokine ligand 20) [108]

2.2.1.3 Monocytes

Blood monocytes are bone marrow-derived phagocytes and, as part of the innate immune system, they can differentiate into either tissue macrophages or myeloid lineage dendritic cells. They participate in the response against viruses, fungi, bacteria and parasites [142] via the production of inflammatory cytokines, phagocytosis and

secretion of nitric oxide (NO), ROS and myeloperoxidase. Monocytes' levels have been related to atherogenesis and, therefore, they have been implicated in cardiovascular disease and peripheral atherosclerosis. As regards metabolic disturbances, the frequency of monocytes has been positively associated with triglycerides, and negatively associated with HDL cholesterol [143].

Murine monocytes can be subdivided in two subsets. Gr1⁺ monocytes, also termed as “inflammatory” monocytes, are responsible for the production of TNF- α , NO and ROS. Further, they secrete type 1 interferon in order to combat viruses, as well as low levels of IL-10 following *in vivo* infection with parasites or bacteria. The second subset or Gr1⁻ monocytes are involved in tissue repair and they can differentiate into macrophages following tissue infiltration [142].

Human monocytes can be categorized into three groups based on the expression of the markers CD14, the bacterial lipopolysaccharide (LPS) co-receptor, and CD16, the low-affinity Fc γ III receptor [100].

CD14⁺⁺CD16⁻ or classical monocytes constitute the major subset of monocytes (80-90%) (Figure 6). On the basis of gene and surface molecules expression, they resemble murine Gr1⁺ monocytes [142], and they express the chemokine receptor CCR2 at a high degree and CX3CR1, as well as C-C chemokine receptor type 5 (CCR5), at lower levels [143, 144]. Classical monocytes produce IL-6, IL-8 and ROS in response to LPS, whereas they secrete high levels of the anti-inflammatory cytokine IL-10 but low levels of TNF- α *in vitro* [142] revealing a possible anti-inflammatory character of this type of cells.

CD14⁺CD16⁺ or intermediate monocytes comprise 5% of total monocytes (Figure 6). They differ from CD14⁺CD16⁻ cells in the expression levels of markers CD43, CD45RA, HLA-DR, epidermal growth factor module-containing mucinlike receptor 2 (EMR2), Ig-like transcript 4 (ILT-4) [145], CD11c, CD16, CD62L, CD163, and CX3CR1. They also resemble murine Gr1⁺ cells in that they possess similar functional properties such as phagocytosis and the secretion of TNF- α and IL-1 in response to LPS stimulation. Moreover, it has been proposed that CD16 expression by CD14⁺ monocytes coincides with activation and differentiation of these cells [142]. Increased CD14⁺ monocyte counts and their activation status were correlated with atherosclerosis and hyperglycemia in obese adults and children [91, 146].

CD14⁻CD16⁺ or non-classical monocytes have a smaller size and granularity, and comprise 7% of total monocytes (Figure 6). They express CCR5 at a lower level compared to intermediate monocytes [144], as well as CD11b and CD163 at a lower degree. Although non- classical monocytes possess anti- inflammatory properties in a steady state, they highly secrete proinflammatory factors including IL-1 β , TNF- α and CCL3 in response to nucleic acids and viruses through a proinflammatory TLR7-TLR 8- MyD88-MEK pathway. Further, they produce IL-1RA but not ROS, as well as lysozyme and myeloperoxidase at low or zero levels [142]. Non- classical monocytes have been implicated in atherogenesis given their positive correlation with atherogenic lipoproteins and their negative correlation with HDL cholesterol [147]. Moreover, it has been demonstrated that their population is under the control of increased glycemia in morbidly obese patients [143].

Both intermediate and non- classical monocytes, i.e. CD16⁺ monocytes, are considered as cells capable to trigger inflammatory reaction and their numbers have been found increased in inflammatory situations such as rheumatoid arthritis, sepsis, chronic kidney disease, and infections [145]. CD16⁺ monocytes possess an enhanced ability of antigen presentation, and increased expression of MHC-II and TNF- α , whereas decreased expression of IL-10 has been detected in CD16⁺ compared to CD16⁻ monocytes [143]. Other studies report that CD16⁺ cells, including CD14⁺CD16⁺, resemble murine Gr1⁻ cells and they respond to LPS and to an array of toll- like receptors (TLRs) through the secretion of IL- 1 β and TNF- α [144, 148, 149]. Although CD16⁻ and CD16⁺ monocytes efficiently face *Aspergillus fumigatus* conidia via phagocytosis, they follow different strategy against conidial germination and the secretion of TNF- α [142].

Considerable recruitment of monocytes into VAT via several candidate chemokine pathways including MCP-1 signaling has been reported [105, 150]. Increased expression of CCR2 by peripheral CD14⁺CD16⁺ cells and CCR5 by peripheral CD14⁺CD16⁻ cells in obese women may reveal increased recruitment of those cells into obese AT [150]. AT- recruited monocytes differentiate into adipose tissue macrophages (ATMs) that exhibit high chemokine and cytokine production and stimulate further recruitment of monocytes into VAT [69]. Those ATMs belong to either M1 subtype that predominate in obese AT, or to M2 subtype that is widely distributed in lean AT [138].

Under overweight and obese condition, monocyte count is increased in peripheral circulation compared to lean subjects [127, 151, 152] and a diminution in their numbers follows fat body reduction [138]. However, this is not a universal finding and the number of study participants should be taken into account when seeking changes in cell counts between lean and obese state [100]. Interestingly, positive [143], no [153, 154] or even negative [155] association between BMI and monocyte counts has been reported.

Further classification of monocytes revealed an elevated number of CD14⁺CD16⁺ and CD14^{dim}CD16⁺ cells in obese compared to non- obese subjects that positively correlated with BMI, fat mass and inflammatory factors such as hsCRP [104, 143, 150, 154]. As for CD14⁺CD16⁻ subset, currently available studies report either similar or decreased levels of these cells in obese compared to lean individuals revealing an inconsistent picture concerning this type of cells [143, 154]. Monocyte numbers decreased following a 6- week very low-energy diet (VLED) intervention in obese subjects compared with baseline [156]. A significant reduction in the number and percentage of non- classical and intermediate subtype was induced following fat mass loss of at least 5% [143].

Despite monocyte numbers, obesity also impacts on their function given the elevated phagocytosis and oxidative burst monocytes exhibit [157]. Monocytes from obese individuals produced ROS at high levels [158] and exhibited an elevated surface expression of integrin CD11b compared to those from lean subjects indicating a more activated phenotype of these cells [155]. Others reported increased expression of the proinflammatory markers IL-6 and TNF- α and decreased expression of the anti-inflammatory IL-10 by monocytes from obese non- diabetic patients compared to their lean counterparts [159]. Further, triglycerides levels detected in the serum of obese adolescents with or without metabolic syndrome have been associated with the expression levels of TNF- α in peripheral monocytes [160]. LPS- induced and basal production of TNF- α by PBMC- isolated monocytes from obese subjects with no other comorbidities was increased compared to those from lean individuals [26]. To this line, PBMCs- isolated monocytes from obese subjects produced lower levels of TNF- α following a VLED weight loss intervention and *in vitro* stimulation with LPS compared to baseline [26].

In vitro experiments have shown that human leptin induces the proliferation and activation of human circulating monocytes via the expression of activation markers, such as CD25 (IL-2 receptor α -chain), CD38, CD69, and CD71 (transferrin receptor) [161], and their fate is directly affected by leptin via apoptosis regulation [157]. Moreover, leptin enhances the secretion of interferon-gamma-inducible protein (IP-10) and interleukin 1 receptor antagonist [15], as well as the secretion of proinflammatory cytokines including TNF- α , IL-6 and IL-12 by monocytes, and their ability to phagocytose [39, 71, 162]. Additionally, healthy overweight men treated with leptin had their monocyte levels reduced [163]. However, it has been reported that oxidative burst in monocytes previously activated is downregulated by human leptin [164].

2.2.2 Adaptive immunity

Lymphocytes

Lymphocytes are the main cell type encountered in lymph and can be identified by the large size of their nucleus. They can be subdivided in three major subsets, T cells (adaptive immunity), B cells (adaptive immunity) and natural killer cells (innate immunity). Under obese and overweight condition, increased circulating lymphocyte numbers have been reported [60] and have been shown to positively correlate with elevated BMI following adjustment for several characteristics, such as ethnicity, age, sex and smoking. However, similar levels of inflammatory cytokine secretion by lymphocytes induced by stimulation with LPS were observed in overweight and lean young adults [100].

2.2.2.1 T cells

T cells that are generally distinguished by the expression of the CD3 marker are produced in bone marrow and they fully mature in thymus. They orchestrate adaptive immunity and they shift from naive to effector state during an immune response [165]. Based on the expression of surface markers, T cells can be subdivided in CD4 and CD8 T cells. CD4 T cells can be further subdivided into T helper and T regulatory cells, whereas CD8 T cells are characterized as T cytotoxic cells depending on their different functions. T helper cells or CD4⁺ cells are further separated in several subtypes mostly based on the production of different cytokines, including Th1 that produce IFN- γ and TNF- α , Th2 that release IL- 4, IL- 5 and IL- 13, Th17 that synthesize IL- 17, IL- 21 and IL- 22, as well as Th22 that produce IL- 22 in the

absence of IL- 17 [69, 166] (Figure 9). T lymphocytes orchestrate obesity- related inflammation via both their ability to produce proinflammatory factors and their cytotoxic activity [167].

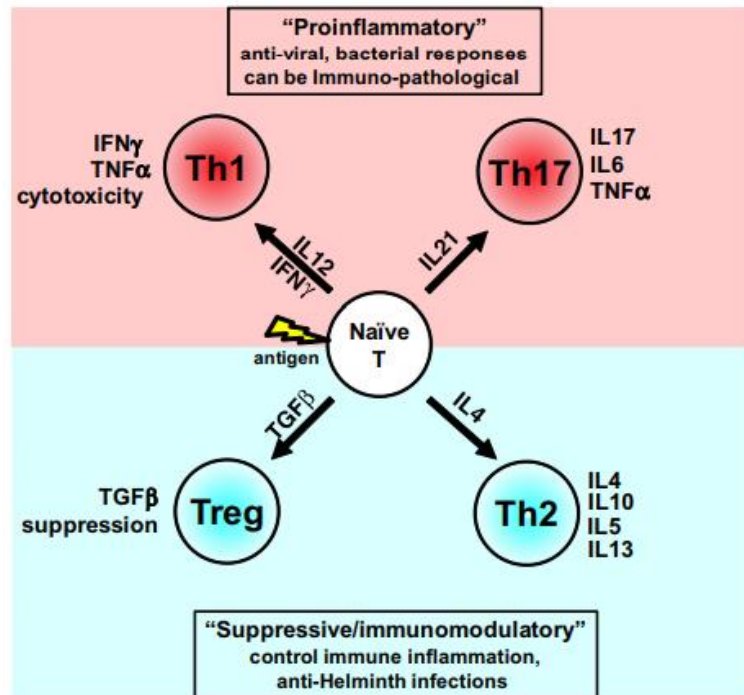


Figure 9. The presence of cytokines in the microenvironment directs naïve T cell differentiation into several subtypes (either proinflammatory or suppressive) following their contact with an antigen [108].

CD3⁺ T cells along with macrophages are the most abundant cells observed in AT. The implication of T lymphocytes in obesity- related inflammation of AT [105], as well as the development of insulin resistance along with lymphocyte infiltration of AT prior to macrophages [105, 168, 169] have been reported. The last fact is supported by the decreased AT infiltration by macrophages and improved insulin signaling following T- cell depletion in HFD- fed mice [169, 170]. In addition, a positive correlation between AT T lymphocyte counts and BMI has been reported based on studies in obese and lean subjects [171].

Nevertheless, data concerning circulating T cell numbers are not so clear. Studies have reported increased levels of circulating T cells by 15- 50% in morbidly obese compared to lean subjects and a positive correlation with adiposity regardless of the

type of studied cohort [40, 92, 101, 127, 172]. However, other studies reported similar CD3⁺ counts between obese and lean adults [153] and children [173], increased CD3⁺ numbers in obese but not in morbidly obese subjects compared to lean individuals [140], and no correlation with BMI in female students [172]. Additionally, similar CD3⁺ T cells percentages were observed between lean, obese and formerly obese women subjected to gastric banding surgery [174], whereas others reported elevated CD3⁺ cell levels in lean compared to obese people [26]. Those variations concerning circulating T cell numbers during obesity could be attributed to differences related to the heterogeneity of T cell pool, the estimation of T cell function and cohort characteristics [100].

CD4⁺ T cells

CD4 T cells are activated by class 2 MHC antigens that are present on the surface of APCs like macrophages and dendritic cells and they trigger the recruitment of other immune cells to the site of inflammation via cytokine production. Their circulating numbers are found elevated in overweight [40], obese [40, 128, 139, 172, 174] and morbidly obese [40, 92, 157, 175] individuals and they positively correlate with BMI [92, 157]. Further, a positive correlation between CD4⁺ T cell numbers and insulin sensitivity (glucose-to-insulin ratio and fasting insulin levels) in non-diabetic morbid obese women has been shown [92]. The increase in CD4⁺ T cell counts may be attributed to an increased proliferative capacity as has been demonstrated in vitro [92]. Importantly, in some cases, their percentage or number did not change following diet- or/ and surgery- induced weight loss [155, 174].

Regulatory T cells (Tregs) are responsible for the maintenance of immune homeostasis through the regulation of immune cell activation and the production of the anti-inflammatory cytokines IL-10 and TGF- β (Figure 9). They usually constitute only 5-15% of circulating CD4⁺ T cell population in mice and humans [41] (Figure 6). These cells actively participate in allergies and peripheral immune tolerance [176], and contribute to the arrangement of an anti-inflammatory environment by inducing M2 polarization via IL- 4, IL- 10 and IL- 13 production [177], reducing M1 polarization and improving insulin sensitivity [178, 179]. Treg cells are differentiated by the regulatory action of transcription factor fox P3 (fork head box P3- foxp3) [180, 181].

During obesity, the number of T reg cells is decreased in rodent [178] and human AT [182] (Figure 8) resulting in the reduction of anti- inflammatory cytokines and a subsequent obesity- induced insulin resistance [169, 170, 178]. Similarly, their circulating levels have been found decreased in T2D patients [183, 184] as well as in obese compared to lean individuals (Figure 8) and have been negatively associated with body weight, BMI and plasma leptin levels [185-187]. As a result, the Th1/Tregs ratio is positively associated with BMI [183].

Treg cells depletion using foxp3- DTR results in an increased transcription of inflammatory genes in VAT and development of insulin insensitivity [178], whereas treatment with Thioridazone (TZD) is associated with increased numbers of Treg cells in AT and a subsequent amelioration of inflammation and insulin resistance. TZD is an agonist of peroxisome proliferator-activated receptor gamma (PPAR- γ); the latter possesses an anti- inflammatory role, controls Tregs accumulation in VAT and adipocyte differentiation, and it is highly expressed in VAT but not in peripheral Tregs. Moreover, IL- 2 administration results in upregulation of regulatory T cells and improves insulin signaling during obesity [188]. Conversely, a direct inhibition of Treg- cell anti- inflammatory function by elevated levels of insulin during obesity was described, thus inducing TNF- α production by macrophages and subsequent inflammation [189].

Other studies report increased mRNA expression of the transcription factor Foxp3, a marker used to identify Treg cells, in the AT of obese compared to lean individuals accompanied by an increase in cytokines produced by Treg cells, IL- 10 and TGF- β [190, 191]. Another study reported increased circulating Treg cell numbers in morbidly obese patients and a positive association with BMI [92], whereas no difference among weight groups in children was suggested by others [192].

It has been suggested that Treg cells percentage might serve as a metabolic state index and individuals having Treg cells $> 1.06\%$ are at a 9.6- fold higher risk of developing an inflammatory obese phenotype [185]. Further, mouse and human Treg cells generation and proliferation are directly affected by leptin [176] and a negative correlation between leptin levels and circulating Treg percentage has been reported (Figure 7) [185]. Inhibition of proper leptin signaling leads to enhanced proliferation of Tregs along with loss of their suppressive character, whereas resistance to leptin

signaling might lead to increased levels of Tregs [71]. Conversely, adiponectin has an indirect positive effect on Tregs proliferation (Figure 7) since an increase in CD4⁺CD25⁺Foxp3⁺ Treg cells frequency and a diminution in T cell proliferation and IL- 2 production have been observed in co- culture experiments of dendritic cells treated with adiponectin and T cells [193].

CD4⁺ T cells can be also characterized by the expression of the leukocyte common antigen isoforms, CD45RA and CD45RO, and the expression of the homing chemokine receptor CCR7 and can be subdivided into four subtypes: naïve (N, CD45RA⁺CCR7⁺), central memory (CM, CD45RO⁺CCR7⁺), effector memory (EM, CD45RO⁺CCR7⁻) and terminally differentiated effector memory cells (TEMRA, CD45RA⁺CCR7⁻). CCR7 has been involved in the stimulation and maintenance of central and peripheral tolerance, as well as in the migration of dendritic, T and B cells into secondary lymphoid organs [194]. Importantly, a sequential differentiation of T cells through the stages Naïve → CM → EM → TEMRA takes place, the latter of which cannot differentiate further.

Alterations in the expression of CD45 isoforms have been associated with metabolic diseases, including T2D and hypothyroidism [195], alcoholic cirrhosis and hepatitis C [196, 197]. A reduction in CD4⁺CD45RA⁺ (29.45 ± 8.90 NASH vs. 43.29 ± 6.62 CNT; $p=0.008$) whereas an increase in CD4⁺CD45RO⁺ (72.99 ± 5.09 NASH vs. 60.38 ± 5.88 CNT; $p=0.013$) compartment was reported in NASH patients compared to healthy subjects. NASH development is accompanied by the development of insulin resistance and the presence of risk factors for the metabolic syndrome, including central obesity [198]. Another study reported a positive correlation between CD4⁺ and CD4⁺CD45RO⁺ T cells with characteristics of metabolic syndrome in a sample of 439 apparently healthy men [153].

Elevated levels of memory (CD4⁺CD45RO⁺) cells positively correlated with protection against T1D in a study that included identical twins [199]. A study including 54 T1D and 12 healthy children reported similar expression of CD45RA⁺, CD45RO⁺ and CCR7⁺ in CD4⁺ cells between diabetic children and controls. A positive correlation between CD4⁺CD45RA⁺ and CD4⁺CCR7⁺ in both T1D and healthy children was observed. However, a negative correlation between

CD4⁺CD45RO⁺ cells and CD4⁺CD45RA⁺/ CD4⁺CCR7⁺ cells was reported in healthy children [194].

Koch et al. (2008) reported an age- associated but not statistically significant diminution in naïve CD4⁺ T cells, as well as an increase in CM but not in TEMRA cells. However, a marked increase in TEMRA cells and a reduction in naïve cells from the elderly were observed in CD8⁺ T cells [200].

Studies discussing the presence of naïve/ memory CD4⁺ T cell compartment exclusively during obesity with no other existing co-morbidities are limited in number. Decreased CD4⁺CD45RO⁺ T cell counts in obese compared to healthy individuals ($0.52 \pm 0.18 \times 10^3 \text{ cells/mm}^3$ OB vs. $0.66 \pm 0.20 \times 10^3 \text{ cells/mm}^3$ CNT; $p < 0,01$) were reported in a study that included 34 obese and 50 healthy subjects, whereas their levels increased following VLED- induced weight loss in 23 obese subjects. Differences in CD4⁺CD45RA⁺ cell counts between obese- healthy individuals and their levels following weight reduction did not reach statistical significance [26]. Further, obesity positively correlated with lower percentages of naïve T cells (CD4⁺CD45RA⁺CCR7⁺) and higher percentages of effector memory T cells (CD4⁺CD45RO⁺CCR7⁻) in a study that included 187 subjects [60].

Both CD4⁺CD45RA⁺ and CD4⁺CD45RO⁺ T cells express the long isoform of leptin receptor and are directly affected by leptin signaling. More specifically, leptin regulates the proliferation of naïve T cells and IL-2 production by those cells [41, 70]. Conversely, leptin affects the proliferation of memory T cells to a lesser extent via Th1- cell responses induction [70] whereas others suggest the prevention of memory T cells proliferation by leptin [41].

Chemokine receptor CXCR3, also known as GPR9, is a 38 kD transmembrane G-protein- coupled receptor that binds to the chemokines CXCL9, CXCL10, and CXCL11 [201, 202]. CXCR3 belongs to the CXC chemokine receptor family and is highly expressed by Th1 cells, NK cells, dendritic cells, alveolar macrophages, eosinophils, mast cells, and human airway epithelial cells, and at low levels by Th2 cells [203]. CXCR3 expression on CD4⁺ and CD8⁺ T cells takes place during their activation state [204, 205]. The interaction between CXCR3 ligands and CXCR3 promotes the polarization of effector T cell recruitment into inflamed tissue, and mediates Th1 trafficking and maturation. As a result, several cellular processes are

triggered, including changes in the cytoskeleton, integrin activation and chemotactic migration. CXCR3 trafficking has been implicated in several inflammatory and autoimmune diseases, such as rheumatoid arthritis, Crohn's disease, multiple sclerosis, and chronically inflamed liver.

Studies in mice have shed light into the role of CXCR3 in T cell recruitment into VAT during obesity. CXCR3 knockout mice fed with a HFD had fewer T cells in VAT compared to control mice on the same diet. Moreover, diet-induced obese CXCR3 deficient mice were more insulin sensitive, and expressed lower mRNA levels of various proinflammatory genes in AT, such as MCP-1, and higher mRNA levels of anti-inflammatory genes, including Foxp3, IL-10 and arginase-1, than their obese littermates [206]. Another study reported no difference in weight gain between CXCR3 deficient and control mice both fed with a HFD for 20 weeks; the former were characterized by decreased VAT infiltration of immature myeloid cells and by improved glucose tolerance, though [207].

Downregulation of CXCR3 and its ligands (CXCL9-11) was observed in cultured progenitor cells derived from 18 obese African-American women compared to their control littermates revealing a disturbance of the CXCR3 pathway under obese condition [208]. Moreover, Hueso et al. [209] reported elevated systemic levels of the CXCR3 ligands CXCL10 and CXCL11 that were associated with increased BMI and insulin resistance in 25 morbidly obese patients who had undergone laparoscopic Roux-Y-gastric bypass surgery.

In a study using human blood samples from healthy donors, it was demonstrated that upregulation of CXCR3 on memory CD8⁺ T cells mediates their migration to sites of inflammation, as well as their differentiation. Moreover, higher expression of CXCR3 by CD8⁺ (~70%) than by CD4⁺ (~20%) T cell compartment was detected [210]. In a group of newly diagnosed T1D patients and diabetic children, Lohmann [211] and Hedman [194], respectively, reported, among others, decreased percentages of CD4⁺CXCR3⁺ cells in diabetic patients compared to healthy controls revealing a possible reduced function of Th1 cells in T1D. Lower percentages of CXCR3⁺ T cells in circulation and lymph nodes along with higher levels of those cells at sites of inflammation may reveal a critical role of this receptor in the infiltration of inflammatory sites by pathogenic T cells [212].

CD8⁺ T cells

T cytotoxic or CD8⁺ cells actively participate in anti- viral and anti- tumoral immunity via their cytolytic activity (perforin, granzyme, and Fas- induced apoptosis) and secretion of proinflammatory cytokines including TNF- α and IFN- γ [100]. They are activated by class 1 MHC molecules presented by APCs [213] and their numbers have been positively associated with BMI [40]. Three- to four- fold increase in CD8 T cell numbers has been reported in obese compared to lean individuals whereas CD8- produced IFN- γ is also elevated in obesity. Increased IFN- γ stimulates macrophage infiltration and M1 polarization contributing to insulin resistance development [69]. Conversely, insulin sensitivity is associated with a reduction in CD8⁺ T cells levels under obese condition [169].

Memory and local effector CD8⁺ T cell numbers have been found elevated in human and rodent obese AT [169, 171, 214-216] and agents produced by these cells contribute to macrophage AT infiltration, differentiation and chemotaxis [169, 217]. CD8⁺ effector T cells depletion that precedes mouse obesity induction results in inhibition of AT infiltration by M1 macrophages and the subsequent enhanced glucose tolerance with no evident effect on AT resident Th1 cells and M2 macrophages numbers or adiposity. Moreover, immunological depletion of CD8⁺ effector cells ameliorated AT inflammation and insulin sensitivity. However, adoptive transfer of CD8⁺ cells into HFD- fed CD8- deficient mice promoted the production of proinflammatory cytokines, VAT infiltration by macrophages, as well as development of insulin insensitivity. Data obtained from *in vitro* studies showed that macrophages had a greater migratory capacity when they were co- cultured with CD8⁺ cells isolated from obese mice compared to those ones isolated from lean mice [169]. Jiang et al. [216] reported that VAT CD8⁺ T cell activation is stimulated by Th1 cytokine IFN- γ *in vitro*.

Despite the observed CD8⁺ increase under obese condition, reduced CD8⁺ T cells in 34 obese compared to 50 lean individuals [26], as well as in 10 morbidly obese compared to 10 healthy, normal weight women [157] have been reported in two different studies. Similarly, low levels of CD8⁺ cells have been reported in several other studies [125, 174, 218]; those results may be attributed to the small sample size though. It is also worth mentioning that CD8⁺ T lymphocytes were more abundant in MHO than in MUO individuals [125]. Further, other studies reported no difference in

CD8⁺ T lymphocyte numbers in obese and normal weight subjects [92, 127, 219]. Weight loss interventions based on either very low calorie diet or surgery did not significantly impact on CD8⁺ T cell number [125] or percentage [220], respectively.

2.2.2.2 B cells

B lymphocytes participate in humoral immunity by secreting antibodies and constitute a far smaller population of lymphocytes in both adipose tissue [221] and circulation [100] (Figure 6) compared to T cells.

The contribution of leptin in hematopoiesis and lymphopoiesis has been demonstrated indicating its pivotal role in the orchestration of immune system function [15]. Reduced numbers of peripheral B and T lymphocytes have been observed in obese ob/ob and db/db mice that exhibit lymphoid organ atrophy and immune dysregulation [222]. When recombinant leptin was supplied to obese mice for seven days, normal myelopoiesis was induced and a twofold increase of the levels of B cells was observed accompanied by a twofold and threefold increase in the numbers of pre- B and immature B cells, respectively [223]. Another study reports a minor increase in CD19⁺ B cells enhanced by leptin treatment that supports the beneficial effects of weight loss on proinflammatory factors [163]. However, no correlation between leptin and B or T lymphocyte counts in postmenopausal obese women has been reported elsewhere [224].

The remarkable presence of several types of lymphocytes including B cells in obese AT has been demonstrated [9, 20, 215]. B cell counts have been found elevated in mouse VAT during diet- induced obesity and have been associated with the development of insulin resistance [221].

Data revealing the association between obesity and circulating B cell levels are inconsistent. Elevated frequency of B cells has been observed in overweight [140] and obese subjects [127, 140, 225] compared to lean control sample. Moreover, B cell levels were related to increased risk for metabolic syndrome and obesity [225]. The most profound correlation between BMI and B cell frequency has been observed in women [140]. However, a lack of association between B cell numbers and BMI during obesity has been reported in other studies [139, 172].

As regards B cell capacity, it has been demonstrated that B cells are less functional and produce more proinflammatory and less anti-inflammatory agents in both young and elderly obese subjects compared to lean individuals based on *ex vivo* data [226]. A similar pattern regarding the production of cytokines by B lymphocytes has been demonstrated by Jagannathan et al. [227]. More specifically, increased secretion of the proinflammatory cytokine/chemokine IL-8 and reduced production of the anti-inflammatory cytokine IL-10 by B cells of obese T2D patients have been reported.

B cells also contribute to the production of the proinflammatory cytokines IFN- γ and IL-17 by T cells [226] and play a significant role in the development of insulin resistance based on data obtained from DIO mouse models [221]. Further, decreased levels of the inflammatory IFN- γ and IL-6, increased levels of the anti-inflammatory IL-10, elevated counts of Treg cells in VAT and protection against insulin resistance have been observed in obese B cell deficient mice compared to obese WT ones [228]. Based on these data, it could be proposed that VAT infiltration by macrophages and T cells follows the presence of B cells in VAT that drive T cell and ATM activation and subsequent inflammation during obesity [9, 20, 168].

2.2.2.3 Natural Killer T (NK T) cells

NK T cells possess properties that lie between innate and adaptive immunity and share similar characteristics to that of NK and T cells. More specifically, they are specialized T cells expressing NK1 and CD3 markers that recognize lipid antigens presented by CD1d molecules, but not peptide antigens presented by MHC-1 and MHC-2 molecules [69, 93, 105, 229]. Based on the type of T-cell receptor (TCR) they express and on their antigen specificity, NK T cells can be categorized in three groups: invariant NK T (iNKT), type II NK T, and NK T-like lymphocytes [166]. They produce a variety of proinflammatory cytokines such as TNF- α and IFN- γ , and anti-inflammatory cytokines including IL-4 and IL-13 [69] thus mediating Th1 and Th2 responses [97]. NK T cells are involved in a variety of pathological conditions, including autoimmune diseases (e.g. multiple sclerosis, rheumatoid arthritis and T1D) [230], microbial infection, metabolic syndrome and cancer [108, 231] and they are typically found in the liver and, to a lesser extent, in circulation, WAT and spleen [105].

Although VAT is enriched in iNKT lymphocytes (15% of total leucocytes) compared to blood samples [166], their number in peripheral circulation, AT and liver is reduced during obesity [105, 230-232]. Others suggest that, although there is a decrease in NKT cells number in the liver under obese condition, ATMs stimulate a slight increase in their levels in AT [233].

According to a recent study, iNKT circulating levels are increased in a group of MHO individuals (i.e. obese subjects who do not suffer from chronic inflammation and insulin resistance) compared to MUO (i.e. obese patients with metabolic abnormalities, chronic inflammation and insulin resistance) and metabolically unhealthy normal-weight individuals (i.e. patients who suffer from metabolic abnormalities and insulin resistance but have normal weight), whereas their numbers are decreased compared to metabolically healthy normal-weight subjects (i.e. individuals protected from metabolic disabilities). Those observations indicate that fat accumulation and its related chronic inflammation but not body weight affect iNKT percentage [229]. Furthermore, weight loss triggers an increase in their numbers in both humans and mice [230].

The frequency of NK T lymphocytes is regulated by leptin that has a negative effect on their numbers based on results obtained from healthy overweight men treated with leptin [163]. It is noteworthy that AT iNKT cells enhance the proliferation of Tregs and the activation of anti-inflammatory macrophages [234]. However, iNKT depletion in combination with high-fat diet provision in mouse models had contradictory effects on insulin resistance and AT inflammation [93] making their role in obesity-induced inflammation unclear.

2.3 Personalized nutrition

The term “personalized nutrition” refers to an approach that aims at the design and subsequent development of specific nutritional advice, products, or services based on each person’s characteristics in order to achieve health increase or preservation. The nature of those characteristics may be genetic, medical, nutritional or phenotypic. Several related terms including precision nutrition, nutritional genomics, nutrigenomics, and nutrigenetics are often used instead of the term “personalized nutrition” [235]. Nutrigenomics or nutrigenetics are used to describe the impact of

genetic variations on individual's response to diet regarding several aspects of health [236].

The application of personalized nutrition is favored either when improvement of public health is needed or when groups requiring specific dietary management (e.g. old people, pregnant women) or suffering from specific diseases need to be nutritionally guided. At personal level, a person's goals regarding performance in competitive sports, desired food preferences, or body dimensions (e.g. through muscle building) could also be achieved through personalized nutrition [235]. It is of great importance that, except for genetic variation, environmental factors should be taken into account during dietary planning, especially in the case of diet-related chronic diseases [237].

Several studies about the use of personalized information in dietary planning have been published so far. In 2015, Zeevi et al [238] designed a machine-learning algorithm using a 800-person cohort and recording responses to 46,898 meals, that requires data concerning biochemical and anthropometric characteristics, personal habits and gut microbiota in order to predict a subject's postprandial glycemic response to real-life meals. The results of the use of this algorithm in a randomized controlled dietary study suggested that personalized diets may contribute to alterations in elevated postprandial blood glucose levels and subsequent beneficial metabolic effects. Another study from the same group [239] suggested that microbiome based information obtained prior to test meal consumption can be used to predict glycemic response to that meal.

In 2016, maybe one of the most outstanding randomized controlled studies [240] concerning personalized nutrition was published, namely the Food4Me Study. This study paved the way for the effective use of the internet to deliver dietary advice. More than 1600 individuals from seven European countries participated in the study and were randomized into four different groups (individual baseline diet, individual baseline diet plus phenotype [blood biomarkers and anthropometry], individual baseline diet plus phenotype plus genotype, and conventional diet) in order to determine the effectiveness of personalized nutrition in changing diet and the aspect of personalization that mostly affects that change. Nutritional advice was delivered to participants via internet and, after a 6-month intervention, it was demonstrated that

any aspect of personalized nutrition was more effective than conventional “one size fit all” approach. The fact that dietary advice was personalized urged participants to develop and sustain a healthier lifestyle highlighting the need for developing cost effective interventions to improve public health.

A limitation of the Food4Me Study is that outcomes of any kind of intervention were restricted to a 3- or a 6- month intervention. However, Lara et al. [241] reported that dietary changes observed at 6 months of intervention may be sustained for at least a year.

Except for the Food4Me Study, the effectiveness of the delivery of personalized nutritional advice via internet has been also widely discussed [242-246]. Increased consumption of fruits and vegetables [247], as well as body weight reduction [2748250] were the outcomes of personalized intervention compared to non-personalized advice reported in several reviews and meta- analyses.

Few studies have focused on genotype- based interventions and their impact on a healthier lifestyle. Joost [251] and Hietaranta-Luoma [252] both concluded that further research is needed in order to model dietary advice on genotype, whereas the limited number and quality of the available studies make the effect of genotype knowledge on successful intervention unclear [253]. Similarly, a prospective longitudinal cohort study including 2,240 individuals reported that knowledge of the results of genomic testing does not affect exercise or fat intake after 3 or 12 months [254].

BMI has a strong genetic background (40-80% heritability) as indicated by family and twin studies, and is affected by genes expressed in the hypothalamus and are involved in appetite regulation [255]. One such gene is fat- mass and obesity- associated (FTO) whose introns 1 and 2 contain 89 common variants [14] (Figure 10).

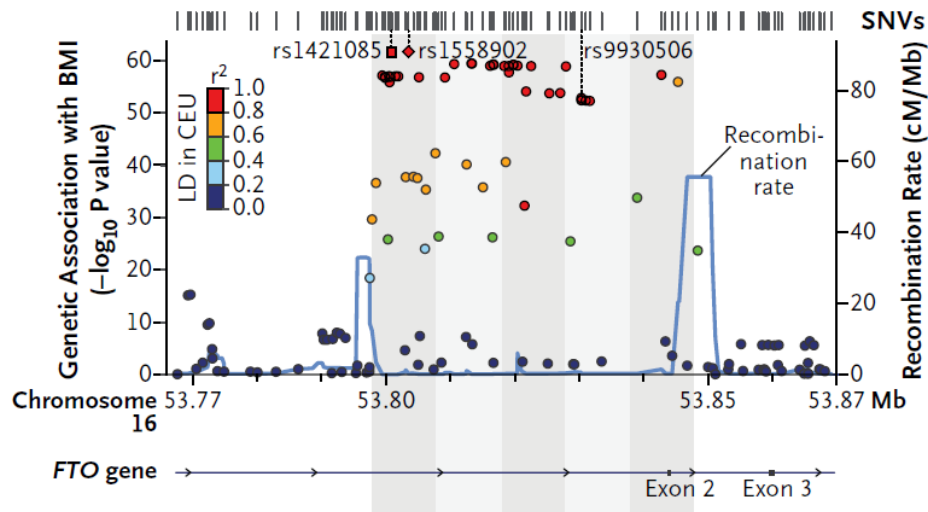


Figure 10. Genetic association for FTO locus variants with BMI (LD: linkage disequilibrium, CEU: population of Utah residents with western and northern European ancestry, gray shading describes consecutive 10-kb parts) [14]

The strong association of variants in the first intron of the FTO gene with obesity has been reported in several studies [256]. Homozygosity for the FTO risk allele AA (rs9939609) resulted in a 3 kg increase in body weight and in a 1.7- fold increased probability of being obese than homozygosity for the lower- risk allele TT [257]. The effect of FTO SNP rs9939609 on changes in BMI and obesity is evident by the age of 7 and continue to exist in the prepubertal period and beyond [257]. Moreover, physical activity has been shown to affect the impact of FTO genetic susceptibility on obesity [256].

In a prospective study including 51 overweight or obese American veterans [258], subjects received one of four types of diet (balanced, low-carbohydrate, low-fat, or Mediterranean) based on their genotype regarding 7 obesity- related polymorphisms [ApoA2, Adiponectin, C1Q and Collagen Domain Containing (ADIPOQ), FTO, Potassium Channel Tetramerization Domain Containing 10 (KCTD10), Lipase C, Hepatic Type (LIPC), Methylmalonic Aciduria (Cobalamin Deficiency) CbIB Type (MMAB), and PPARG], whereas 21 out of 51 individuals served as the control group (standard balanced diet). No difference in weight loss due to nutrigenetic- guided and conventional diet was observed. Further, individuals with low- risk obesity-associated SNPs had a greater weight loss at 8 weeks (5.0% vs 2.9%, respectively; P=

0.02) and BMI reduction at 24 weeks (6.4% vs 3.6% respectively; $P= 0.03$) compared to all other participants.

On the contrary, a Canadian randomized controlled trial including 138 individuals aged 20-35 years reported that nutritional advice based on the ACE genotype successfully led to significant changes in sodium intake at 12 months in individuals with the ACE risk allele compared to the group receiving general population- based recommendation (-287.3 ± 114.1 mg/day vs. 129.8 ± 118.2 mg/day, $p = 0.008$) [236]. This was the first study to examine the impact of genotype- based advice on modification of dietary lifestyle.

Qi et al. [259] examined the role of the insulin receptor substrate 1 (IRS1) variant rs2943641 in improvement of insulin resistance and weight loss in response to four diets. Weight loss interventions were part of the Pounds Lost Trial [260] and varied in macronutrient components. 738 overweight adults were genotyped and were assigned to one of the four diets for 2 years. As a result, participants with the CC genotype showed greater weight loss and decreases in insulin levels than those without CC genotype when they followed a high- carbohydrate/ low- fat diet. It is worth- mentioning that this was the first study to evaluate the effect of gene- diet interactions on improvement of insulin resistance along with weight loss in a long- term randomized clinical trial and highlights the significance of an intervention based on personalized nutrition in preventing obesity- related diseases.

Arkadianos et al. [261] compared the effects of a genetically-guided and a traditional weight loss diet on BMI and blood glucose levels. For that reason, 50 participants in the intervention group were screened for 24 variants in 19 genes related to metabolism, whereas 43 individuals who did not receive a nutrigenetic test served as the control group. It was demonstrated that personalized diet resulted in improvements in fasting blood glucose levels, better dietary adherence and longer- term maintenance of weight loss as compared to conventional diet.

Meisel et al. [262] reported that healthy individuals being informed about their FTO status in the weight- control recommendation were more confident to control their weight; no effect on behavior change was observed, though. In a group of 683 participants from the Food4Me randomized controlled trial, it was reported that individuals carrying the FTO risk allele and being informed about their genotype

significantly had their body weight (21.34 compared with 22.28 kg, respectively; $P = 0.045$) and waist circumference (22.82 compared with 24.34 cm, respectively; $P = 0.046$) reduced compared to the non-personalized control group who were not informed about their genotype [256]. Further, in a 1- year intervention study including 107 healthy adults, it was found that genetic information regarding apoE gene may impact on dietary fat quality and promote a healthier lifestyle [252].

Significant conclusions regarding the association of gene variants and diet with cardiovascular disease manifestations [263] and T2D incidence [264] were drawn out in two studies including >7,000 participants.

Public interest around personal genomics and, more specifically, nutrigenomics, is noteworthy [265]. In a survey conducted in six European countries with 5,967 participants, 66% of responders were willing to undergo nutrigenomics testing and 27% to participate in a personalized intervention [294]. Nielsen and El- Sohemy (2012) in a randomized controlled study with 149 participants [267] reported that individuals find genotype- based dietary recommendations more useful and understandable than general population based dietary advice and they would be more willing to make changes to their usual diet if genetics- based advice was provided to them. Other studies demonstrate that knowledge of genetic information based on genome analysis affects dietary lifestyle even though the genetic information was not related to any dietary change [268, 269].

It is interesting to mention that in a double- blind, randomized controlled trial with 138 participants, it was demonstrated that individuals prefer to be informed about their personal genetic results by a health care professional or a university research lab than a genetic testing company [265]. The important role of the involvement of healthcare professionals in the communication of genetic results has also been discussed in other studies [270, 271]. Individuals would also prefer to receive personalized nutrition recommendation by registered dietitians [265].

3. OBJECTIVE

This study was designed to identify differences in circulating levels of leukocyte and lymphocyte subclasses between obese and non- obese individuals. Furthermore, the effect of weight loss due to personalized or non- personalized intervention on the frequency of circulating immune cells was also evaluated.

4. METHODS

4.1 Study design

Two groups of participants were included in this study. In the first group, 34 obese volunteers (BMI >30 kg/m²) with no other existing co-morbidities, undergoing a weight loss program were included. Obese participants were assigned to either a personalized intervention group (n=4) who followed a diet based on their genetic background or a conventional diet group (n=7) who followed conventional low-calorie diet. Leukocyte subpopulations were assessed before (n=34) and after a 3-month genotype-based or conventional diet intervention (n=11).

The second group included 15 lean (BMI<25 kg/m²) healthy volunteers.

Informed consent was obtained from all volunteers and venous blood was drawn into 10mL EDTA tubes. Leukocyte subpopulations count was determined either by a cell counter or by means of flow cytometry (Figure 11).

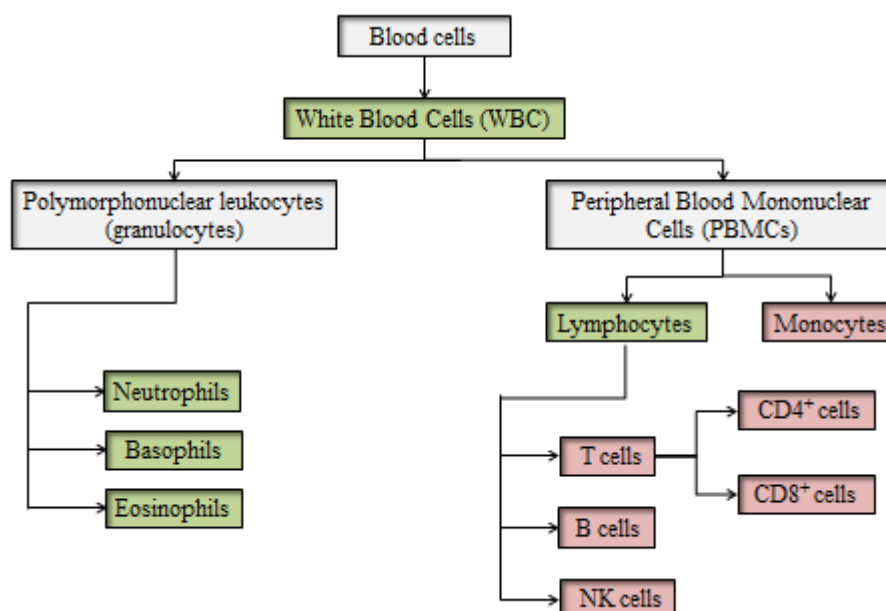


Figure 11. Schematic illustration of immune cells assessed in this study either by cell counter (green boxes) or by means of flow cytometry (red boxes). PBMC subpopulations were further analyzed by flow cytometry.

4.2 Isolation of peripheral blood mononuclear cells (PBMCs)

PBMCs exposure to systemic factors, including inflammatory agents and nutrients might render those cells probable biomarkers to predict early homeostatic energy imbalance [272]. The most commonly used method for the isolation of peripheral blood mononuclear cells (PBMCs), namely monocytes and lymphocytes, is by density gradient centrifugation. This method takes advantage of the property that immune cells possess different densities (Figure 12) and are separated in distinct layers during centrifugation in the presence of a density gradient media, such as Ficoll- Paque medium. Thus, cells possessing a high density will migrate through ficoll whereas cells with a lower density will be found on top of the ficoll layer following centrifugation. As a result, PBMCs- containing layer can be easily extracted and purified.

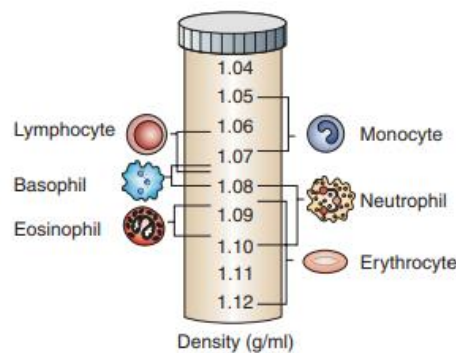


Figure 12. Different densities of human blood cells [273]

PBMCs were isolated from venous blood according to the following protocol.

- Peripheral blood was drawn in the presence of the anti-coagulant ethylenediamine-tetraacetic acid (EDTA) and then transferred to 50 ml falcon tube.
- 10-15 ml of Ficoll-Paque were prepared in a falcon tube.
- Peripheral blood was diluted 1:1 with Roswell Park Memorial Institute 1640 (RPMI).
- Ficoll was overlaid with diluted blood slowly against the wall of tube (10 ml Ficoll for <30 ml diluted blood).

- Cells were separated by spinning at 900g for 20min at 18°C (no brake).
- Following spin, a Pasteur's pipette was used to collect the lymphocytes layer into a fresh tube (Figure 13). It was important to slowly suck and move in circular motion in order to ensure all possible white cloudy part was sucked up into a new falcon tube.
- Lymphocytes layer was topped up to 50 ml with RPMI and spinned at 300g for 10min at 4°C, with brakes. Lymphocytes were washed 2 more times.
- Cells were counted prior last wash using Neubauer's chamber by trypan blue exclusion.
- After determining the number of cells, they were resuspended in appropriate volume of pyrogen- free saline, namely PBS⁺ (1% Human serum, 2mM EDTA) to be used for flow cytometry profiling.

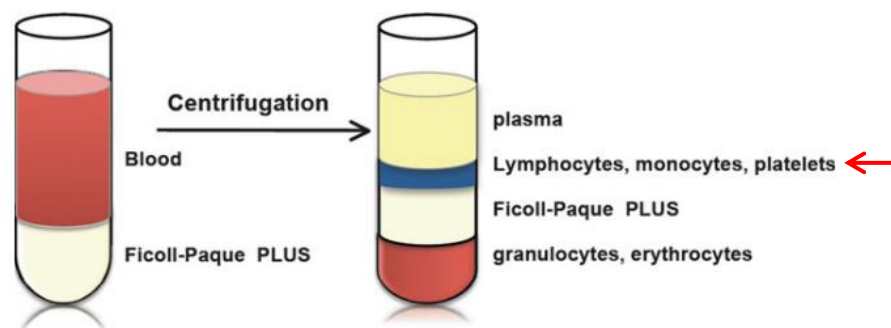


Figure 13. Experimental procedure for PBMCs isolation. First, peripheral blood is layered over ficoll (left part). Then, after centrifugation, blood components are separated into four layers (right part): (1) granulocytes, erythrocytes, (2) ficoll, (3) lymphocytes, monocytes (i.e. PBMCs), platelets (red arrow), and (4) plasma [274].

4.3 Immune profiling using flow cytometry

Flow cytometry is a widely used laser- based technique used for the analysis of the expression of cell surface and intracellular molecules, the definition of cell size and volume, the detection of cell viability, and the characterization of different cell types in a mixed cell population. It was first used in the 1950s for the estimation of cell volume in a rapidly flowing fluid stream during cell passing in front of a viewing

hole. Nowadays, flow cytometers allow the simultaneous detection of an increased number of fluorescent parameters on the same cell (from 1 up to >30) and the extremely rapid collection of information from millions of cells.

The simultaneous multi- parameter analysis of single cells is the most powerful application of flow cytometry. Its functional principle is based on the measurement of fluorescence intensity emitted by fluorescent- labeled antibodies detecting ligands or proteins that bind to cell- associated factors. In order to prepare samples for flow cytometry analysis, a single- cell suspension from tissue samples or cell culture is incubated with fluorochrome- labeled or unlabeled antibodies and are then analyzed.

The three main components of a cytometer are (Figure 14):

- the fluidics system, that is responsible for sample transportation from the container to the flow cell,
- the optical system, that includes excitation light sources, lenses and filters responsible for light collection and spread around the cytometer, as well as the detection system that gives rise to photocurrent generation,
- the electronics, in which the photocurrent is digitized and prepared for further analysis

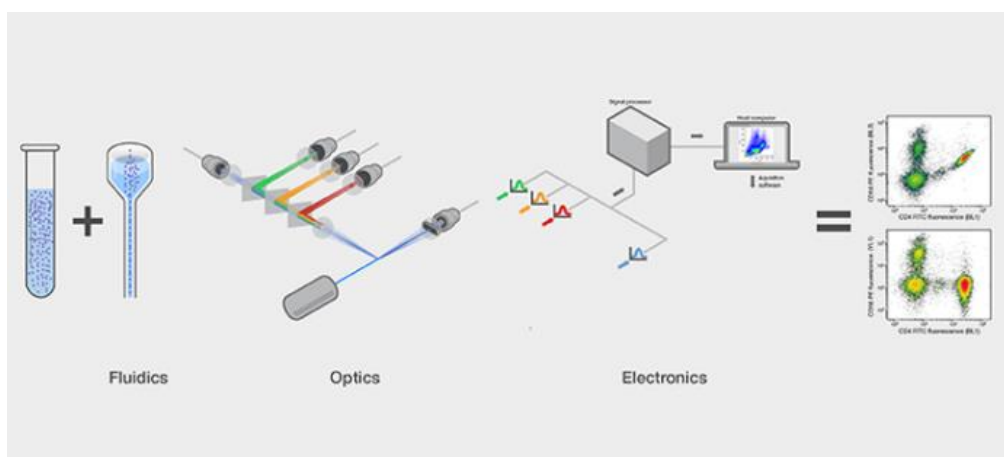


Figure 14. Schematic illustration of the three main parts of a flow cytometer [275]

It is important to mention that instruments used for sorting cells into different containers in real time (Fluorescence activated cell sorting [FACS]), are also consisted by a cell sorting component (Figure 15).

The sample is drawn from the tube or multi- well plate and is injected into the flow chamber. There, laminar stream of sheath fluid focuses the cells through a nozzle and allows only the single pass of cells through the laser light at a time. Cells or particles scatter the light following their route through the laser beam. Forward scatter (FS) is measured by a detector placed in front of the light beam and is indicative of the size of the cell or particle passing in front of the laser. Side scatter (SS) is measured by several detectors placed to the side of the light beam and detects changes in optical density and complexity of the objects. Fluorescence produced by stained cells is detected by fluorescence detectors (Figure 15).

Except for fluorescent dyes used in the experiment, fluorescence may also originate from autofluorescence within a cell. In order to determine the real signal emitted by an antibody, estimation of the background fluorescence is conducted by using unstained cells or isotype antibodies. Isotypes are antibodies with a binding domain that does not target any cell molecule and a constant region that may bind to some receptors on cell surface and dead cells. The isotype control should ideally be the same isotype, in terms of species, heavy and light chain, conjugated to the same fluorophore and have the same F:P ratio (i.e. a ratio indicative of the number of fluorescent molecules detected on an antibody) as the experimental antibody.

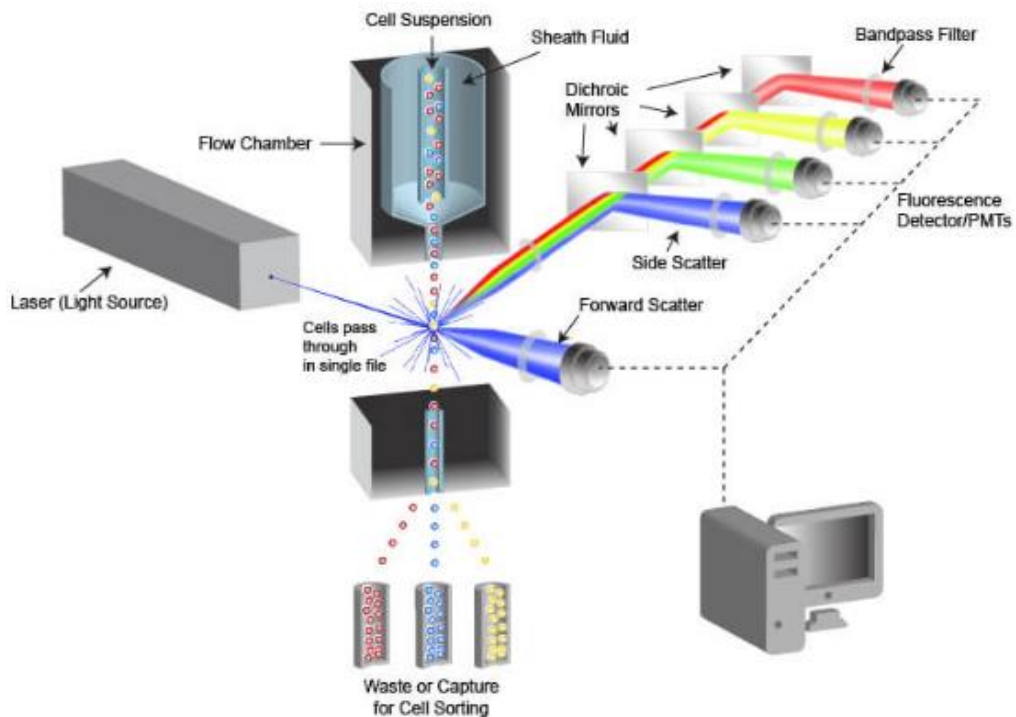


Figure 15. Schematic illustration of flow cytometry system and main parts [276]

We stained isolated PBMCs for flow cytometry profiling according to the following protocol:

- 2×10^6 cell suspension in PBS⁺ were dispensed in three different tubes.
- Antibody mastermix was prepared and 6 μ L of antibody mixture were added in the appropriate tube (Table 1). The dilution of each monoclonal antibody in each tube was 1:10. Singles and isotype controls were also prepared.

Table 1. Antibody mixture used for each staining (St1, St2, St3) for the detection of monocytes, NK cells and T cell subsets

St1	St2	St3
T cells	CD8 ⁺ T cells/ Tregs	Monocytes/ NK cells

CD3 FITC	CD3 FITC	CD45 PE/Dazzle
CXCR3 PE	CD4 PE	CD 14 PE
CD45RO APC		CD16 FITC
CD4 PercPCy5.5	CD127 PECy5	CD15 PECy7
CD45RA PECy7	CD25 PECy7	HLA-DR APCCy7
CCR7 APCCy7	CD8 APCCy7	CD56 APC

- After 30min of incubation on ice in the dark, tubes were centrifuged at 1500rpm for 7min at 4°C.
- Supernatants were discarded and cells were resuspended in 150 µL PBS⁺. DAPI (dilution 1:1000) was added when needed in order to exclude dead cells.
- Cells were then analyzed by flow cytometry (FACS Aria).
- Data acquisition and analysis were performed with the FACS Diva Software version 6.1.3.

4.4 Statistical analysis

GraphPad Prism 6 was used for graph construction and the statistical analysis of results. WBC percentages are expressed as mean± standard error of the mean (SEM). Statistical analysis was performed using the unpaired Mann-Whitney t- test (two-tailed) when comparing cell absolute counts and percentages derived from obese and lean participants. Two-way analysis of variance (ANOVA) was used to assess the statistical significance of the differences in PBMCs subtypes levels between genotype-based and conventional diet following the 3-month intervention. Sidac multiple comparison test assuming that each comparison is independent of the others, was used for post hoc comparison. The threshold for significance was set at $p < 0.05$.

5. RESULTS

5.1 Participants' characteristics

The baseline characteristics of the 49 study participants are depicted in Table 2. As described in “Methods” section, participants were classified according to their BMI and were defined as obese (BMI= 34.45±1.08 kg/m², n=34) or lean (BMI= 22.64±0.52 kg/m², n=15). 71% of them were female (60% non- obese and 76% obese) and mean age was 32.60±2.70 years for lean and 38.21±1.58 years for obese subjects.

Table 2. Baseline characteristics of the participants included in the study (*: mean±SEM).

	Lean	Obese
No.	15	34
Sex ratio, F/M	9/6	26/8
Age, years*	32.60±2.70	38.21±1.58
Weight, kg*	65.30±2.10	96.17±3.41
BMI, kg/m²*	22.64±0.52	34.45±1.08

5.2 Gating strategy in flow cytometry profiling

In order to evaluate the number of immune cells present during obesity, three gating strategies were followed.

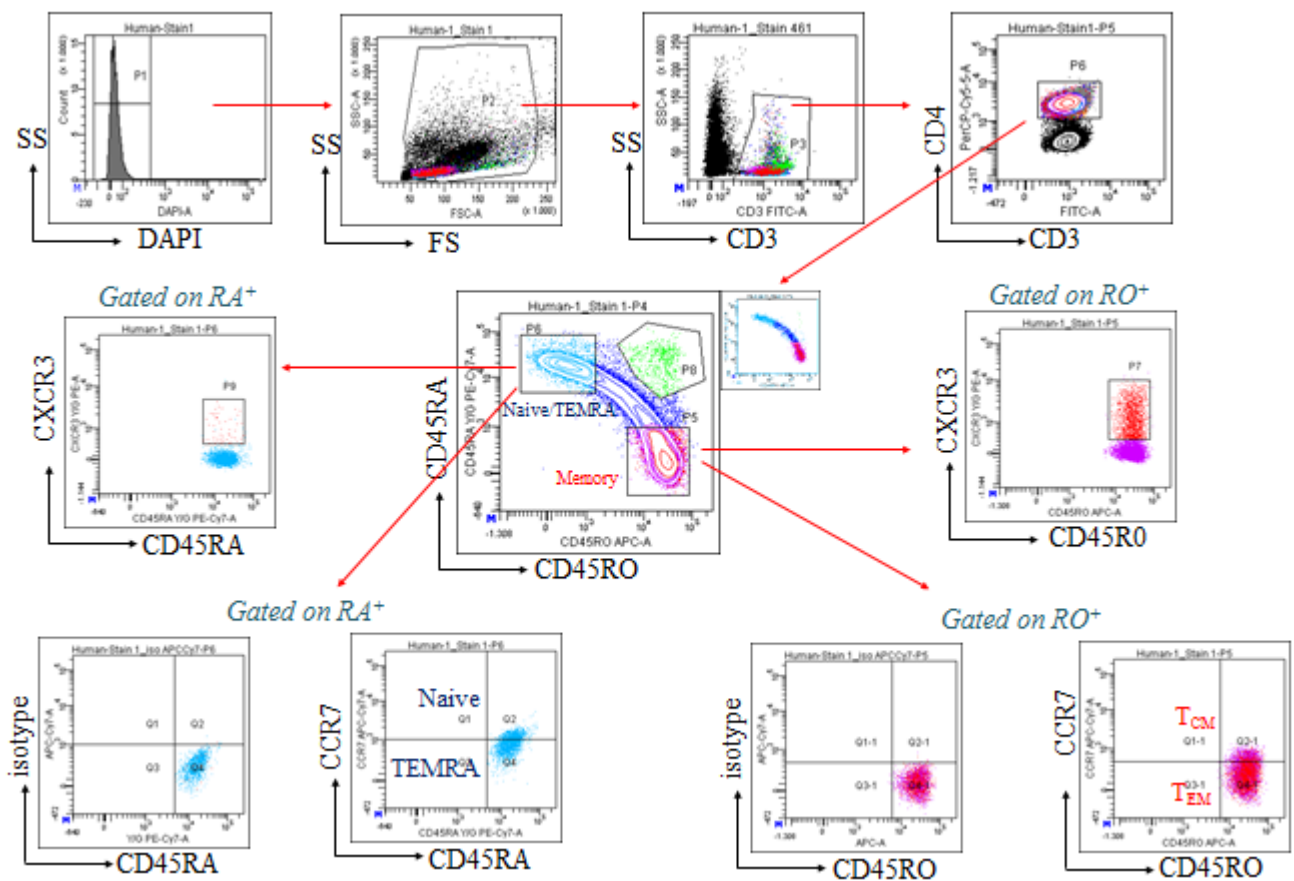
Staining 1

In this strategy, the following cell populations were assessed (Figure 16):

- T cells (CD3⁺)
- CD4⁺ T cells
- Naïve T cells (CD45RA⁺CCR7⁺)
- Central memory T cells (T_{CM}) (CD45RO⁺CCR7⁺)

- Effector memory T cells (T_{EM}) ($CD45RO^+CCR7^-$)
- Terminally differentiated effector memory cells (TEMRA) ($CD45RA^+CCR7^-$)
- $CD45RA^+CD45RO^+$ T cells
- $CD45RA^+CXCR3^+$ T cells
- $CD45RO^+CXCR3^+$ T cells

Figure 16. Gating strategy followed for the assessment of $CD4^+$ T cells subtypes



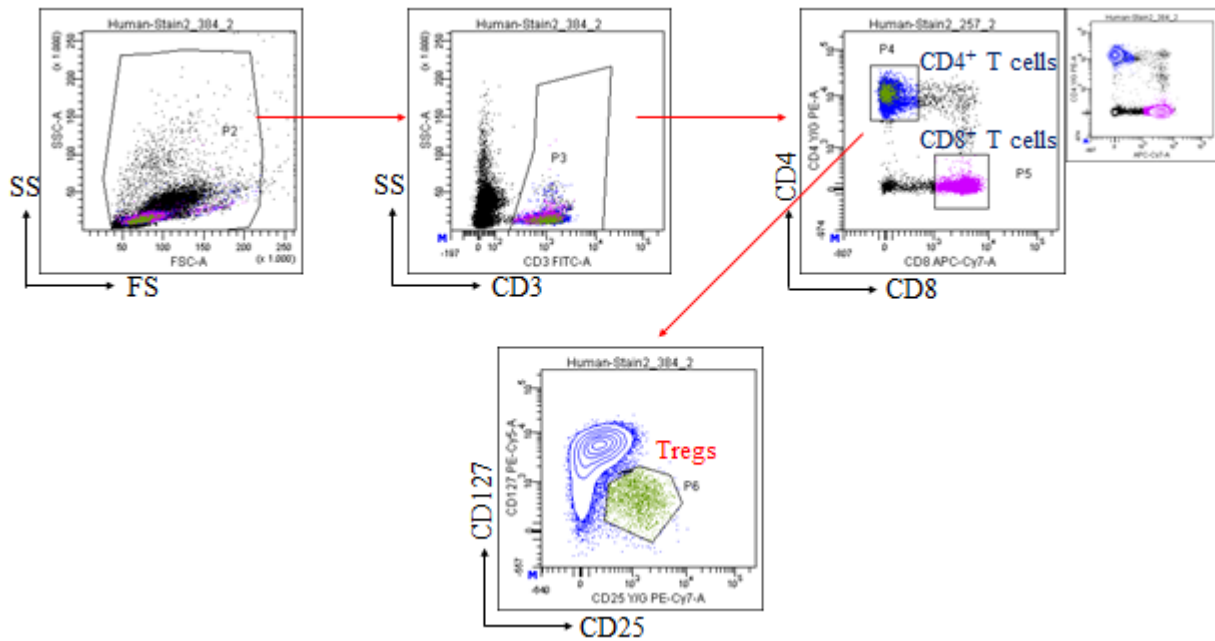
(Staining 1)

Staining 2

In this strategy, the following cell populations were assessed (Figure 17):

- T cells ($CD3^+$)
- $CD4^+$ T cells
- T cytotoxic cells ($CD8^+$)
- Regulatory T cells (Tregs) ($CD127^-CD25^+$)

Figure 17. Gating strategy followed for the assessment of CD8⁺ T cells and T



regulatory cells (Tregs) (Staining 2)

Staining 3

In this strategy, the following cell populations were evaluated (Figure 18):

- Monocytes
 - Classical (CD14⁺CD16⁻)
 - Intermediate (CD14⁺CD16⁺)
 - CD14^{low}CD16⁺
 - Non- classical (CD14⁻CD16⁺)
- NK cells
 - CD56⁺CD16⁺
 - CD56^{bright}CD16⁻
 - CD56^{dim}CD16⁻
- B lymphocytes (CD16⁻CD14⁻HLA-DR⁺)

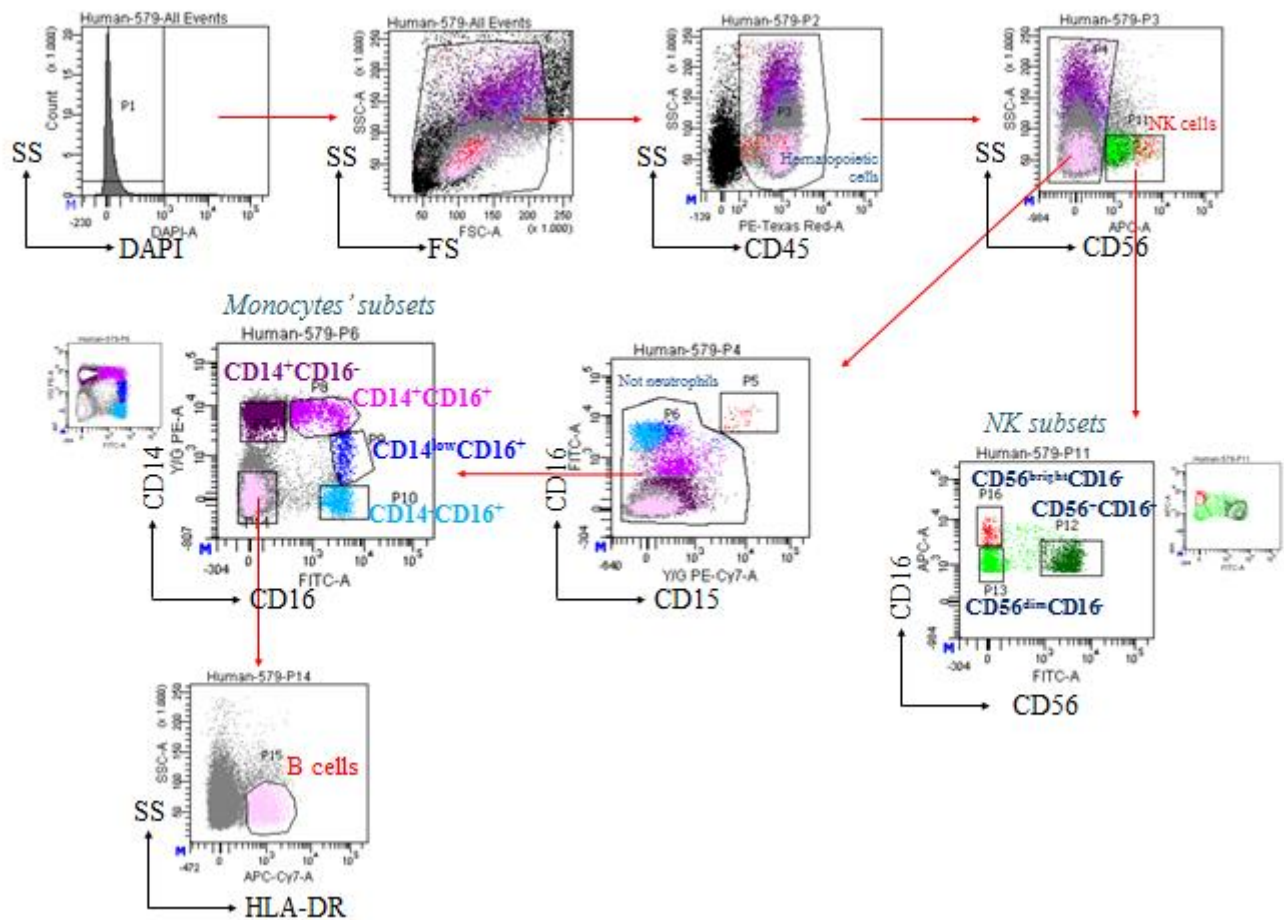


Figure 18. Gating strategy followed for the assessment of B lymphocytes, monocyte and NK subsets (Staining 3)

5.3 Differences in immune cell numbers between lean and obese individuals

Differences in absolute numbers and percentages of immune cells between obese and non-obese participants are summarized in Table 3.

Table 3. Leukocyte and lymphocyte subset counts or percentages in lean and obese individuals. Values are presented as mean \pm standard error of the mean (SEM). (*: p values in bold represent statistical significant differences between the obese and control group, $p < 0.05$)

Type of cell	Lean	Obese	p value*
	mean±SEM		
White blood cells (cells/ μ L)	6423±308.4	6809±439	0.9045
Basophils (% total cells)	0.79±0.1426	0.6543±0.07273	0.4612
Eosinophils (% total cells)	2.75±0.5272	2.628±0.2561	0.6211
Neutrophils (% total cells)	54.15±2.252	54.98±1.556	0.7033
PBMCs (total cells)	1.87x10 ⁷ ±1.957x10 ⁶	2.654x10 ⁷ ±1.533x10 ⁶	0.0037
Classical monocytes (CD14 ⁺ CD16 ⁻) (% total PBMCs)	10.09±1.297	8.475±0.5443	0.4636
Intermediate monocytes (CD14 ⁺ CD16 ⁺) (% total PBMCs)	1.26±0.1848	1.461±0.1768	0.7056
Non-classical monocytes (CD14 ⁻ CD16 ⁺) (% total PBMCs)	2.42±0.4900	3.402±0.6301	0.6309
CD14 ^{low} CD16 ⁺ monocytes (% total PBMCs)	0.5779±0.09208	0.7293±0.08834	0.3861
Lymphocytes (% total cells)	35.74±1.560	34.83±1.364	0.4956
T (CD3 ⁺) lymphocytes (% total PBMCs)	43.73±2.388	48.51±1.395	0.0506
B lymphocytes (% total PBMCs)	6.304±0.6829	6.481±0.4483	>0.9999
NK cells (% total PBMCs)	8.438±0.6743	7.224±0.5447	0.1072
CD56 ^{bright} CD16 ⁻ NK cells (% total PBMCs)	0.2679±0.03839	0.3117±0.04647	0.4064
CD56 ^{bright} CD16 ⁻ NK cells (% NK cells)	3.7±0.6942	4.443±0.5208	0.1446

CD56 ^{dim} CD16 ⁻ NK cells (% total PBMCs)	1.281±0.2568	1.46±0.2241	0.5617
CD56 ^{dim} CD16 ⁻ NK cells (% NK cells)	15.71±2.456	20.35±2.635	0.2161
CD56 ⁺ CD16 ⁺ NK cells (% total PBMCs)	6.287±0.6456	4.897±0.4450	0.0664
CD56 ⁺ CD16 ⁺ NK cells (% NK cells)	72.41±3.591	66.88±3.410	0.3753
CD3 ⁺ CD4 ⁺ (% total PBMCs)	28.89±2.177	32.61±1.637	0.1481
CD3 ⁺ CD4 ⁺ (% CD3 ⁺ cells)	61.27±1.776	63.58±1.608	0.48
CD3 ⁺ CD8 ⁺ (% total PBMCs)	12.63±0.8096	12.4±0.7214	0.7541
CD3 ⁺ CD8 ⁺ (% CD3 ⁺ cells)	27.77±1.853	24.47±1.080	0.1173
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CD45RO ⁻ (% total PBMCs)	10.04±1.418	9.206±0.6649	0.7704
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CD45RO ⁻ (% CD4 ⁺)	35.74±3.385	29.92±1.710	0.2466
CD3 ⁺ CD4 ⁺ CD45RA ⁻ CD45RO ⁺ (% total PBMCs)	10.92±0.8434	13.96±0.6497	0.0124
CD3 ⁺ CD4 ⁺ CD45RA ⁻ CD45RO ⁺ (% total CD4 ⁺)	43.39±3.248	45.9±1.550	0.5408
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CD45RO ⁺ (% total PBMCs)	0.5667±0.5667	0.6106±0.06858	0.4816
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CD45RO ⁺ (% total CD4 ⁺)	1.893±0.3098	2.032±0.2053	0.7031
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CCR7 ⁺ (Naïve) (% total PBMCs)	1.617±0.2635	2.22±0.2686	0.3142
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CCR7 ⁺ (Naïve) (% CD4 ⁺)	6.827±1.243	7.438±0.8730	0.8117
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CCR7 ⁻ (TEMRA) (% total PBMCs)	10.63±1.600	12.01±0.9013	0.3549

CD3⁺CD4⁺CD45RA⁺CCR7⁺ (TEMRA) (% CD4 ⁺)	46.1±4.053	45.96±2.001	0.9023
CD3⁺CD4⁺CD45RO⁺CCR7⁺ (CM) (% total PBMCs)	0.3336±0.05293	0.5962±0.08440	0.1772
CD3⁺CD4⁺CD45RO⁺CCR7⁺ (CM) (% CD4 ⁺)	1.304±0.2253	2.079±0.3258	0.3363
CD3⁺CD4⁺CD45RO⁺CCR7⁻ (EM) (% total PBMCs)	13.76±1.065	16.94±1.183	0.1361
CD3⁺CD4⁺CD45RO⁺CCR7⁻ (EM) (% CD4 ⁺)	41.56±3.024	43.51±1.525	0.7179
CD3⁺CD4⁺CD45RA⁺CXCR3⁺ (% total PBMCs)	0.366±0.06918	0.3265±0.03911	0.8595
CD3⁺CD4⁺CD45RA⁺CXCR3⁺ (% CD4 ⁺)	1.255±0.1832	1.083±0.1346	0.3749
CD3⁺CD4⁺CD45RO⁺CXCR3⁺ (% total PBMCs)	5.032±0.5299	5.316±0.4552	0.7156
CD3⁺CD4⁺CD45RO⁺CXCR3⁺ (% CD4 ⁺)	19.52±1.724	17.28±1.266	0.362
CD3⁺CD4⁺CD127⁻CD25⁺ (T regs) (% total PBMCs)	1.996±0.1423	2.157±0.1446	0.6406
CD3⁺CD4⁺CD127⁻CD25⁺ (T regs) (% CD4 ⁺)	7.06±0.3254	6.559±0.2522	0.1616

White blood cells (WBC)

Increased white blood cell counts were observed in obese (mean± SEM= 6809±439 cells/μL) compared to non- obese participants (mean± SEM= 6423±308.4 cells/μL) but the difference did not reach the levels of statistical significance (Figure 19A).

5.3.1 Polymorphonuclear leukocytes (granulocytes)

Regarding polymorphonuclear leukocytes, a reduction in basophil levels (mean± SEM= 0.65±0.07% vs. 0.79±0.14%) (Figure 19B) and a slight increase in neutrophils' levels (mean± SEM= 54.98±1.56% vs. 54.15±2.25%) (Figure 19C) were observed in obese compared to lean individuals. Furthermore, the percentage of eosinophils in the

obese group was lower than that of controls (mean± SEM= 2.63±0.26% vs. 2.75±0.53%) (Figure 19D).

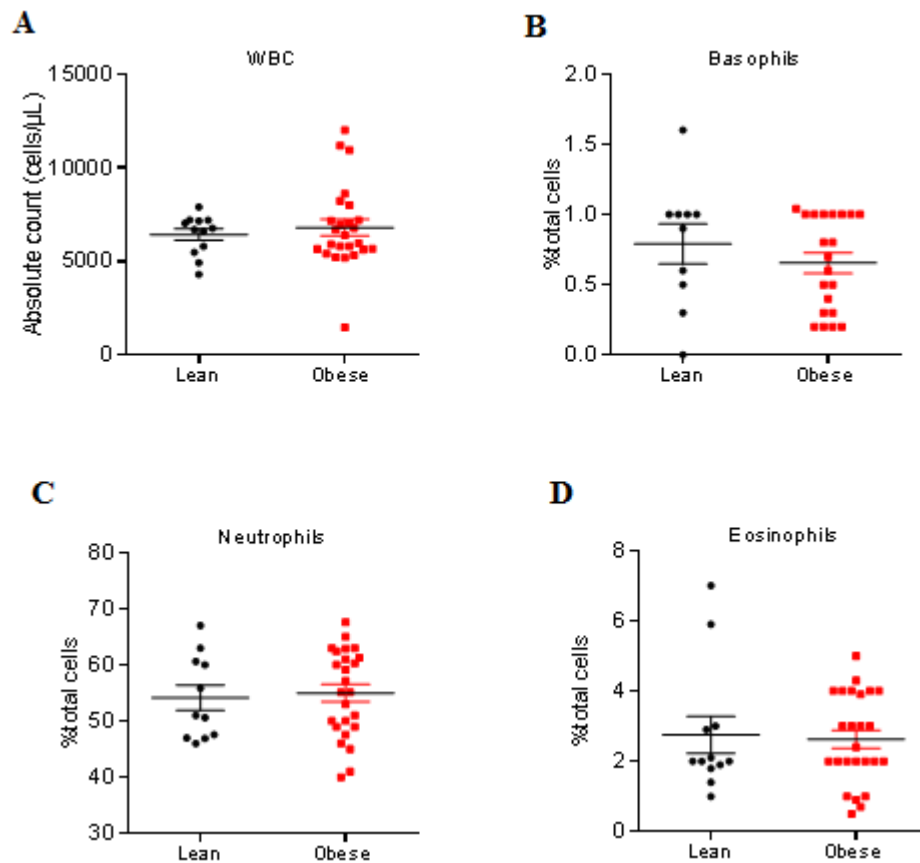


Figure 19. Differences in white blood cell (WBC) counts (n=12 lean/ 25 obese) (A) and granulocytes' [basophils (B) (n=10 lean/ 21 obese), neutrophils (C) (n=11 lean/ 25 obese), eosinophils (D) (n=12 lean/ 25 obese)] percentages between lean and obese participants. Comparisons between groups were performed using a Mann- Whitney t-test. In all cases $p > 0.05$.

5.3.2 Peripheral Blood Mononuclear Cells (PBMCs)

Circulating numbers of PBMCs were significantly higher ($p = 0.0037$) in obese (mean± SEM= $2.65 \times 10^7 \pm 1.53 \times 10^6$ cells) compared to non- obese (mean± SEM= $1.87 \times 10^7 \pm 1.96 \times 10^6$ cells) individuals (Figure 20A).

5.3.2.1 Monocytes

As for monocytes' total percentages, an increase in $CD14^-CD16^+$ (non- classical) (mean± SEM= $3.40 \pm 0.63\%$ vs. $2.42 \pm 0.49\%$) (Figure 20B), $CD14^+CD16^+$

(intermediate) (mean± SEM= 1.46±0.18% vs. 1.26±0.18%) and CD14^{low}CD16⁺ (mean± SEM= 0.73±0.09% vs. 0.58±0.09%) (Figure 20C) subsets in obese compared to lean individuals were observed. However, CD14⁺CD16⁻ (classical) monocytes (Figure 20B) were found decreased in obese (mean± SEM= 8.47±0.54%) compared to non- obese (mean± SEM= 10.09±1.3%) individuals.

5.3.2.2 Lymphocytes

Relative to non- obese subjects (mean± SEM= 35.74±1.56%), obese participants experienced a slight reduction in lymphocytes' total percentage (mean± SEM= 34.83±1.36%) (Figure 20D).

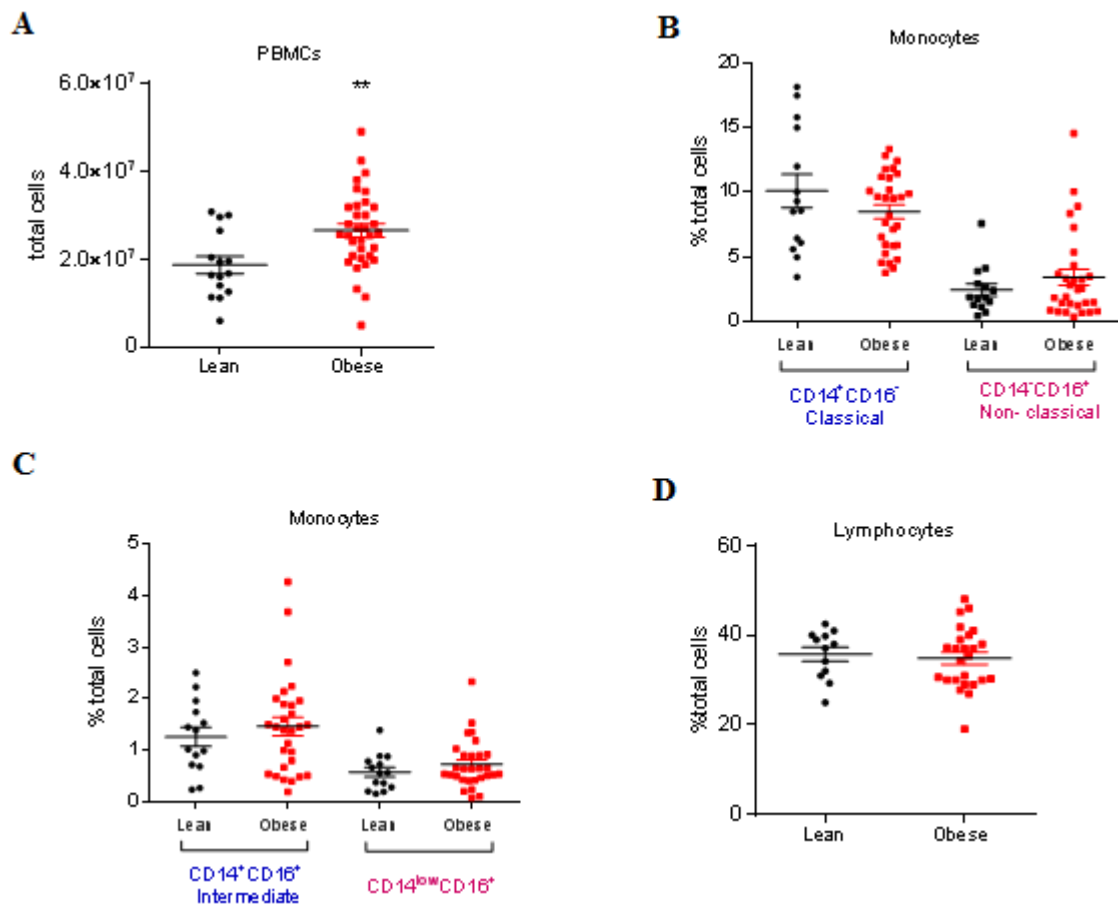


Figure 20. Differences in PBMCs counts (n=15 lean/ 34 obese) (A), as well as in monocytes' subsets [CD14⁺CD16⁻ (classical), CD14⁻CD16⁺ (non- classical) (B), CD14⁺CD16⁺ (intermediate), CD14^{low}CD16⁺ (C)] (n=14 lean/ 29 obese) and lymphocytes' percentages (n=12 lean/ 25 obese) (D) between lean and obese

individuals. Comparisons between groups were performed using a Mann-Whitney t-test. **: $p=0.0037$

Lymphocyte compartment

Elevated T cell ($CD3^+$) (mean \pm SEM = $48.51 \pm 1.39\%$ vs. $43.73 \pm 2.39\%$) ($p=0.0506$) (Figure 21A), decreased NK cell (mean \pm SEM = $7.22 \pm 0.54\%$ vs. $8.44 \pm 0.67\%$) (Figure 21B) and similar levels of B cells (mean \pm SEM = $6.48 \pm 0.45\%$ vs. $6.30 \pm 0.68\%$) (Figure 21C) were observed in obese compared to lean individuals.

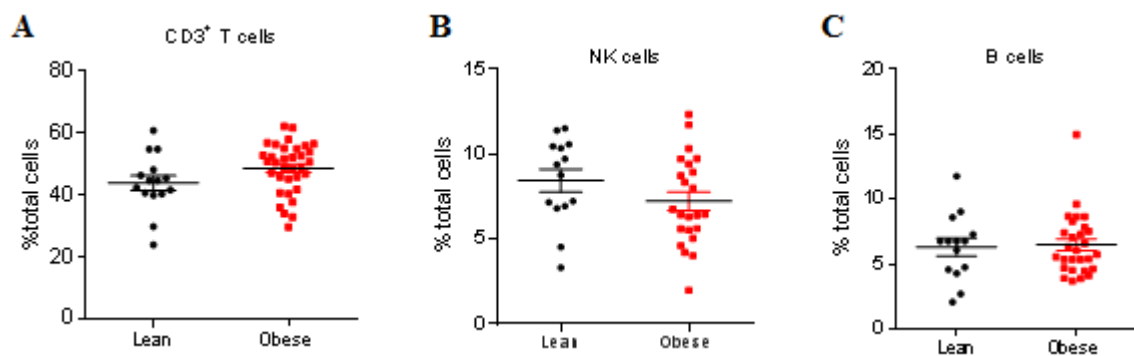


Figure 21. Differences in T lymphocytes ($CD3^+$) ($n=15$ lean/ 34 obese) (A), NK cells ($n=14$ lean/ 23 obese) (B) and B lymphocytes ($n=14$ lean/ 28 obese) (C) levels between lean and obese individuals. Comparisons between groups were performed using a Mann-Whitney t-test. In all cases $p>0.05$.

NK cell compartment

Total percentages of CD56^{bright}CD16⁻ (mean± SEM=0.31±0.05% vs. 0.27±0.04%) (Figure 22A) and CD56^{dim}CD16⁻ (mean± SEM= 1.46±0.22% vs. 1.28±0.26%) (Figure 22B) NK cells were elevated in obese individuals. A reduction in CD56⁺C16⁺ levels (Figure 22C) in the same group (mean± SEM= 4.9±0.44%) compared to non- obese participants (mean± SEM= 6.29±0.64%) was observed though (p=0.0664). Similar observations were reported even when cell percentages regarding NK cell compartment were examined (CD56^{bright}CD16⁻:4.44±0.52% vs. 3.7±0.69%, CD56^{dim}CD16⁻: 20.35±2.63% vs. 15.71±2.46%, CD56⁺C16⁺: 66.88±3.41% vs. 72.41±3.59%) (Figure 22D-F).

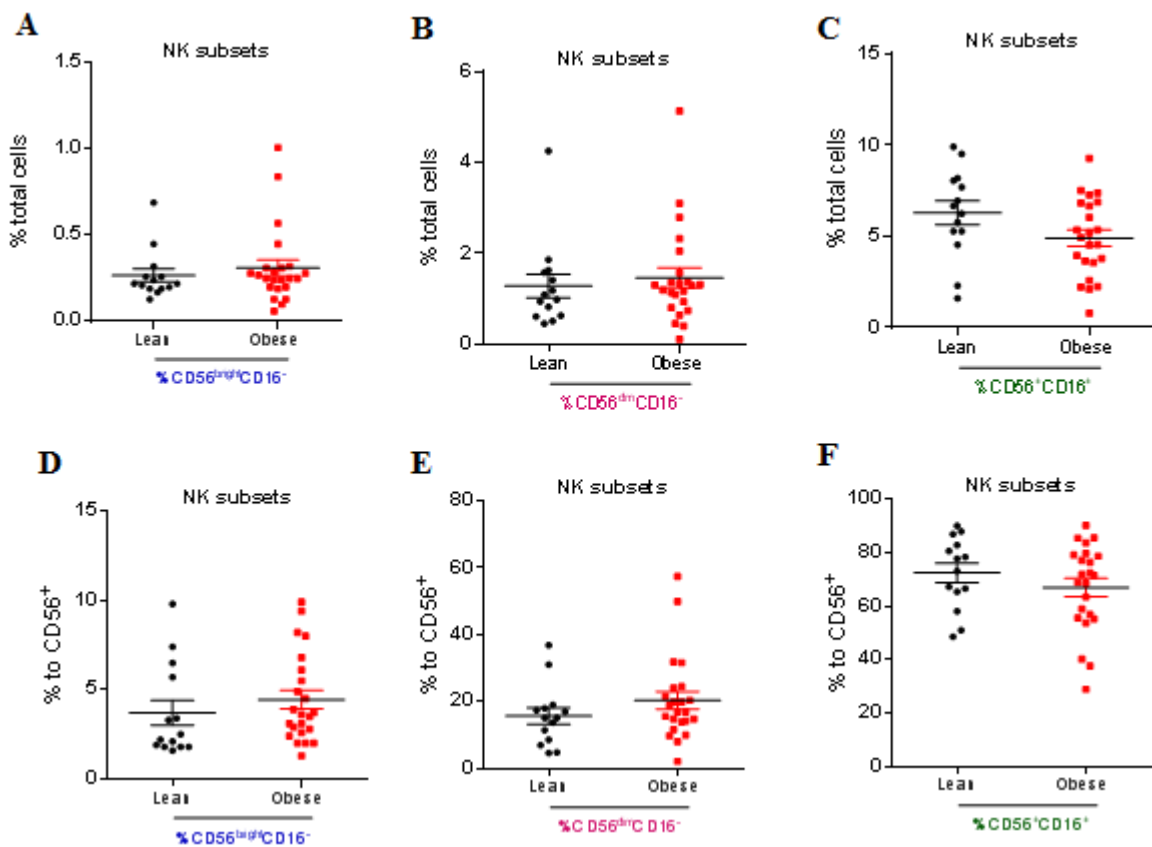


Figure 22. Total and % percentage to total NK cells (CD56⁺) of CD56^{bright}CD16⁻ (A, D), CD56^{dim}CD16⁻ (B, E), and CD56⁺C16⁺ (C, F) NK cells, respectively, in obese (n=23) and lean (n=14) group. Comparisons between groups were performed using a Mann- Whitney t- test. In all cases p>0.05.

T lymphocyte compartment

In obese individuals, total levels of CD4⁺ T cells were higher (mean± SEM= 32.61±1.64% vs. 28.89±2.18%) (Figure 23A) whereas total percentage of CD8⁺ T cells was slightly lower (mean± SEM= 12.40±0.72% vs. 12.63±0.81%) (Figure 23B) than those of controls. Regarding CD3⁺ T cell compartment, CD4⁺ T cells were increased (mean± SEM= 63.58±1.61% vs. 61.27±1.78%) (Figure 23C) and CD8⁺ T cells were decreased (mean± SEM= 24.47±1.08% vs. 27.77±1.85%) (Figure 23D) in obese compared to non- obese participants.

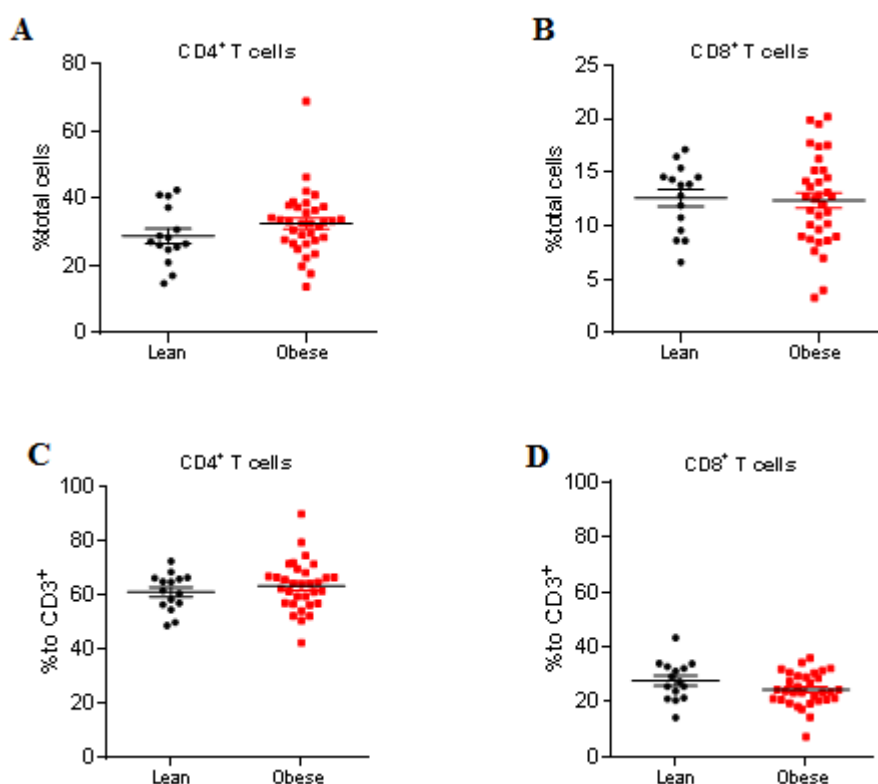


Figure 23. Total (n=15 lean/ 34 obese) and % percentage to T lymphocytes (CD3⁺) (n=15 lean/ 32 obese) of CD4⁺ (A, C) and CD8⁺ (B, D) T cells, respectively, in obese and lean participants. Comparisons between groups were performed using a Mann-Whitney t- test. In all cases p>0.05.

CD4⁺ T cells compartment

CD4⁺ T cells were further assessed based on the expression of CD45RA/CD45RO markers. More specifically, total CD4⁺CD45RA⁺ T cells (Naïve/ TEMRA) were

decreased in obese individuals (mean± SEM= 9.21±0.66% vs. 10.04±1.42%) (Figure 24A). The levels of CD4⁺CD45RO⁺ T cells (Memory) were elevated in obese participants (mean± SEM= 13.96±0.65% vs. 10.92±0.84%) and the difference between the obese and control group reached the levels of statistical significance (p=0.0124) (Figure 24B). Furthermore, total percentage of CD4⁺CD45RA⁺CD45RO⁺ T cells was slightly increased in the obese group (mean± SEM= 0.61±0.07% vs. 0.57±0.12%) (Figure 24C).

When cell levels were examined regarding their distribution in CD4⁺ T cell compartment, decreased levels of CD4⁺CD45RA⁺ (mean± SEM= 29.92±1.71% vs. 35.74±3.38%) (Figure 24D) and increased levels of CD4⁺CD45RO⁺ (mean± SEM= 45.90±1.55% vs. 43.39±3.25%) (Figure 24E) and CD4⁺CD45RA⁺CD45RO⁺ (mean± SEM= 2.03±0.21% vs. 1.89±0.31%) (Figure 24F) T cells were observed in obese compared to lean individuals.

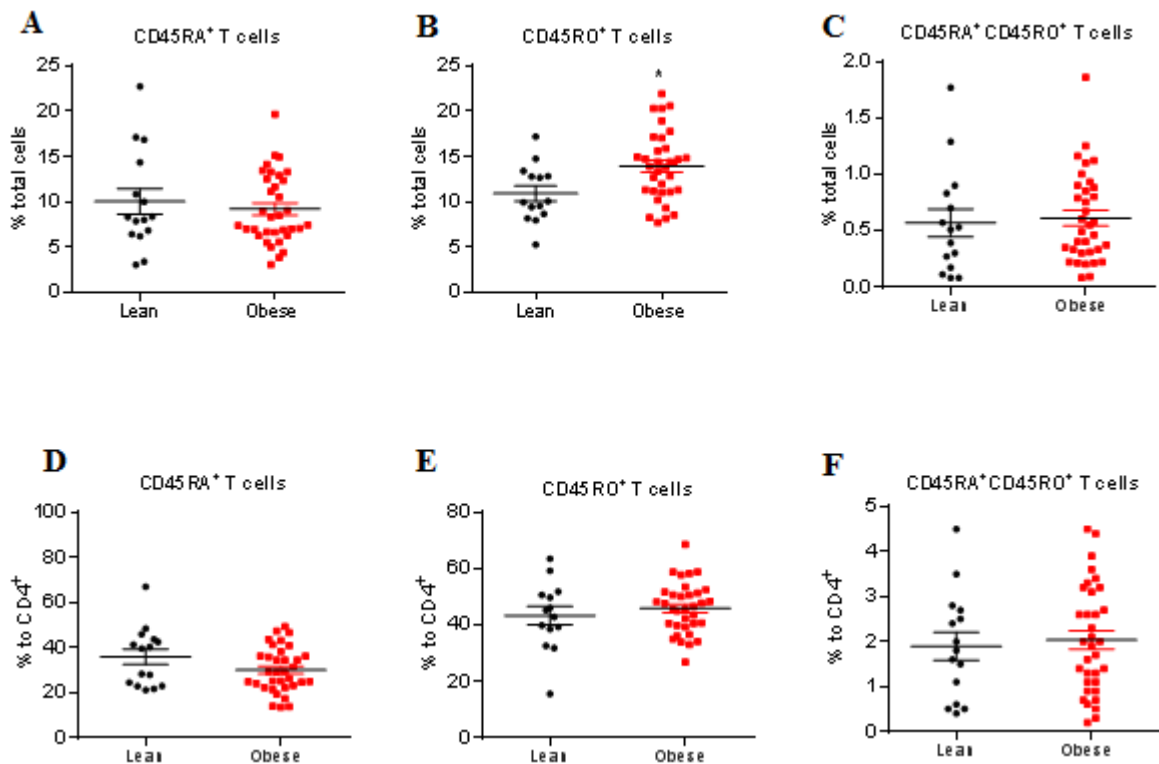


Figure 24. Total and % percentage to CD4⁺ T lymphocytes of CD4⁺CD45RA⁺ (n=15 lean/ 34 obese) (A, D), CD4⁺CD45RO⁺ (n=14 lean/ 34 obese) (B, E) and CD4⁺CD45RA⁺CD45RO⁺ (n=15 lean/ 34 obese) (C, F) T cells, respectively, in obese

and lean individuals. Comparisons between groups were performed using a Mann-Whitney t- test. *: $p=0.0124$

The expression of the marker CCR7 was used for the classification of cells belonging to CD45RA and CD45RO compartment.

Relative to non- obese individuals, obese subjects experienced noteworthy increases in total levels of $CD4^+CD45RA^+CCR7^+$ (Naïve) (mean \pm SEM= $2.22\pm0.27\%$ vs. $1.62\pm0.26\%$) (Figure 25A) and $CD4^+CD45RA^+CCR7^-$ (TEMRA) (mean \pm SEM= $12.01\pm0.90\%$ vs. $10.63\pm1.6\%$) (Figure 25B) T cells. Regarding their distribution in $CD4^+$ T cell compartment, naïve T cells were increased in obese group (mean \pm SEM= $7.44\pm0.87\%$ vs. $6.83\pm1.24\%$) (Figure 25C) whereas TEMRA T cells were about the same at both groups (mean \pm SEM= $45.96\pm2.00\%$ vs. $46.10\pm4.05\%$) (Figure 25D).

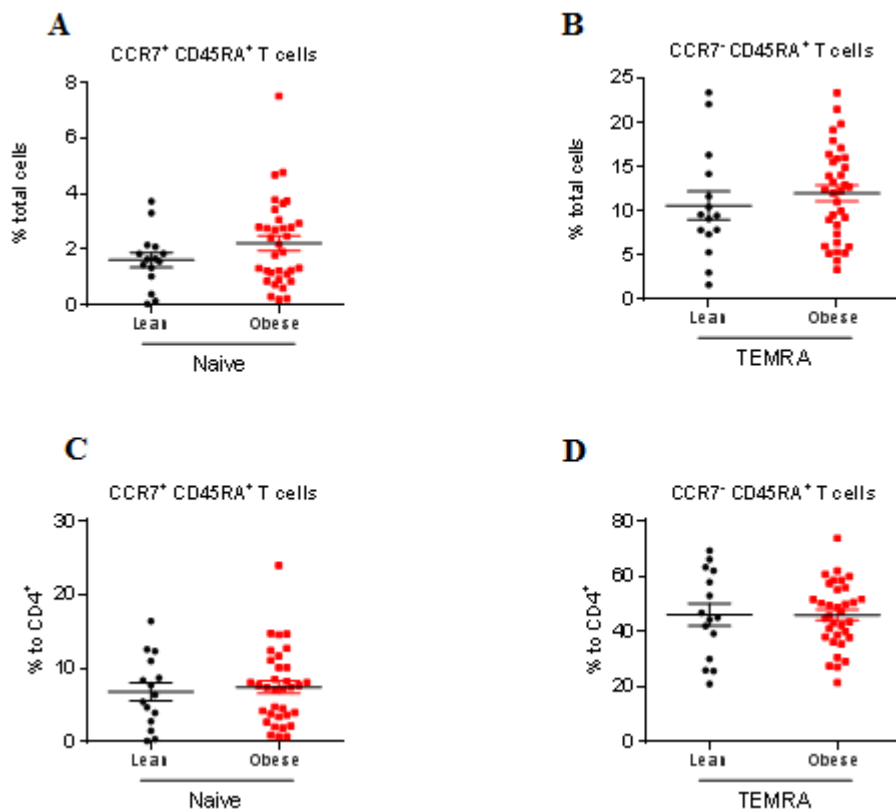


Figure 25. Total and % percentage to $CD4^+$ T lymphocytes of $CD4^+CD45RA^+CCR7^+$ (Naïve) (A, C) and $CD4^+CD45RA^+CCR7^-$ (TEMRA) (B, D) T cells, respectively, in obese ($n=34$) and lean ($n=15$) participants. Comparisons between groups were performed using a Mann-Whitney t- test. In all cases $p>0.05$.

As for memory cells, total $CD4^+CD45RO^+CCR7^+$ (CM) (mean \pm SEM= 0.60 \pm 0.08% vs. 0.33 \pm 0.05%) (Figure 26A) and $CD4^+CD45RO^+CCR7^-$ (EM) (mean \pm SEM= 16.94 \pm 1.18% vs. 13.76 \pm 1.06%) (Figure 26B) were elevated in obese participants compared to the control group. This increase in both groups was reserved even when the classification in $CD4^+$ T cell compartment was evaluated (CM: 2.08 \pm 0.32% vs. 1.30 \pm 0.22%, EM: 43.51 \pm 1.52% vs. 41.56 \pm 3.02%) (Figure 26C, D).

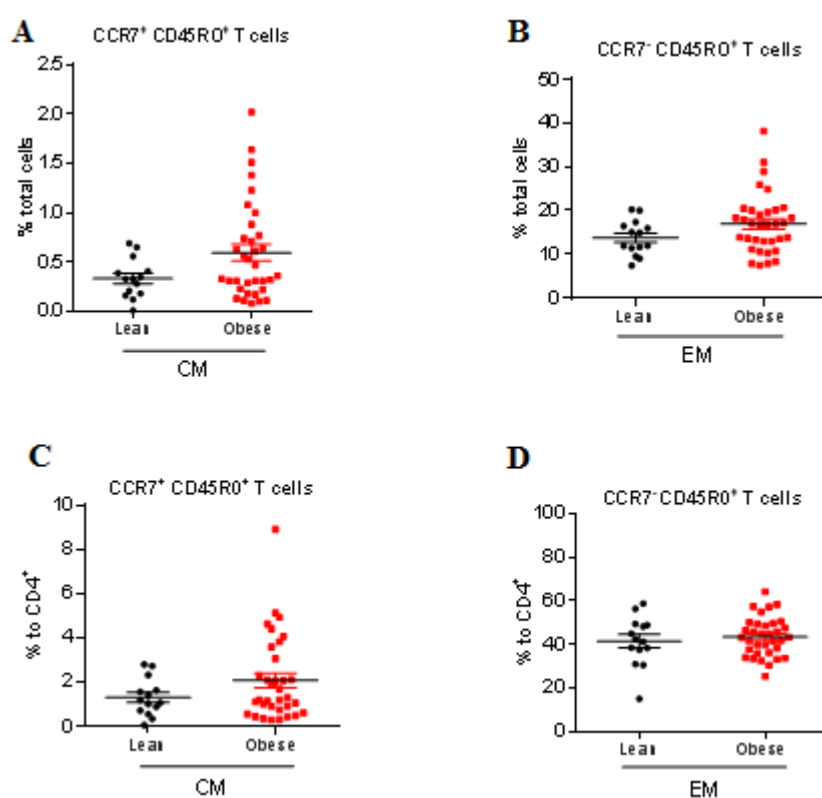


Figure 26. Total and % percentage to $CD4^+$ T lymphocytes of $CD4^+CD45RO^+CCR7^+$ (CM) (A, C) and $CD4^+CD45RO^+CCR7^-$ (EM) (B, D) T cells, respectively, in obese (n=34) and control (n=14) group. Comparisons between groups were performed using a Mann-Whitney t-test. In all cases $p > 0.05$.

The expression of the CXCR3 marker by $CD4^+CD45RA^+$ and $CD4^+CD45RO^+$ T cells was also evaluated. Total $CD4^+CD45RA^+CXCR3^+$ T cells were decreased (mean \pm SEM= 0.33 \pm 0.04% vs. 0.37 \pm 0.07%) (Figure 27A) whereas $CD4^+CD45RO^+CXCR3^+$ were increased (mean \pm SEM= 5.32 \pm 0.45% vs. 5.03 \pm 0.53%) (Figure 27B) in obese

compared to lean participants. Furthermore, regarding their distribution in CD4⁺ T cell compartment, both CD45RA⁺CXCR3⁺ (mean± SEM= 1.08±0.13% vs. 1.25±0.18%) (Figure 27C) and CD45RO⁺CXCR3⁺ (mean± SEM= 17.28±1.27% vs. 19.52±1.72%) (Figure 27D) were decreased in the obese group.

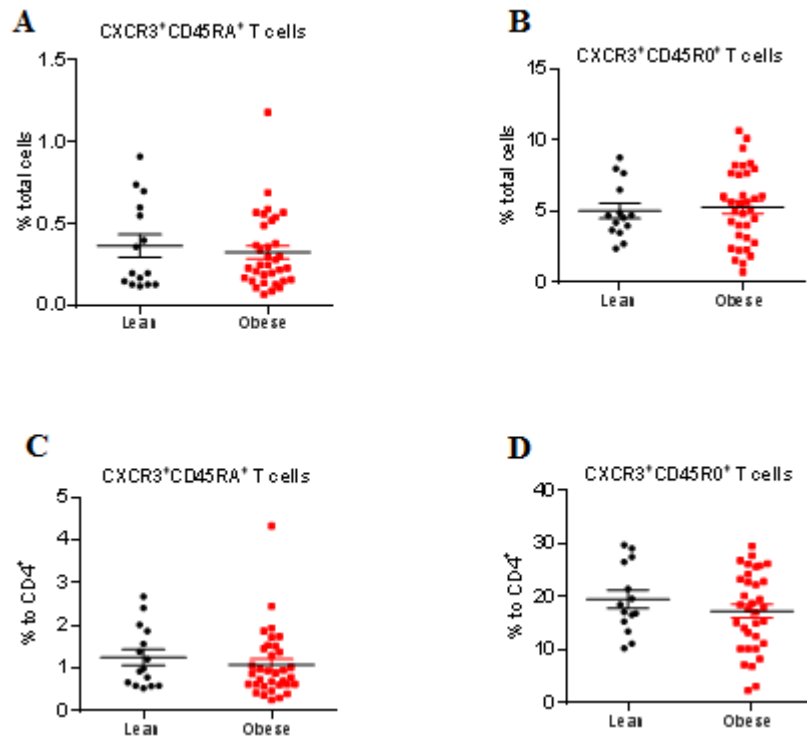


Figure 27. Total and % percentage to CD4⁺ T lymphocytes of CD4⁺CD45RA⁺CXCR3⁺ (n=15 lean/ 34 obese) (A, C) and CD4⁺CD45RO⁺CXCR3⁺ (n=14 lean/ 34 obese) (B, D) T cells, respectively, in obese and control participants. Comparisons between groups were performed using a Mann-Whitney t-test. In all cases $p > 0.05$.

The last subtype of CD4⁺ T lymphocytes examined was the anti-inflammatory Treg cells. Their total levels were elevated in obese compared to lean participants (mean± SEM= 2.16±0.14% vs. 2.00±0.14%) (Figure 28A). However, their levels were decreased in the obese group regarding their distribution in CD4⁺ T cell compartment (mean± SEM= 6.56±0.25% vs. 7.06±0.32%) (Figure 28B).

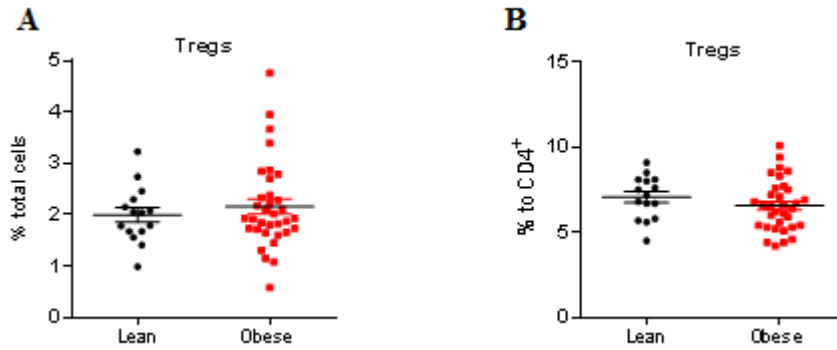


Figure 28. Total (A) and % percentage to CD4⁺ T lymphocytes (B) of Treg cells in obese (n=34) and control (n=15) group. Comparisons between groups were performed using a Mann-Whitney t-test. In all cases p>0.05.

5.4 Effect of weight reduction on immune phenotype induced by genotype-based and conventional diet

The effect of genotype-based diet on the expression of inflammatory and anti-inflammatory markers by immune cells compared to conventional intervention was evaluated (Table 4).

Marked weight reduction (8.23±4.29%) was observed throughout the 3-month period of intervention. More specifically, 8.76±3.82% and 7.30±5.5% weight loss was reported in participants who followed conventional and personalized intervention, respectively, but the difference between the two groups did not reach the levels of statistical significance.

Table 4. Leukocyte and lymphocyte subset counts or percentages before and after conventional and genotype-based intervention. Values are presented as mean± standard error of the mean (SEM). (ns: not significant, *: p≤0.05, **: p≤0.01)

Type of cell	Conventional diet	Genotype-based diet	Significance (convent)

	Baseline		3 months		Significance	Baseline		3 months		Significance	Genotype vs. diet
	Mean	SEM	Mean	SEM		Mean	SEM	Mean	SEM		
PBMCs (total cells)	2E+07	3E+06	2E+07	2E+06	ns	4E+07	4E+06	3E+07	5E+06	ns	** at baseline
Classical monocytes (CD14⁺CD16⁻) (% total PBMCs)	9.333	1.423	10.74	2.167	ns	8.358	1.42	5.81	1.381	ns	ns
Intermediate monocytes (CD14⁺CD16⁺)	1.373	0.434	2.137	1.165	ns	1.445	0.364	1.298	0.49	ns	ns
Non-classical monocytes (CD14⁻CD16⁺)	5.137	1.89	2.42	0.444	ns	3.768	1.17	5.7	2.374	ns	ns
CD14^{low}CD16⁺ monocytes (% total PBMCs)	0.777	0.123	0.45	0.127	ns	0.718	0.245	0.67	0.204	ns	ns
B lymphocytes (% total PBMCs)	9.01	1.062	6.13	1.135	ns	9.49	3.196	7.817	2.268	ns	ns
T (CD3⁺) lymphocytes (% total PBMCs)	44.41	5.058	46.77	3.824	ns	62.34	16.88	47.15	6.201	ns	ns
CD3⁺CD4⁺ (% total PBMCs)	29.95	3.632	33.28	3.851	ns	40.77	9.542	32.72	5.707	ns	ns
CD3⁺CD4⁺ (% CD3⁺ cells)	64.77	5.635	68.47	5.446	ns	67.63	2.266	62.4	7.17	ns	ns
CD3⁺CD8⁺ (% total PBMCs)	9.729	1.672	9.633	1.138	ns	11.72	2.611	9.03	1.101	ns	ns
CD3⁺CD8⁺ (% CD3⁺ cells)	20.37	2.832	21.28	3.49	ns	20.37	1.761	21.53	4.191	ns	ns
CD3⁺CD4⁺CD45RA⁺CD45RO⁻ (% total PBMCs)	8.55	1.232	12.58	1.308	ns	8.313	1.658	10.43	1.919	ns	ns

CD3 ⁺ CD4 ⁺ CD45RA ⁺ CD45RO ⁻ (% CD4 ⁺)	30.2 1	4.39 5	38.9 6	3.38	ns	27	5.06 2	32.2 3	3.06 5	ns	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁻ CD45RO ⁺ (% total PBMCs)	13.0 3	1.72 6	14.3 4	2.15 5	ns	15.3 8	2.03 8	15.2 6	2.61 5	ns	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁻ CD45RO ⁺ (% total CD4 ⁺)	45.6 7	4.76 3	42.0 1	2.93 7	ns	49.8 5	5.35 8	48.2	6.25 9	ns	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CD45RO ⁺ (% total PBMCs)	0.53 1	0.13 1	0.54 7	0.21 5	ns	0.61 3	0.20 5	0.37 5	0.10 6	ns	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CD45RO ⁺ (% total CD4 ⁺)	2.04 3	0.54	1.5	0.43 7	ns	2.1	0.75 6	1.17 5	0.22 9	ns	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CCR7 ⁺ (Naïve) (% total PBMCs)	2.36 7	0.68 2	2.34 9	0.58 9	ns	3.76	1.27 9	0.68	0.11	*	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CCR7 ⁺ (Naïve) (% CD4 ⁺)	7.76 3	2.04 7	6.37 4	1.36 2	ns	12.0 5	3.98 2	2.29 5	0.49	*	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CCR7 ⁻ (TEMRA) (% total PBMCs)	9.34 1	1.11 1	13.8 8	1.90 9	ns	9.11	1.44	16.3 3	4.23 9	ns	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CCR7 ⁻ (TEMRA) (% CD4 ⁺)	44.5 3	3.95 2	56.6 1	2.76 2	ns	37.5 3	3.63 5	63.2 2	7.72 7	**	ns
CD3 ⁺ CD4 ⁺ CD45RO ⁺ CCR7 ⁺ (CM) (% total PBMCs)	0.77 6	0.25 5	0.56 6	0.14 9	ns	0.37 5	0.16 6	0.19 8	0.02 7	ns	ns
CD3 ⁺ CD4 ⁺ CD45RO ⁺ CCR7 ⁺ (CM) (% CD4 ⁺)	2.53 7	0.69 6	1.57 9	0.34 7	ns	1.14 8	0.49 3	0.62 5	0.07 5	ns	ns
CD3 ⁺ CD4 ⁺ CD45RO ⁺ CCR7 ⁻ (EM) (% total PBMCs)	18.5 2	4.34 4	19.5 1	3.72 4	ns	19.1 7	3.05 1	20.3 9	4.50 3	ns	ns
CD3 ⁺ CD4 ⁺ CD45RO ⁺ CCR7 ⁻ (EM) (% CD4 ⁺)	42.8 9	4.31	40.0 9	2.93 9	ns	47.8 5	6.54 2	47.4	6.13 5	ns	ns
CD3 ⁺ CD4 ⁺ CD45RA ⁺ CXCR3 ⁺ (% total PBMCs)	0.35 3	0.06	0.45 7	0.11 5	ns	0.25	0.09 9	0.51 8	0.17 1	ns	ns

CD3 ⁺ CD4 ⁺ CD45RA ⁺ CXCR3 ⁺ (% CD4 ⁺)	1.27 9	0.25	1.27 9	0.19 8	ns	0.82 3	0.31 1	1.70 3	0.52 8	ns	ns
CD3 ⁺ CD4 ⁺ CD45RO ⁺ CXCR3 ⁺ (% total PBMCs)	5.69 9	0.99 3	5.40 1	1.14 8	ns	3.95 5	0.94 5	5.54 5	0.74 6	ns	ns
CD3 ⁺ CD4 ⁺ CD45RO ⁺ CXCR3 ⁺ (% CD4 ⁺)	19.6 5	2.53 6	15.5 8	2.40 6	ns	12.5 5	2.48 3	18.5	3.58 4	ns	ns
CD3 ⁺ CD4 ⁺ CD127 ⁻ CD25 ⁺ (T regs) (% total PBMCs)	1.86 4	0.24 4	2.19	0.36	ns	2.60 5	0.73 6	2.71 3	0.42 7	ns	ns
CD3 ⁺ CD4 ⁺ CD127 ⁻ CD25 ⁺ (T regs) (% CD4 ⁺)	6.18 6	0.50 7	6.65 7	0.73	ns	6.22 5	0.39 7	8.37 5	0.24 6	ns	ns

Peripheral Blood Mononuclear Cells (PBMCs)

Participants who followed a 3- month genotype- based diet had their circulating levels of PBMCs decreased (baseline: $3.83 \times 10^7 \pm 3.61 \times 10^6$ cells, 3 months: $2.77 \times 10^7 \pm 4.58 \times 10^6$ cells) whereas those who followed conventional diet had a mild increase in PBMCs total count (baseline: $1.96 \times 10^7 \pm 3.32 \times 10^6$ cells, 3 months: $2.12 \times 10^7 \pm 2.05 \times 10^6$ cells) (Figure 29). However, the difference between the two groups reached the levels of statistical significance only at the beginning of the intervention ($p \leq 0.05$).

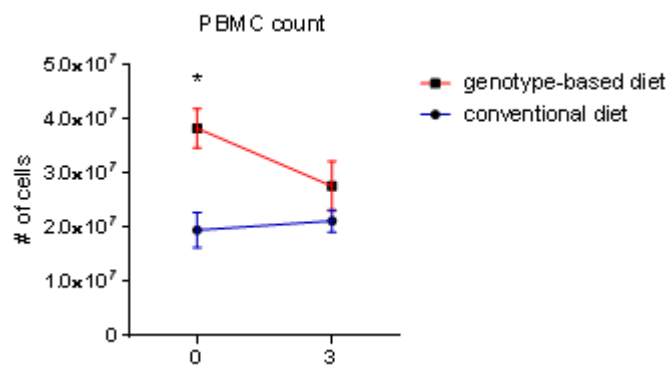


Figure 29. Differences in PBMC total count in genotype- based (n=4) and conventional (n=7) group. X axis: months after the beginning of the intervention.

Comparisons between groups were performed using two- way analysis of variance (ANOVA). *: $p \leq 0.05$

5.4.1 Monocytes

Personalized intervention resulted in a reduction in total levels of classical (baseline: $8.36 \pm 1.42\%$, 3 months: $5.81 \pm 1.38\%$) (Figure 30A) and intermediate (baseline: $1.44 \pm 0.36\%$, 3 months: $1.30 \pm 0.49\%$) (Figure 30B) monocytes. Conversely, individuals who followed conventional diet had their classical (baseline: $9.33 \pm 1.42\%$, 3 months: $10.74 \pm 2.17\%$) (Figure 30A) and intermediate (baseline: $1.37 \pm 0.43\%$, 3 months: $2.14 \pm 1.16\%$) (Figure 30B) monocytes increased throughout the 3- month period.

Furthermore, total percentage of non- classical monocytes was found increased in individuals who followed genotype- based diet (baseline: $3.77 \pm 1.17\%$, 3 months: $5.7 \pm 2.37\%$) and decreased in the conventional group (baseline: $5.14 \pm 1.89\%$, 3 months: $2.42 \pm 0.44\%$) (Figure 30C). At the end of the intervention, the personalized group had more non- classical monocytes than the non- personalized group.

A slight reduction in $CD14^{\text{low}}CD16^+$ monocytes was observed in participants who followed genotype- based intervention (baseline: $0.72 \pm 0.24\%$, 3 months: $0.67 \pm 0.20\%$). Similarly, the non- personalized group had their total levels of the same monocyte subset decreased (baseline: $0.78 \pm 0.12\%$, 3 months: $0.45 \pm 0.13\%$) and their levels were lower at 3 months than the genotype- based group (Figure 30D).

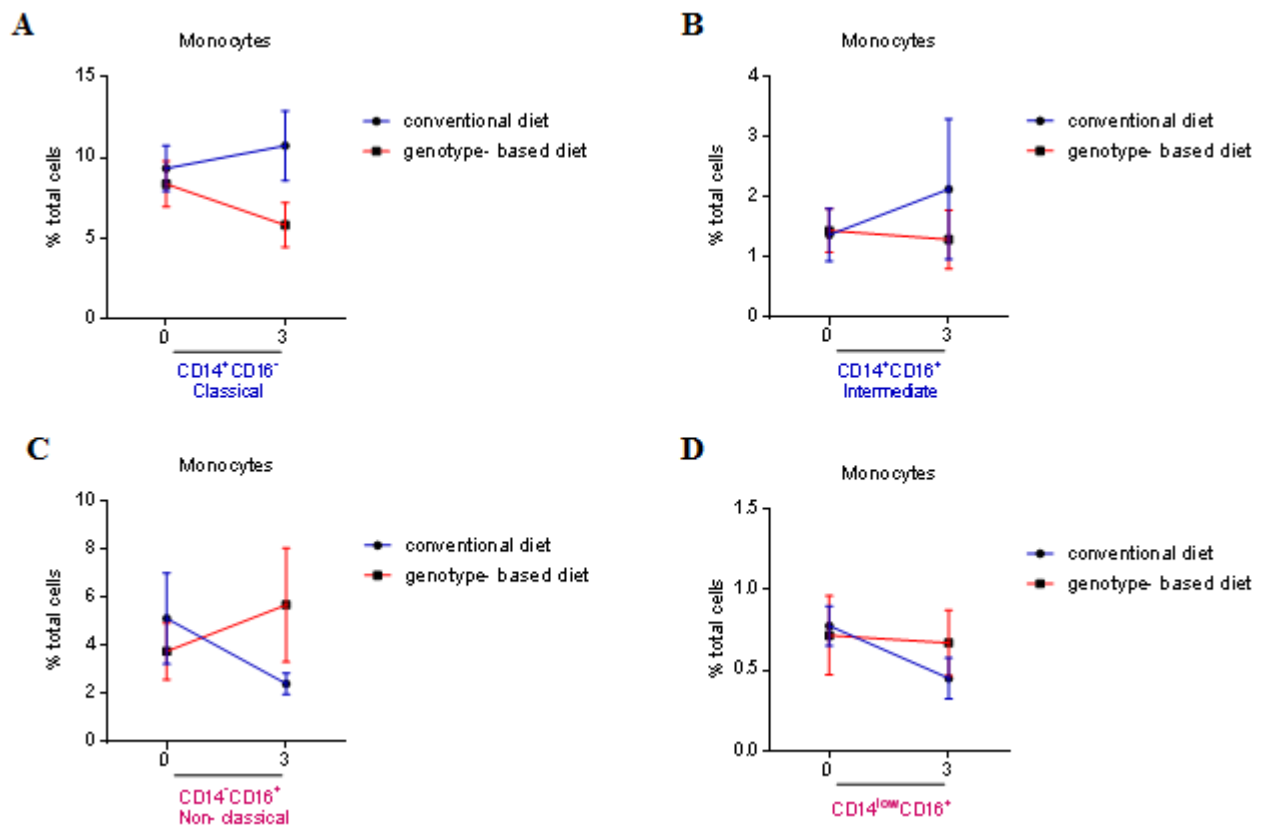


Figure 30. Total percentages of monocytes' subtypes [CD14⁺CD16⁻ (classical) (A), CD14⁺CD16⁺ (intermediate) (B), CD14⁻CD16⁺ (non- classical) (C), CD14^{low}CD16⁺ (D)] in personalized (n=4) and conventional (n=3) group. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two- way analysis of variance (ANOVA). In all cases p>0.05.

5.4.2 Lymphocytes

5.4.2.1 B lymphocytes

At the beginning of the intervention, both groups had similar total levels of B lymphocytes (genotype- based: 9.49±3.20%, conventional: 9.01±1.06%) (Figure 31A). After the 3- month diet, both groups had their B cells decreased, but a milder decrease in their levels was observed in individuals belonging to the genotype- based group (7.82±2.27%) compared to the conventional group (6.13±1.13%).

5.4.2.2 CD3⁺ T cells

Individuals who were assigned to the genotype- based intervention group had their total CD3⁺ T cell levels decreased throughout the 3- month period (baseline: 62.34±16.88%, 3 months: 47.15±6.20%). Conversely, a slight increase in those cells in the non- personalized group was reported (baseline: 44.41±5.06%, 3 months: 46.77±3.82%). Similar T lymphocyte levels between the two intervention groups were observed at 3 months (personalized: 47.15±6.20%, conventional: 46.77±3.82%) (Figure 31B).

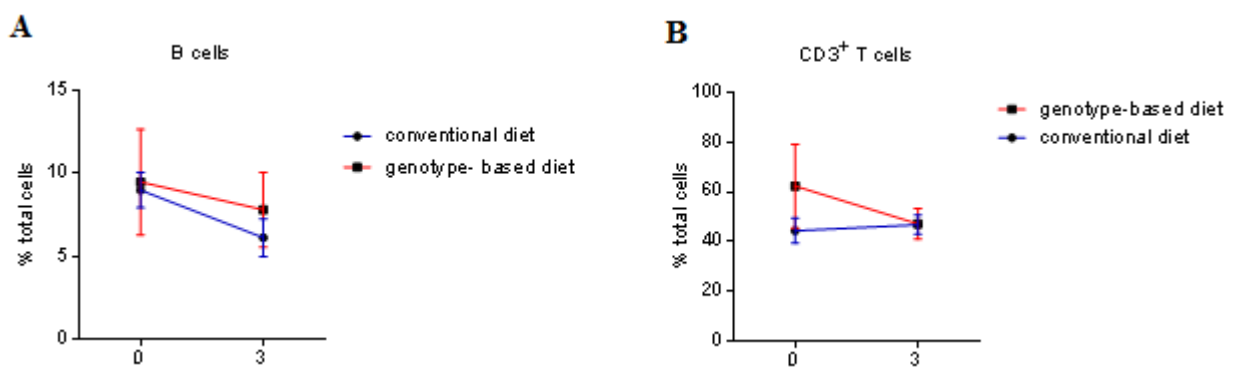


Figure 31. Differences in B lymphocytes' (n=3 conventional/ 3 personalized) (A) and CD3⁺ T cell total percentage (n=6 conventional/ 3 personalized) (B) in genotype-based and conventional group. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two- way analysis of variance (ANOVA). In all cases p>0.05.

CD4⁺ and CD8⁺ T cells

After dieting, participants belonging in the personalized group had marked decreases in total percentages of CD4⁺ (baseline: 40.76±9.54%, 3 months: 32.72±5.71%) (Figure 32A) and CD8⁺ T lymphocytes (baseline: 11.72±2.61%, 3 months: 9.03±1.10%) (Figure 32B). An increase in CD4⁺ T cell levels was reported in the conventional group (baseline: 29.95±3.63%, 3 months: 33.28±3.85%) but at the end of the intervention cell percentages were similar in personalized (32.72±5.71%) and non- personalized group (33.28±3.85%) (Figure 32A). Moreover, no difference in CD8⁺ T cells was observed in the conventional group throughout the 3- month intervention (baseline: 9.73±1.67%, 3 months: 9.63±1.14%) (Figure 32B).

Relative to CD3⁺ T cell compartment, CD4⁺ T cell levels differed at baseline and the genotype- based group had increased levels of those cells (genotype-based: 67.63±2.26%, conventional: 64.77±5.63%). After the 3- month intervention, CD4⁺ T cell percentage increased in the conventional group (68.47±5.44%), decreased in the genotype- based group (62.4±7.17%), and cell levels of the latter were lower compared to those of the conventional group (Figure 32C). As for CD8⁺ T cell levels relative to CD3⁺ T cells, an increase was reported in participants belonging to both groups (genotype- based: 20.37±1.76% at baseline, 21.53±4.19% at 3 months, conventional: 20.37±2.83% at baseline, 21.28±3.49% at 3 months). It is noteworthy that the percentage of CD8⁺ cells to CD3⁺ lymphocytes was similar at the beginning and at the end of the intervention in both groups (Figure 32D).

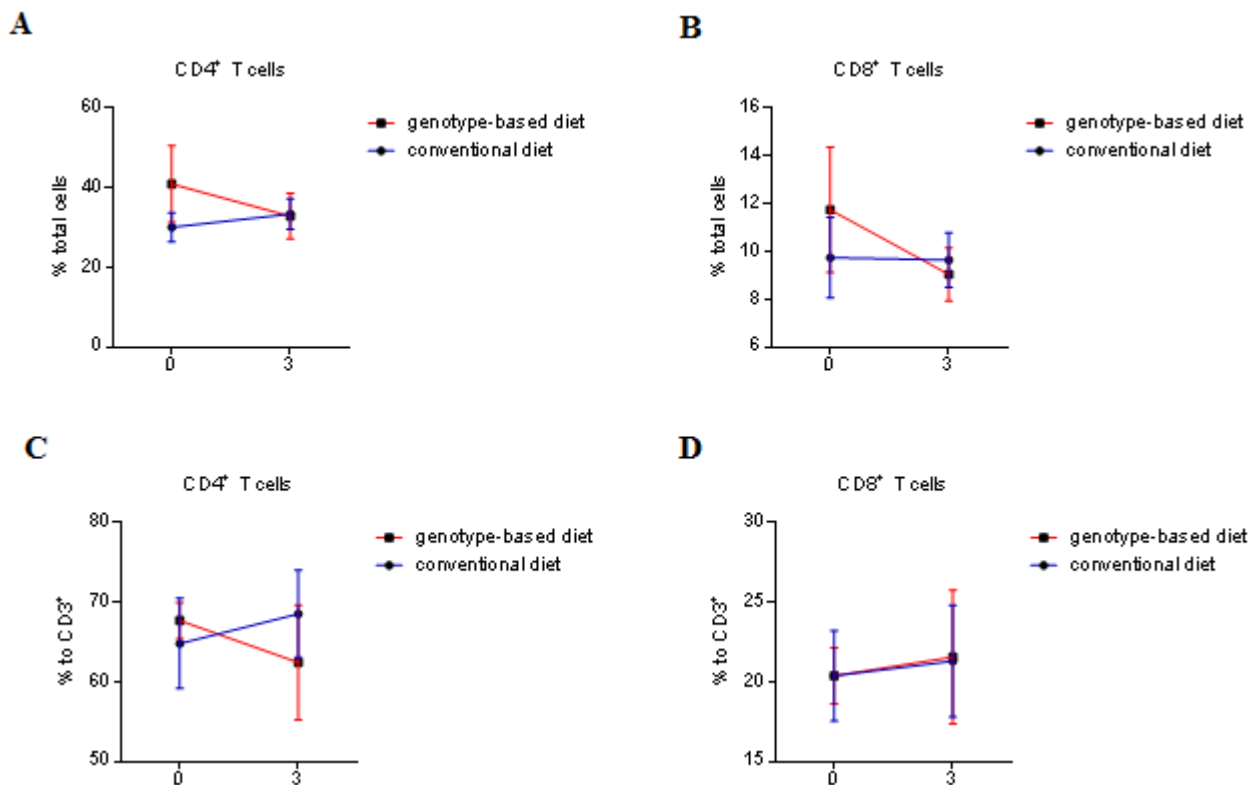


Figure 32. Total (n=7 conventional/ 4 personalized) and % percentage to T lymphocytes (CD3⁺) (n=6 conventional/ 3 personalized) of CD4⁺ (A, C) and CD8⁺ (B, D) T cells, respectively, in genotype- based and conventional group. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two- way analysis of variance (ANOVA). In all cases p>0.05.

CD4⁺ T cells compartment

Taking CD4⁺ T cell classification into account based on the expression of the CD45RA/CD45RO markers, a marked increase in total CD4⁺CD45RA⁺ (Naïve/TEMRA) T cells was reported in both groups (genotype- based: 8.31±1.66% at baseline, 10.42±1.92% at 3 months, conventional: 8.55±1.23% at baseline, 12.58±1.31% at 3 months) (Figure 33A). The increase in the non- personalized group was more prominent but the values between the two groups remained not significantly different.

Similarly, participants who followed conventional intervention had their CD4⁺CD45RO⁺ (Memory) T cells increased throughout the 3- month period (baseline: 13.03±1.73%, 3 months: 14.34±2.15%). A slight reduction in those cells was observed in the genotype- based group, though (baseline: 15.38±2.04%, 3 months: 15.26±2.61%), but their total levels remained elevated compared to those of the non- personalized group (Figure 33B).

Furthermore, subjects who followed personalized diet experienced a marked reduction in CD4⁺CD45RA⁺CD45RO⁺ T cell levels (baseline: 0.61±0.20%, 3 months: 0.37±0.11%), whereas those cells were about the same in the conventional group before (0.53±0.13%) and after (0.55±0.21%) the intervention (Figure 33C). At the end of the 3- month period, participants following the conventional diet had more CD45RA⁺CD45RO⁺ T cells than those who followed genotype- based intervention.

Regarding CD4⁺ T cell compartment, the relative percentage of CD4⁺CD45RA⁺ T cells to CD4⁺ cells was increased in both groups following the 3- month diet period (genotype- based: 27.00±5.06% at baseline, 32.22±3.06% at 3 months, conventional: 30.21±4.39% at baseline, 38.96±3.38% at 3 months) (Figure 33D). As in the case of naïve/ TEMRA T cells total percentage, their final levels regarding CD4⁺ T cells were elevated in the conventional group.

During the intervention period, relative percentage of memory T cells to CD4⁺ T cells markedly decreased in participants belonging to both groups (genotype- based: 49.85±5.36% at baseline, 48.2±6.26% at 3 months, conventional: 45.67±4.76% at baseline, 42.01±2.94% at 3 months) (Figure 33E) with a greater reduction in the conventional group.

As opposed to absolute percentages $CD4^+CD45RA^+CD45RO^+$ T cells, their relative percentages to $CD4^+$ T cells were decreased in both dieting groups. It is noteworthy that similar baseline levels were reported (genotype-based: $2.1\pm 0.76\%$, conventional: $2.04\pm 0.54\%$) but participants who followed genotype-based diet had lower levels of those cells at the end of the intervention (genotype-based: $1.17\pm 0.23\%$, conventional: $1.5\pm 0.44\%$) (Figure 33F).

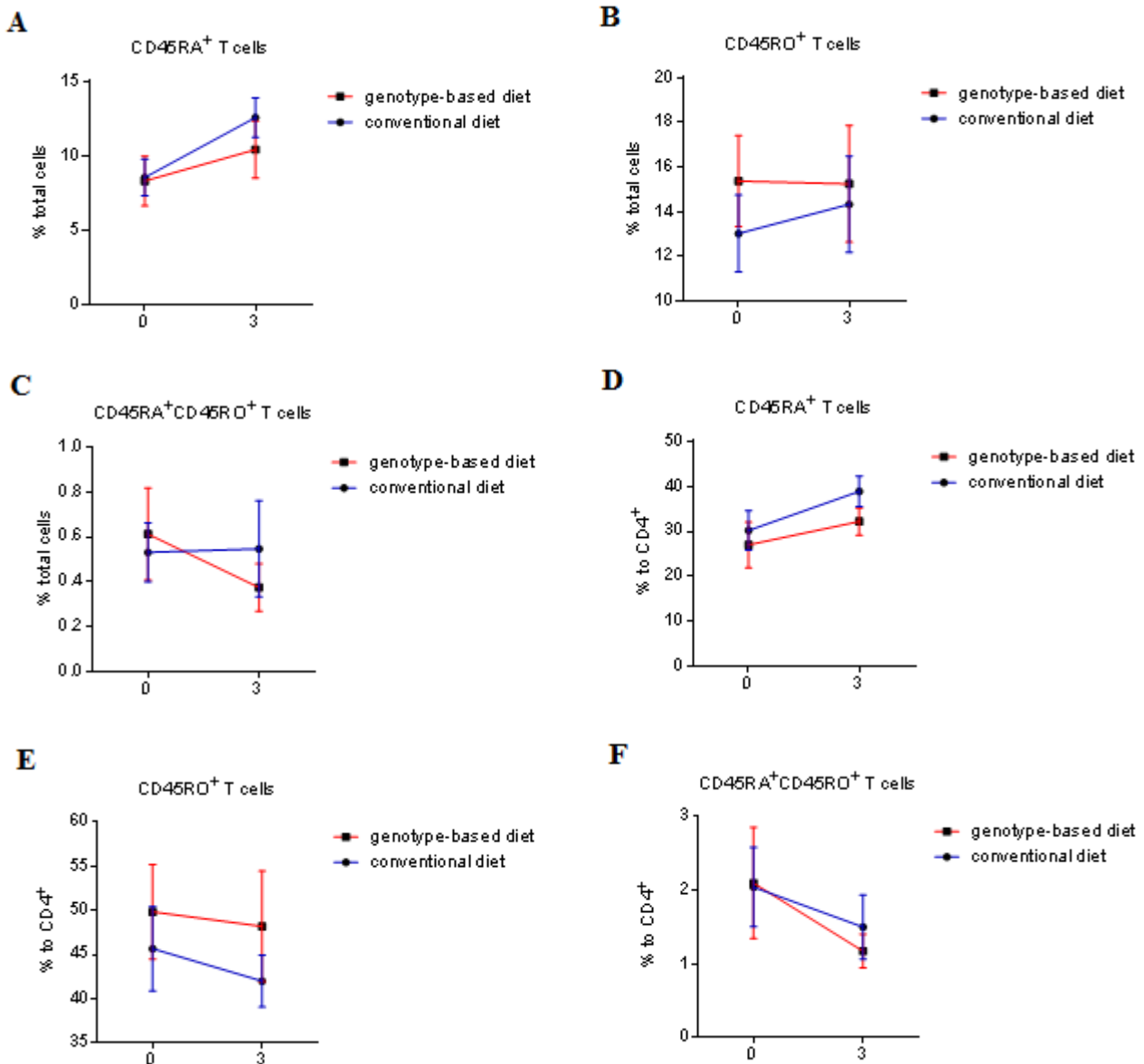


Figure 33. Total and % percentage to $CD4^+$ T lymphocytes of $CD4^+CD45RA^+$ (A, D) $CD4^+CD45RO^+$ (B, E) and $CD4^+CD45RA^+CD45RO^+$ (C, F) T cells, respectively, in participants following genotype-based ($n=4$) and conventional ($n=7$) intervention. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two-way analysis of variance (ANOVA). In all cases $p>0.05$.

Baseline total levels of CD4⁺CD45RA⁺CCR7⁺ (Naïve) T cells were similar to those at the end of the intervention in subjects who followed conventional diet (baseline: 2.37±0.68%, 3 months: 2.35±0.59%). However, total levels of naïve T cells were significantly lower ($p \leq 0.05$) at the end of the 3- month period in participants following personalized diet (baseline: 3.76±1.28%, 3 months: 0.68±0.11%) (Figure 34A).

Regarding total CD4⁺CD45RA⁺CCR7⁻ (TEMRA) T cells, both groups had similar levels at the beginning of the intervention (genotype-based: 9.11±1.44%, conventional: 9.34±1.11%). A more profound increase was observed in the genotype-based group at the end of the intervention resulting in higher final TEMRA levels compared to the conventional group (genotype-based: 16.32±4.24%, conventional: 13.88±1.91%) (Figure 34B).

A significant reduction ($p \leq 0.05$) in relative percentage of naïve T cells to CD4⁺ cells was reported in participants who followed personalized intervention throughout the 3-month period (baseline: 12.04±3.98%, 3 months: 2.29±0.49%). Furthermore, a slight reduction in relative percentage of those cells was observed in the non- personalized group (baseline: 7.76±2.05%, 3 months: 6.37±1.36%). At the end of the intervention, naïve T cell percentage to CD4⁺ T cells was elevated in the conventional group compared to genotype- based group (Figure 34C).

Conversely, relative percentage of TEMRA T cells to CD4⁺ cells increased significantly ($p \leq 0.01$) with intervention in subjects following a personalized diet (baseline: 37.53±3.63%, 3 months: 63.21±7.23%) (Figure 34D). The reduction in TEMRA T cell relative levels to CD4⁺ cells observed in the conventional group comparing baseline and 3- month intervention values (baseline: 44.53±3.95%, 3 months: 56.61±2.76%) did not reach the levels of statistical significance. It is interesting to mention that TEMRA baseline levels were lower and TEMRA final levels were higher in the personalized group compared to the non- personalized.

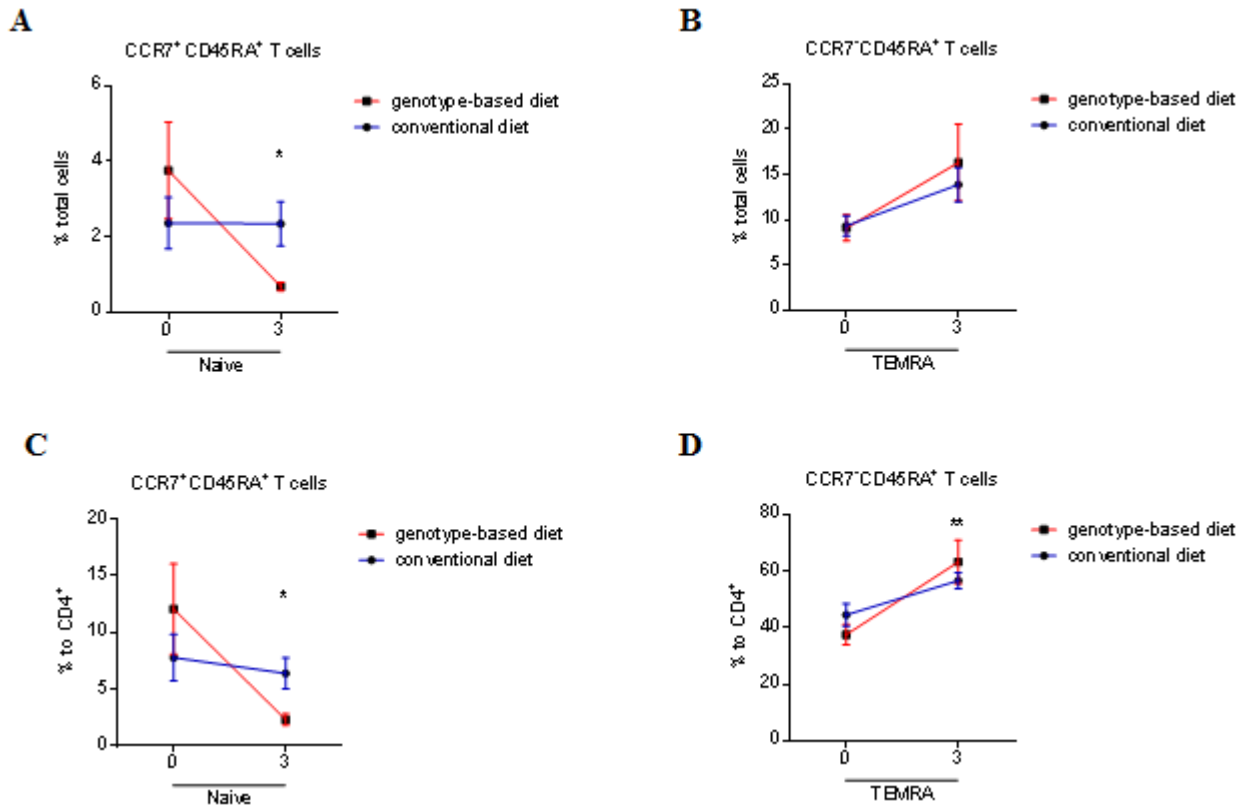


Figure 34. Total and % percentage to CD4⁺ T lymphocytes of CD4⁺CD45RA⁺CCR7⁺ (Naïve) (A, C) and CD4⁺CD45RA⁺CCR7⁻ (TEMRA) (B, D) T cells, respectively, in genotype- based (n=4) and conventional (n=7) group. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two- way analysis of variance (ANOVA). *: p \leq 0.05, **: p \leq 0.01

During the 3- month diet intervention period, total (genotype- based: 0.37 \pm 0.16% at baseline, 0.20 \pm 0.03% at 3 months, conventional: 0.77 \pm 0.25% at baseline, 0.56 \pm 0.15% at 3 months) (Figure 35A) and relative percentage to CD4⁺ cells (genotype- based: 1.15 \pm 0.49% at baseline, 0.62 \pm 0.07% at 3 months, conventional: 2.54 \pm 0.69% at baseline, 1.58 \pm 0.35% at 3 months) (Figure 35B) of CD4⁺CD45RO⁺CCR7⁺ (CM) cells markedly decreased in personalized and conventional group. It is noteworthy that baseline and final levels of CM cells were lower in subjects who followed personalized diet (Figure 35A, B).

Conversely, individuals following both types of diet had their total CD4⁺CD45RO⁺CCR7⁻ (EM) T cell levels increased at the end of the intervention (genotype- based: 19.16 \pm 3.05% at baseline, 20.38 \pm 4.50% at 3 months, conventional:

18.52±4.34% at baseline, 19.50±3.72% at 3 months) (Figure 35C) with a more profound increase observed in the personalized group. Regarding CD4⁺ T cell compartment, similar relative EM T cell percentage to CD4⁺ cells was observed in genotype- based group at the beginning and at the end of the intervention (baseline: 47.85±6.54%, 3 months: 47.40±6.13%). A reduction in those cells was reported in the conventional group at 3 months, though (baseline: 42.89±4.31%, 3 months: 40.09±2.94%) (Figure 35D). Both baseline and final relative levels of EM cell to CD4⁺ cells were lower at non- personalized compare to the personalized group.

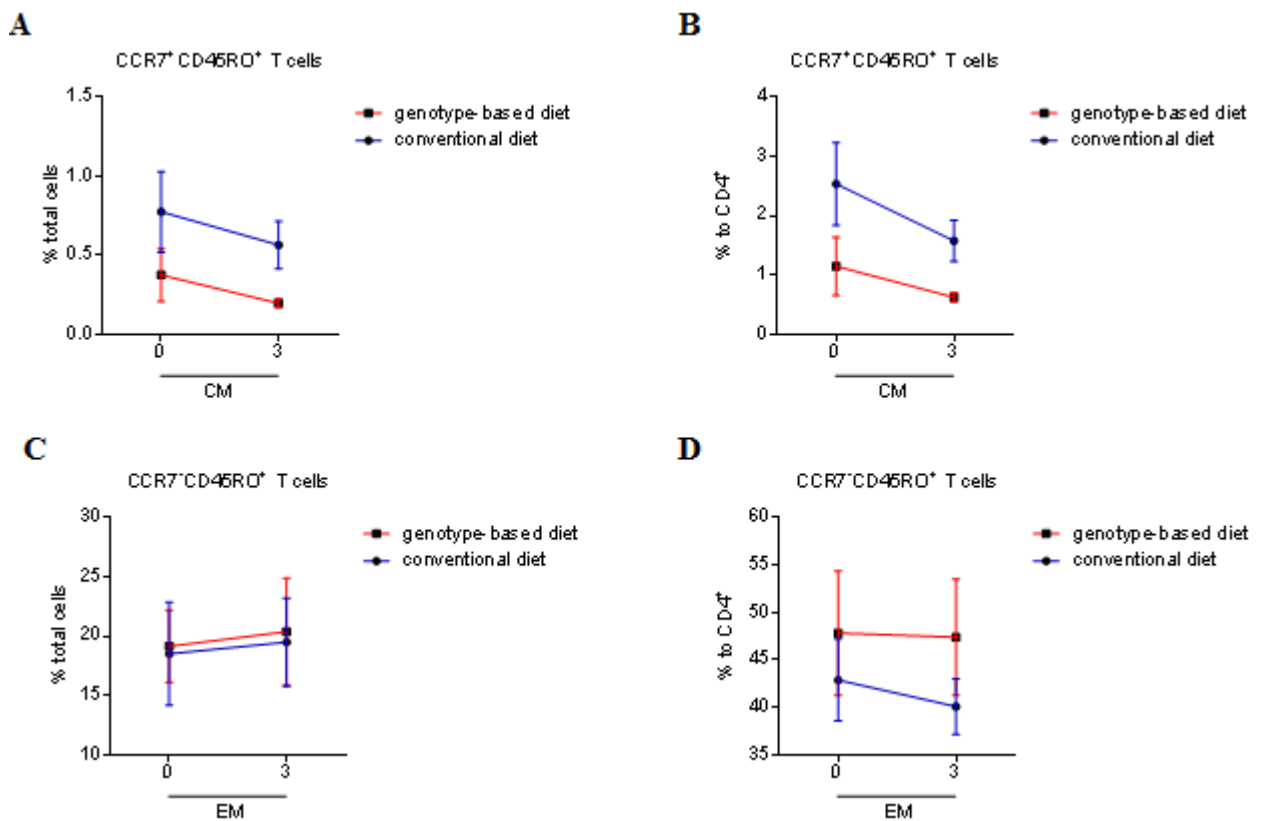


Figure 35. Total and % percentage to CD4⁺ T lymphocytes of CD4⁺CD45RO⁺CCR7⁺ (CM) (A, B) and CD4⁺CD45RO⁺CCR7⁻ (EM) (C, D) T cells, respectively, in subjects following personalized (n=4) and conventional (n=7) diet. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two- way analysis of variance (ANOVA). In all cases p>0.05.

Genotype- based intervention resulted in a marked increase in total levels of CD4⁺CD45RA⁺CXCR3⁺ (baseline: 0.25±0.10%, 3 months: 0.52±0.17%) (Figure 36A) and CD4⁺CD45RO⁺CXCR3⁺ (baseline: 3.96±0.94%, 3 months: 5.54±0.74%)

(Figure 36B) T cells. A less prominent increase in $CD4^+CD45RA^+CXCR3^+$ cells was observed in subjects following conventional diet (baseline: $0.35\pm0.06\%$, 3 months: $0.46\pm0.11\%$) (Figure 36A) and resulted in lower final levels of those cells compared to the personalized group. Lower total levels of $CD4^+CD45RO^+CXCR3^+$ cells were reported in conventional group at the end of the intervention (baseline: $5.70\pm0.99\%$, 3 months: $5.40\pm1.15\%$) (Figure 36B) but both intervention groups had similar total levels of those cells at 3 months. Those facts contributed to an immune phenotype characterized by increased $CD4^+CD45RA^+CXCR3^+$ cells in personalized group compared to the conventional group at the end of the 3- month intervention.

Similarly, relative percentage of $CD4^+CD45RA^+CXCR3^+$ (baseline: $0.82\pm0.31\%$, 3 months: $1.70\pm0.53\%$) (Figure 36C) and $CD4^+CD45RO^+CXCR3^+$ (baseline: $12.55\pm2.48\%$, 3 months: $18.50\pm3.58\%$) (Figure 36D) cells to $CD4^+$ cells increased with genotype- based intervention. Relative levels of $CD4^+CD45RA^+CXCR3^+$ cells were similar to those of baseline in the conventional group (baseline: $1.28\pm0.25\%$, 3 months: $1.28\pm0.20\%$) (Figure 36C). Participants belonging to the conventional group had their relative percentage of $CD4^+CD45RO^+CXCR3^+$ cells to $CD4^+$ cells decreased throughout the 3- month period (baseline: $19.65\pm2.54\%$, 3 months: $15.57\pm2.41\%$) (Figure 36D). At the end of the intervention, both cell levels were increased in the personalized group.

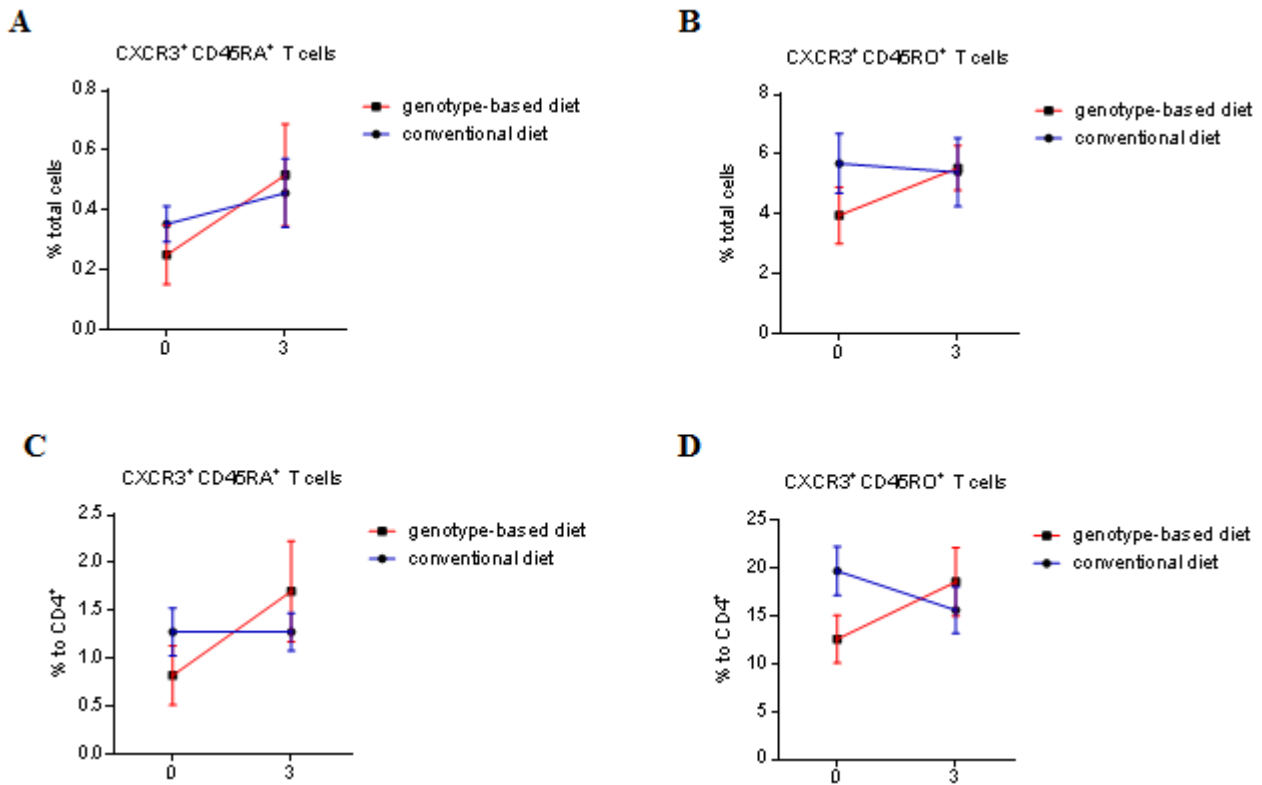


Figure 36. Total and % percentage to CD4⁺ T lymphocytes of CD4⁺CD45RA⁺CXCR3⁺ (A, C) and CD4⁺CD45RO⁺CXCR3⁺ (B, D) T cells, respectively, in personalized (n=4) and conventional (n=7) group. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two- way analysis of variance (ANOVA). In all cases p>0.05.

Finally, total levels of Treg cells increased in participants who followed both the 3-month genotype- based (baseline: 2.60±0.74%, 3 months: 2.71±0.43%) and conventional diet (baseline: 1.86±0.24%, 3 months: 2.19±0.36%) (Figure 37A). Although this increase was less profound in the personalized group, higher total levels of Treg cells were observed in individuals following personalized diet.

Regarding CD4⁺ T cell compartment, both groups had similar relative Tregs percentage to CD4⁺ cells at the beginning of the intervention (genotype- based: 6.22±0.40, conventional: 6.19±0.51%). Personalized diet resulted in a more profound increase in Tregs relative percentage (8.37±0.25%) compared to conventional diet (6.66±0.73%) (Figure 37B).

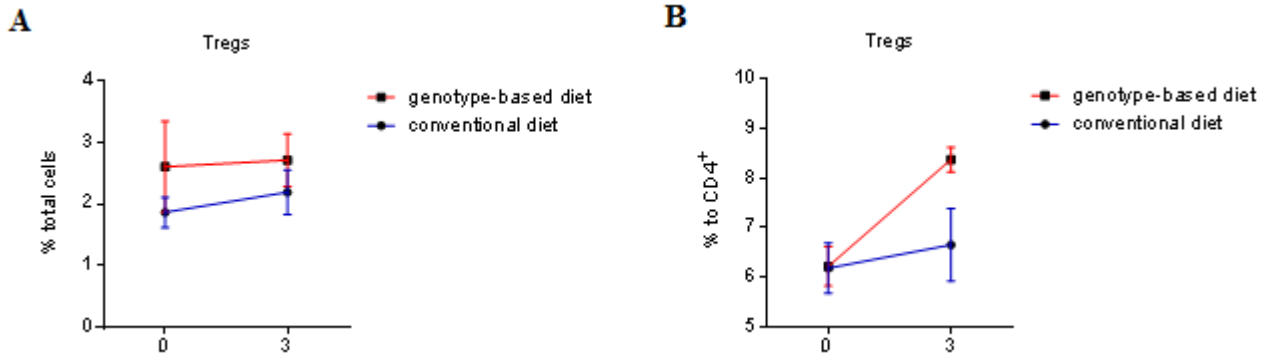


Figure 37. Total (A) and % percentage to CD4⁺ T lymphocytes (B) of Treg cells in participants following personalized (n=4) and conventional (n=7) intervention. X axis: months after the beginning of the intervention. Comparisons between groups were performed using two- way analysis of variance (ANOVA). In all cases p>0.05.

6. DISCUSSION

Obesity is associated with low level chronic inflammation and deregulated immunity. This link is highlighted by the elevated levels of various proinflammatory factors including TNF- α , IL- 6 and CRP, in the serum of obese individuals, the dysregulation of leptin that mediates the cross- talk between immune function and physiologic mechanisms that control body weight and by the increased incidence of several types of cancer among obese individuals [157].

The involvement of lymphocyte dysregulation in the pathogenesis of diabetes, atherosclerosis and steatohepatitis, i. e. co- morbidities related to obesity, along with the impaired cellular immune function observed in obesity- related cancer, reveal the effect of variations in lymphocyte number and/ or function on immune response during obesity. To this line, leptin, the levels of which are upregulated in the case of excess body weight, modulates T- cell proliferation and apoptosis, as well as monocyte apoptosis, revealing a profound role of this hormone in the regulation of immunity [157].

Our results regarding WBC counts in obesity are in line with literature (Table 5) suggesting a positive correlation with BMI. Few studies report no correlation between WBC numbers and adiposity but this fact may be attributed to the limited number of participants examined (<20 lean and obese participants in 3 out of 4 studies, Table 5).

Table 5. Summary of studies evaluating the effect of human obesity on major classes of circulating leukocytes and T cell subclasses (\uparrow : increased cell numbers or percentages in obese compared to non- obese individuals, \downarrow : decreased cell numbers or percentages in obese compared to non- obese individuals, -: no statistical difference between obese and non- obese individuals)

Type of cell	Overall change of circulating cell population frequency and/ or numbers during obesity	References
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White blood cells	↑	40, 91, 127, 139, 140, 151, 152, 172, 174, 175, 218, 283
	–	92, 150, 219, 229
Basophils	↑	175, 283
	–	91, 151, 152, 172
Eosinophils	↑	104, 175
	–	91, 151, 152, 172
Neutrophils	↑	127, 139, 140, 152, 172, 175, 283, 284
	–	91, 151, 229
Monocytes	↑	91, 127, 140, 151, 152, 175, 219, 283
	–	92, 139, 144, 150, 172
	↓	155
Classical monocytes (CD14⁺CD16⁻)	–	144
	↓	143, 150
Intermediate monocytes (CD14⁺CD16⁺)	↑	104, 143, 150
	–	144
Non-classical monocytes (CD14⁻CD16⁺)	↑	143
Lymphocytes	↑	40, 60, 127, 152, 172, 174, 175, 283
	–	91, 92, 139, 151, 219, 229
T lymphocytes (CD3⁺)	↑	92, 127, 138, 139
	–	172, 174, 219

	↓	26
B lymphocytes	↑	127, 140, 225
	–	92, 139, 172
NK cells (CD56⁺)	↓	121, 125
CD56⁺C16⁺ NK cells	↑	138
	–	92, 127, 139, 172
	↓	140
CD3⁺CD4⁺ cells	↑	40, 92, 127, 138, 157, 172, 174
	–	219
	↓	26
CD3⁺CD8⁺ cells	↑	40, 138
	–	92, 127, 172, 219
	↓	26, 157, 174, 218, 125
CD3⁺CD4⁺CD45RA⁺CD45RO⁻ cells	–	26
CD3⁺CD4⁺CD45RA⁻CD45RO⁺ cells	↓	26
CD3⁺CD4⁺CD45RA⁺CCR7⁺ (Naïve) cells	↑	92
	↓	60
CD3⁺CD4⁺CD45RA⁺CCR7⁻ (TEMRA) cells	↑	92
CD3⁺CD4⁺CD45RO⁺CCR7⁺ (CM) cells	↑	92
CD3⁺CD4⁺CD45RO⁺CCR7⁻ (EM) cells	↑	60

	–	92
T reg cells	↑	92
	↓	185, 186, 187, 231, 285

The involvement of granulocytes in immune dysfunction during obesity is not clear. Neutrophils, the most abundant type of polymorphonuclear leukocytes, were found slightly increased in obese participants. This upregulation in neutrophils levels is supported by several other studies whereas an absence of correlation between obesity and cell numbers are reported by few of them (Table 5). The conflicting relationship between excess body weight and granulocytes' levels might be attributed to basophils and eosinophils. Despite the fact that the percentage of basophils and eosinophils was found decreased in obese individuals in our study, published data report either positive or no correlation with increasing BMI for both subsets of granulocytes (Table 5). Although obesity and both eosinophils and basophils are related to allergic inflammation, current information about circulating levels of those cells in the case of excess body weight are rather inconsistent.

A statistical significant increase in PBMCs count reported in obese participants reveals an upsurge in cells that constitute the lymphocyte and monocyte compartment. Conclusions regarding the effect of different types of intervention could not be easily drawn because baseline levels of PBMCs differed a lot between the two intervention groups. Generally speaking, personalized diet was more efficient at the improvement of obesity- related inflammation represented by the reduction of total PBMCs counts.

As for monocyte compartment, the majority of studies report an increase in monocytes' numbers and/ or percentages along with increasing adiposity. A small number of studies report no association and one study reports a negative association between monocyte levels and BMI. It is noteworthy that only a limited number of participants are included in that study (16 obese and 12 normal- weight individuals) (Table 5).

Monocytes represent a heterogeneous population and their classification based on the expression of the CD14 and CD16 surface markers reveals important alterations during obesity.

Regarding classical monocytes, our results are in line with published data reporting a reduction in this type of monocytes in obese compared to lean individuals (Table 5). A lack of association between those cells and increasing BMI is reported in a study published by de Matos in which only 9 obese and 8 lean participants were included [144]. When the type of diet was examined, personalized diet resulted in a reduction whereas conventional intervention contributed to an increase in classical monocytes. Those results indicate that conventional diet is more efficient in the enforcement of the anti – inflammatory character of immunity represented by classical monocytes.

Conversely, intermediate monocytes were found elevated in obese participants and this increase is reported by several other studies (Table 5). As mentioned above, de Matos et al. reported no difference between lean and obese subjects regarding CD14⁺CD16⁺ but this observation may be due to the limited number of participants included in this study [144]. These cells along with non- classical monocytes are related to the initiation of immune response in case of an inflammatory situation. Consequently, they are expected to be upregulated in obesity. Similar to classical monocytes, intermediate monocytes were found elevated due to conventional diet compared with baseline whereas personalized diet resulted in a moderate reduction in their levels.

A marked increase in CD14⁻CD16⁺ and CD14^{low}CD16⁺ monocytes was observed in obese participants compared with lean subjects emphasizing the proinflammatory role of those cells in obesity- related low grade systemic inflammation. In 2011, Poitou et al. [143] reported a 2- fold increase of CD14^{dim}CD16⁺ monocytes in obese individuals with noteworthy additional effects of diabetes. Weight loss due to non- personalized diet resulted in a reduction in CD14⁻CD16⁺ and CD14^{low}CD16⁺ monocyte levels, whereas personalized diet contributed to a marked increase in non- classical monocytes and to a less profound reduction in CD14⁻CD16⁺ cells. Consequently, in the case of CD14⁻CD16⁺ and CD14^{low}CD16⁺ monocytes, personalized intervention seems to be more efficient in the restriction of the proinflammatory character of obese state represented by those cells.

Regarding the second subtype of PBMCs, the majority of studies report an upregulation in lymphocyte levels during obesity although in some cases the difference between lean and obese individuals did not reach the levels of statistical significance (Table 5). Our results are not in accordance with published data given the slight reduction in obese participants but this observation may be due to the limited number of participants included in our study.

When lymphocyte classification is taken into account, a marked reduction in NK cell ($CD56^+$) total levels was reported in the obese group. Those observations are in line with a study including 52 morbidly obese [26 MHO (BMI= $46.8 \pm 7.3 \text{ kg/m}^2$), 26 MUO (BMI= $47.5 \pm 12.2 \text{ kg/m}^2$)] and 11 lean controls [125]. NK cells were less abundant in severely obese participants compared with lean controls (9.1% versus 12.3% of total peripheral lymphocytes, $p=0.03$). Similarly, O' Shea et al. [121] reported a significant reduction in $CD56^+$ NK cell levels in morbidly obese patients ($n=40$) compared to lean healthy ($n=20$) subjects (7.6% versus 16.6%, $p=0.0008$).

When the expression of the CD16 marker was evaluated in order to further classify NK cells, the major NK subtype, i. e. $CD56^+CD16^+$ cells, were found decreased in obese compared to lean individuals. This reduction is responsible for the total reduction of NK cells in the obese group given the reported increase in relative levels of the other two NK subtypes ($CD56^{\text{bright}}CD16^-$, $CD56^{\text{dim}}CD16^-$) in obese compared to lean participants. As for $CD56^+CD16^+$ NK cells in obesity, current literature reveals a complex picture reporting elevated [138], similar [92, 127, 139, 172] or even decreased [140] levels of those cells in obese subjects (Table 5). Due to the participation of NK cells in both innate immunity against infection and in immune response against malignancy, studying those cells is of great interest given the fact that obesity predisposes to elevated risk of several types of cancer. According to currently published data, reduction in NK numbers/ function might be more prominent in morbidly but not in mildly obese individuals compared to lean subjects [100] but this association has to be further addressed.

The second component of the lymphocyte compartment, i. e. B cells, was found slightly elevated in obese participants and genotype- based diet resulted in a less profound reduction in their numbers following the 3- month intervention period. To this line, obesity was associated with elevated B cell numbers in several studies [127,

140, 225]. Nevertheless, others [92, 172, 139] reported similar levels of B cells in the obese and non- obese group and found no correlation with BMI [172].

An increase in CD3⁺ T cells, i. e. the third component of lymphocyte compartment, was reported in obese participants. Several other groups reported an upregulation of those cells in case of excess body weight (Table 5). Nevertheless, others reported similar levels of those cells in obese individuals but only ≤ 25 participants were included in those studies (Table 5). Weight reduction did not induce significant changes in total percentages of T cells and a more profound reduction was reported in the genotype- based group. It is interesting to mention that Tanaka et al. [26] reported a statistical significant upregulation ($p < 0.001$) in CD3⁺ cells in non- obese (n=50) compared to obese (n=34) subjects. Furthermore, 23 obese participants were subjected to a VLED that resulted in a marked weight reduction and a significant increase ($p < 0.05$) in T lymphocytes compared to the baseline value.

Further classification of CD3⁺ T cells revealed an upregulation in total percentage of CD4⁺ cells in obese individuals that is in line with current literature (Table 5). In contrast, Tanaka et al. [26] reported a reduction in those cells in obese subjects who also had their CD4⁺ cells increased following VLED ($p < 0.05$). Moreover, in a study published by Fink et al. [219], no difference between lean and obese individuals regarding CD4⁺ cells was reported but only 22 participants (9 obese and 13 non- obese) were included in this study. Our results regarding the type of diet used for the induction of weight loss indicate an increase and a reduction in non- personalized and in personalized group, respectively, whereas both groups have similar final levels of CD4⁺ cells.

A not significant reduction in the second subset of T lymphocytes, i. e. CD8⁺ cells, was reported in obese participants. The majority of studies report either decreased or similar CD8⁺ numbers between obese and non- obese state (Table 5). Nevertheless, Magrone et al. [138] reported an upregulation in obese subjects (7×10^5 versus 2×10^5 , $p < 0.0001$), whereas morbid obesity was associated with a higher CD8⁺ count in another study [40]. A noteworthy reduction in total CD8⁺ cells was observed in obese participants who followed genotype- based intervention. The latter is in line with a study [215] in which 9 obese women following a very- low- calorie diet program were

enrolled. After dieting, obese subjects had both their CD8⁺ total number (from 467/m1 to 336/m1, p<0.05) and percentage (from 21% to 16%, p<0.02) decreased.

Those inconsistencies in literature regarding CD8⁺ numbers in obesity may originate from the more destructive behavior of these cells once they get activated as compared to CD4⁺ T lymphocytes. The latter cells respond to several signals induced by increased adiposity, including cytokines and adipokines that stimulate their differentiation and proliferation. On the other hand, CD8⁺ cells are less prone to adipokine activation thus they only get activated following CD4⁺ T cell activation by fat- induced adipokine production. As a result, it is more possible to detect the effect of fat accumulation on CD8⁺ T cell number in extreme BMI condition as compared to lean state [40].

As for CD4⁺ and CD8⁺ cell distribution in T lymphocyte compartment, the increase reported in overall CD3⁺ T cells could be attributed to the increase in CD4⁺ cells given the reduction reported in CD8⁺ cells. Similar to total percentages, a trend towards the reduction of CD4⁺ cells to CD3⁺ lymphocytes is observed in participants following personalized intervention. Conversely, results regarding CD8⁺ cells to CD3⁺ cells are similar in the personalized and non- personalized group.

When the classification of CD4⁺ T cells based on the expression of the markers CD45RA/CD45RO was examined, a statistical significant increase of memory T cells in the obese group was reported. In contrast, obese subjects had significantly lower memory T cells than lean control subjects in a study published by Tanaka et al. [26] (See “Introduction” section). Among the functional features of memory cells, they have already been exposed to the antigen and still exist in its absence; they also possess enhanced activity in case of re- exposure and solicit immune response [277], and they have been strongly associated with obese condition [60]. Furthermore, 3-month genotype- based type of diet induced a reduction in memory cell levels (total percentage and relative percentage to CD4⁺ T cells), whereas conventional diet resulted in an increase in total percentage of those cells. Similarly, in the study mentioned above, weight reduction resulted in a significant increase in CD4⁺CD45RO⁺ cells ($0.56 \pm 0.22 \times 10^3$ cells/mm³ at baseline, $0.73 \pm 0.32 \times 10^3$ cells/mm³ at refeeding, p<0.001) [26].

CD45RA⁺ T cells, representing both the first and final stage of differentiation of T cells, i. e. naïve/ TEMRA cells, were found elevated in lean individuals and were increased to a greater extent due to conventional intervention. Others reported no difference in CD4⁺CD45RA⁺ cells between lean and obese individuals and weight loss did not cause significant alterations in their levels [26].

CD4⁺CD45RA⁺CD45RO⁺ cells are among the less studied cells included in our study according to current literature. They resemble naïve T cells in the inhibition of immunoglobulin production by B lymphocytes, and they resemble memory T cells in the expression of mRNA and the production of IFN- γ . CD4⁺CD45RA⁺CD45RO⁺ cells were found slightly upregulated in obese participants and personalized diet induced a marked reduction in their levels following the 3- month intervention period. Given the fact that those cells are a transient stage of differentiation in the process of transformation from naïve to memory cells, they are expected to be found at greater numbers in secondary lymphoid organs than in the periphery. In circulation, their frequency is <1% and the expression of CD45 isoforms by the majority of intermediate cells is reported at low density [278].

Within the CD4⁺ T cell compartment, CD45RA⁺ cells were found decreased in obese participants. The overall increase in CD4⁺ T cells in the obese group could be attributed to the increase reported in CD45RA⁻CD45RO⁺ and CD45RA⁺CD45RO⁺ cells.

Studying the expression of the CCR7 marker by CD4⁺ T cells revealed noteworthy observations regarding the sequential differentiation of CD4⁺ cells from naïve to TEMRA cells, with central memory and effector memory representing the intermediate stages.

Our results regarding the total percentage of naïve T cells are in line with a study published by Van der Weerd [92] reporting a significant increase in morbidly obese (n=8) compared to lean (n=11) individuals. However, Mauro et al. [60] observed a marked reduction in naïve T cells in obese individuals in a much larger group of participants (n=187). Naïve T lymphocytes represent cells responding to pathogens that the immune system has not yet encountered and may further differentiate into memory cells. Given the strong inflammatory response that is activated during obesity, we expect that fewer cells will remain in the undifferentiated stage. It is

noteworthy that participants following the genotype- based diet significantly had their naïve T cells decreased (total percentage and relative percentage to CD4⁺ T cells).

Central memory T cells possessing little or no effector function proliferate and differentiate into effector cells in response to stimulation by antigens. A noteworthy increase in total percentage of central memory T cells was observed in obese subjects and similar observations are reported in another study [92]. Both types of diet (i.e. personalized and non- personalized) resulted in a marked reduction in total and relative to CD4⁺ cells levels following the 3- month intervention period.

Effector memory T cells possess immediate effector function. No lymph- node homing receptors are reported in those cells and they are mostly encountered in tissues and circulation. According to our results, obese participants had elevated percentages of this type of cells compared to lean subjects. Similarly, Mauro et al. [60] demonstrated a significant association between increased effector memory T cells and obese condition. In contrast, effector memory T cell counts in obese individuals did not significantly differ from controls in another study [92]. Given the chronic systemic inflammation reported in obesity, the differentiation of naïve T cells into memory T cells and the subsequent marked upsurge of effector memory T cells in obese individuals are expected. In addition, except for the reduction of effector memory cell percentage to CD4⁺ T cells in response to conventional diet, no other marked changes regarding the type of intervention used to induce weight loss were reported.

TEMRA T cells are cytolytic cells possessing lower homeostatic proliferation capacity and shorter telomeres than naïve, central memory and effector memory T cells. In our study, TEMRA cells were found elevated in the obese group. Our results are line with those from a study published by Van der Weerd [92] reporting significant increases in TEMRA cells in obese participants compared to lean controls. Generally, weight reduction induced an upregulation in TEMRA T cell levels with a statistical significant increase reported in the group following the genotype- based 3- month intervention (% percentage to CD4⁺ T cells).

The overall increase reported in total CD4⁺ T cells in obese individuals could be predominantly attributed to the increase in central memory T cells and to a lesser extent to the increase reported in naïve and effector memory T cells. TEMRA T cells

did not exhibit any difference between lean and obese participants regarding their distribution in CD4⁺ T cell compartment.

The expression of the CXCR3 marker in obesity has not been extensively studied. Except for a study examining plasma levels of the CXCR3 ligand, CXCL10, in morbidly obese patients [209], no studies investigating the peripheral expression of CXCR3 in case of obesity with no other existing co-morbidities have been published so far. Our results indicate a reduction of naïve/ TEMRA cells and an upregulation of memory cells expressing the CXCR3 marker in obese participants. Thus, memory cells more than naïve/ TEMRA cells possess a possible active role in the orchestration of the accumulation of inflammatory T cells in fat sites in obesity. In addition, following weight loss, personalized intervention results in an overall increase in both CXCR3⁺ memory and CXCR3⁺ naïve/ TEMRA cells, whereas non- personalized intervention results in a moderate upregulation in naïve/ TEMRA cells and in a less profound reduction in memory cells.

The extensive investigation of Treg cells in obesity is supported by the fact that low grade systemic inflammation observed in obese individuals might be indicative of impaired Tregs function and/ or number [279]. The involvement of the anti-inflammatory Treg cells in obesity has been largely evaluated by several studies. The majority of them report a significant reduction in circulating Treg cell total count or percentage in obese compared to non- obese subjects (Table 5). This reduction might be attributed to their active recruitment to sites of inflammation [185].

In spite of the reported downregulation, Van der Weerd [92] reported an increase in circulating Treg cell counts in morbidly obese adults and a positive correlation with BMI. Our results are line with the latter study indicating an upregulation in Tregs total percentage in the obese group. However, Tregs percentage to CD4⁺ T cells was decreased in obese compared to non- obese subjects. Similarly, Wagner [185] and Agabiti- Rosei [186] reported that the percentage of Treg cells from CD4⁺ T cells was lower in obese compared to non- obese individuals (median: 1.2% versus 0.73%, $p=0.038$, and $4.11\pm 1.60\%$ versus $2.69\pm 1.81\%$ OB, $p<0,01$, respectively). Furthermore, both types of diet induced an upregulation in Tregs levels following weight loss with genotype- based type of diet resulting in a more marked increase in their relative levels regarding CD4⁺ T cells. Those results indicate that personalized

intervention is more efficient at the enhancement of the anti-inflammatory mechanism represented by Treg cells via limitation of obesity-related inflammation.

It is widely accepted that individuals respond differently to dietary factors. According to results from several studies, the delivery of personalized intervention results in outstanding improvements in dietary intake behavior compared to “one fits all” approach, and forces individuals to sustain healthy changes to their usual lifestyle. However, the number of well-designed randomized controlled trials reflecting the efficacy of personalized intervention is limited and noteworthy results obtained until now mostly derive from observational studies with a low level of reproducibility. Thus, larger and better-quality studies are needed in order to elucidate the exact role of personalized recommendation, especially the one based on genetic information, in diet and lifestyle modifications.

Similarly, there is a lack of knowledge regarding the factors that cause interindividual differences in response to pieces of diet and their persistence over time. Results from intervention studies based on personalized information seem to be useful and they should be definitely be conducted in a larger scale in order to draw the right conclusions about the role of interindividual differences in responses to dietary interventions.

Today, most of the available services in the area of personalized nutrition are based on limited published evidence regarding their safety or efficacy [235], and their clinical utility and analytical validity are a matter of concern. For that reason, worldwide government bodies make an effort to effectively control the distribution and familiarize consumers with genetic tests [280-282].

It is evident that current literature is characterized by conflicting data regarding most of the cells included in our study. Those variations might be attributed to differences in the BMI of participants. More specifically, a dose-dependent effect of BMI on the levels of circulating leukocytes, lymphocytes and T cells has been reported [26, 127]. Furthermore, existing co-morbidities and intake of multiple medications by obese patients might also serve as confounding factors that affect the frequency and function of immune cells, and contribute to differences between published data [157].

Well- designed studies evaluating immune cell frequency and function from circulation and adipose tissue from the same person are indispensable in order to examine whether circulating immune cells might be used as biomarkers for short-term clinical trial outcomes [108]. Understanding how immune cells are altered in obesity will probably lead to treatment for diseases in which dietary intake behavior regulates clinical outcome.

In summary, it is evident that obesity directly affects the regulation of the inflammatory and immune response. Our data demonstrate that obesity is associated with an increased frequency of circulating PBMCs and memory T cells confirming the proinflammatory status of obese individuals. Furthermore, the 3- month genotype- based type of intervention induced a statistical significant reduction in naïve T cells (total and % percentage to CD4⁺ T cells) and a statistical significant increase in TEMRA cells (relative percentage to CD4⁺ T cells). That observation indicates that weight loss is in line with a more differentiated status of CD4⁺ T cells but further studies are needed in order to confirm this trend in the intermediate stages, i.e. central and effector memory T cells.

7. REFERENCES

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8. APPENDIX

8.1 STATISTICAL ANALYSIS

Statistical significant results obtained from the statistical analysis (see “Methods” section) are presented below.

8.1.1 Differences in immune cell levels between lean and obese individuals

8.1.1.1 Peripheral blood mononuclear cells (PBMCs)

t test		
1	Table Analyzed	Total cells
2		
3	Column B	Obese
4	vs.	vs.
5	Column A	Lean
6		
7	Mann Whitney test	
8	P value	0.0037
9	Exact or approximate P value?	Exact
10	P value summary	**
11	Significantly different? (P < 0.05)	Yes
12	One- or two-tailed P value?	Two-tailed
13	Sum of ranks in column A,B	244.0 , 981.0
14	Mann-Whitney U	124.0
15		
16	Difference between medians	
17	Median of column A	1.680e+007
18	Median of column B	2.580e+007
19	Difference: Actual	9.000e+006
20	Difference: Hodges-Lehmann	8.100e+006

8.1.1.2 CD3⁺CD4⁺CD45RA⁻CD45RO⁺ T cells (Memory)

t test		
1	Table Analyzed	%CD45RA-CD45RO+ tota
2		
3	Column B	Obese
4	vs.	vs.
5	Column A	Lean
6		
7	Mann Whitney test	
8	P value	0.0124
9	Exact or approximate P value?	Exact
10	P value summary	*
11	Significantly different? (P < 0.05)	Yes
12	One- or two-tailed P value?	Two-tailed
13	Sum of ranks in column A,B	234.0 , 942.0
14	Mann-Whitney U	129.0
15		
16	Difference between medians	
17	Median of column A	10.01
18	Median of column B	14.07
19	Difference: Actual	4.065
20	Difference: Hodges-Lehmann	2.950

8.1.2 Effect of genotype- based diet- induced weight reduction on immune phenotype

8.1.2.1 Peripheral blood mononuclear cells (PBMCs)

2way ANOVA Multiple comparisons		A	B	C	D
		Data Set-A	Data Set-B	Data Set-C	Data Set-D
		Y	Y	Y	Y
1	Compare each cell mean with the other cell mean in that row.				
2					
3	Number of families	1			
4	Number of comparisons per family	2			
5	Alpha	0.05			
6					
7	Sidak's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
8					
9	conventional diet - genotype-based diet				
10	0	-1.878e+007	-3.029e+007 to -7.265e+006	Yes	**
11	3	-6.443e+006	-1.796e+007 to 5.070e+006	No	ns

8.1.2.2 CD4⁺CD45RA⁺CCR7⁺ cells (Naïve) (% total PBMCs)

2way ANOVA Multiple comparisons		A	B	C	D
		Data Set-A	Data Set-B	Data Set-C	Data Set-D
1	Compare each cell mean with the other cell mean in that column.	Y	Y	Y	Y
2					
3	Number of families	1			
4	Number of comparisons per family	2			
5	Alpha	0.05			
6					
7	Sidak's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
8					
9	0 - 3				
10	conventional diet	0.01857	-2.237 to 2.274	No	ns
11	genotype-based diet	3.080	0.09647 to 6.064	Yes	*

8.1.2.3 CD4⁺CD45RA⁺CCR7⁺ cells (Naïve) (% CD4⁺)

2way ANOVA Multiple comparisons		A	B	C	D
		Data Set-A	Data Set-B	Data Set-C	Data Set-D
1	Compare each cell mean with the other cell mean in that column.	Y	Y	Y	Y
2					
3	Number of families	1			
4	Number of comparisons per family	2			
5	Alpha	0.05			
6					
7	Sidak's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
8					
9	0 - 3				
10	conventional diet	1.389	-5.109 to 7.886	No	ns
11	genotype-based diet	9.750	1.155 to 18.35	Yes	*

8.1.2.4 CD4⁺CD45RA⁺CCR7⁻ cells (TEMRA) (% CD4⁺)

2way ANOVA Multiple comparisons		A	B	C	D
		Data Set-A	Data Set-B	Data Set-C	Data Set-D
1	Compare each cell mean with the other cell mean in that column.	Y	Y	Y	Y
2					
3	Number of families	1			
4	Number of comparisons per family	2			
5	Alpha	0.05			
6					
7	Sidak's multiple comparisons test	Mean Diff.	95% CI of diff.	Significant?	Summary
8					
9	0 - 3				
10	conventional diet	-12.08	-25.30 to 1.141	No	ns
11	genotype-based diet	-25.68	-43.17 to -8.193	Yes	**

8.2 INSTRUMENTS- DEVICES

Equipment and instruments- devices that were used in our study are summarized in the following table.

INSTRUMENT- DEVICE	MODEL	MANUFACTURER
Blood collection tubes	REF 368841	BD Vacutainer
Laminar flow hood	NU-437	Labgard
P20 pipetman	Cat. number: F123600	Gilson
P200 pipetman	Cat. number: F123601	Gilson
P1000 pipetman	Cat. number: F123602	Gilson
Centrifuge	Multifuge 3SR	Heraeus
Light microscope	DM IRE2	Leica
Cell sorter	FACS ARIA III	BD

8.3 REAGENTS

Reagents that were used in our study are summarized in the following table.

Experimental procedure	Reagent	Manufacturer	Catalog number
PBMCs isolation	RPMI Medium1640 (1X) + GlutaMAX	gibco	61870-010
	Ficoll-Paque PLUS	GE Healthcare Bio-Sciences AB	17-1440-03
PBMCs counting	Trypan Blue solution	Sigma- Aldrich	72571
	PBS pH 7.2 (10X) Phosphate Buffered Saline	gibco	70013-016
Flow cytometry	PBS pH 7.4 (1X) Phosphate Buffered Saline	gibco	10010-015
	Distilled Water	gibco	15230-097
	Ethylenediaminetetraacetic acid disodium salt solution (EDTA)	Sigma-aldrich	E7889
	FITC anti-human CD3	BioLegend	317306
	PE anti-human CD183 (CXCR3)	BioLegend	353706
	APC anti-human CD45RO	BioLegend	304210
	PerCP/Cy5.5 anti-human CD4	BioLegend	300530
	PE/Cy7 anti-human CD45RA	BioLegend	304126
	APC/Cy7 anti-human CD197 (CCR7)	BioLegend	353212
	PE anti-human CD4	BioLegend	300508
	PE/Cy5 anti-human CD127 (IL-7Ra)	BioLegend	351324
	PE/Cy7 anti-human CD25	BioLegend	356107
	APC/Cy7 anti-human CD8	BioLegend	344714
	APC/Cy7 Mouse IgG2a, κ isotype Ctrl	BioLegend	400230
	APC anti-human CD56 (NCAM)	BioLegend	318309
APC/Cy7 anti-human HLA-DR	BioLegend	307618	
PE/Cy7 anti-human CD15 (SSEA-1)	BioLegend	323030	

FITC anti-human CD16	BioLegend	302006
PE anti-human CD14	BioLegend	325606
PE-CF594 Mouse Anti- Human CD45	BD Horizon	562279
DAPI	Calbiochem	268298
