

1 Review

2 Obesity, Inflammation, Toll-like Receptor 4 and Fatty 3 Acids

4
5 Marcelo Macedo Rogero^{1,2,*}, Philip C. Calder^{3,4}

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7 ¹ Nutritional Genomics and Inflammation Laboratory, Department of Nutrition, School of Public Health,
8 University of São Paulo, 01246-904 São Paulo, Brazil; mmrogero@usp.br

9 ² Food Research Center (FoRC), 05508-000 São Paulo, Brazil.

10 ³ Human Development and Health Academic Unit, Faculty of Medicine, University of Southampton,
11 Southampton, United Kingdom; P.C.Calder@soton.ac.uk

12 ⁴ NIHR Southampton Biomedical Research Centre, University Hospital Southampton NHS Foundation
13 Trust and University of Southampton, Southampton, UK.

14 * Correspondence: mmrogero@usp.br; Tel.: +55-11-30617850

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18 **Abstract:** Obesity leads to an inflammatory condition directly involved in the etiology of
19 cardiovascular diseases, type 2 diabetes mellitus and certain types of cancer. The classic
20 inflammatory response is an acute reaction to infections or to tissue injuries, and it tends to move
21 towards resolution and homeostasis. However, the inflammatory process observed in individuals
22 affected by obesity and metabolic syndrome differs from the classical inflammatory response in
23 certain respects. This inflammatory process manifests itself systemically and is characterized by a
24 chronic low-intensity reaction. The toll-like receptor (TLR) 4 signaling pathway is acknowledged as
25 one of the main triggers of the obesity-induced inflammatory response. The aim of the present
26 review is to describe the role played by the TLR4 signaling pathway in the inflammatory response
27 and its modulation by saturated and omega-3 polyunsaturated fatty acids. Studies indicate that
28 saturated fatty acids can induce inflammation by activating the TLR4 signaling pathway.
29 Conversely, omega-3 polyunsaturated fatty acids, such as eicosapentaenoic acid and
30 docosahexaenoic acid, exert anti-inflammatory actions through attenuation of the activation of the
31 TLR4 signaling pathway by either lipopolysaccharides or saturated fatty acids.

32
33 **Keywords:** inflammation; Toll-like receptor 4; obesity; fatty acids

36 1. Obesity

37
38 Obesity is a multifactorial and polygenic condition that has become a very concerning public
39 health issue affecting both developed and developing countries [1-3]. Overweight individuals
40 (defined as body mass index [BMI] ≥ 25 kg/m²) account for approximately 30% of the global
41 population, i.e., 2.1 billion people, of whom more than 600,000 are classified as obese (defined as
42 BMI ≥ 30 kg/m²) [4]. The analysis conducted by the *Global Burden of Disease Study 2013* showed that
43 the overweight prevalence increased to 27.5% of adults and 47.1% of children in the past three
44 decades [5]. The prevalence of obesity is currently higher in developed countries; nevertheless,
45 approximately two-thirds of the obese population lives in developing countries [6]. Based on the
46 current scenario, it is estimated that up to 50% of the global population will be classified as
47 overweight or obese by 2030 [7]. Approximately 35% of adult individuals and 17% of children and

48 adolescents (2 to 19 years old) are considered obese (defined by values above the 95th percentile of
49 the BMI curve of these age groups) in the United States. It is estimated that approximately 300,000
50 people die due to obesity in the U.S. every year, which is the second highest cause of preventable
51 death [8].

52 Cardiovascular diseases, type 2 diabetes (DM2), non-alcoholic fatty liver disease and cancer
53 stand out among the main health issues responsible for morbidity related to the obesity [9]. Obesity
54 treatment and the treatment of its associated complications in developing countries has led to
55 significant cost increases in healthcare. Costs linked to DM2, in particular, stand out, since 20%–30%
56 of overweight people present with a DM2 diagnosis, while 85% of diabetic patients are overweight
57 or obese [10]. Calle et al. [11] conducted a prospective study of more than one million men and
58 women and found that the lowest mortality rates, for all causes, in both men and women, occur in
59 individuals with BMIs between 23.5 and 24.9 and 22.00 and 23.4 kg/m², respectively. Another study
60 including 900,000 adult individuals found that BMIs above 25 kg/m² were associated with a 30%
61 increase in general mortality rate per each 5 kg/m² increase [12].

62 Obesity results from the interactions of different factors, including genetic, metabolic,
63 behavioral and environmental ones. Accordingly, the dramatic increase in obesity prevalence rates
64 suggests that behavioral and environmental components are the main factors responsible for
65 obesity, with an emphasis on eating habits and exercise. With regard to eating, modern societies
66 converge to an eating pattern called the Western diet, which is characterized by the intake of foods
67 with high energy densities. Such densities derive from the high contents of fat and carbohydrate,
68 especially sugars, found in these food types, a fact that contributes to obesity development [13,14].

69 The profile of fatty acids present in a diet may also be relevant to obesity. It is worth
70 highlighting that, according to anthropological and epidemiological studies, humans from the
71 Paleolithic Era—40,000 years ago—consumed a ratio of omega-6 (ω -6) to omega-3 (ω -3)
72 polyunsaturated fatty acids of approximately 1, mainly due to a high intake of marine and vegetable
73 sources of ω -3 polyunsaturated fatty acids (PUFAs). However, there was a significant increase in the
74 intake of lipids, *trans* fatty acids and ω -6 PUFAs after the Industrial Revolution, as well as a small
75 increase in the intake of ω -3 fatty acids; meanwhile, intakes of vitamins C and E decreased. Such
76 changes are particularly relevant if one takes into account the participation of these nutrients in the
77 inflammatory response, which is linked to the physiopathology of different non-transmissible
78 chronic diseases, such as obesity, DM2, cardiovascular diseases, hypertension and cancer [15–17].

79

80 **2. Inflammation, Adipose Tissue and Obesity**

81

82 Inflammation is a central component of innate immunity, and microorganism destruction is
83 the prime function of the inflammatory response, a process that involves the participation of effector
84 cells in contact with pathogens living in the infected tissue. Microbial components, such as
85 lipopolysaccharides (LPS) found in the cell wall of Gram negative bacteria, can trigger an
86 inflammatory response through their interactions with cell-surface receptors found, for instance, in
87 cells from the immune system, such as macrophages and neutrophils. Inflammation in response to
88 microorganisms involves increased synthesis and secretion of a number of mediators, including
89 chemokines and cytokines. The latter include tumor necrosis factor (TNF)- α and interleukin (IL)-1

90 which act on endothelial cells and leukocytes to promote the recruitment and activation of
91 leukocytes in the inflammatory area [18,19].

92 Inflammation can be classified as acute or chronic. Acute inflammation presents via three
93 principal components: (i) changes in the vascular caliber, which result in increased blood flow in the
94 inflammatory focus; (ii) structural changes in the microcirculation, which favor the exit of plasma
95 proteins and leukocytes from the blood to the tissue; and (iii) adhesion and transmigration of
96 leukocytes from the microcirculation to the tissue as well as their further activation, which allows
97 the elimination of harmful agents. As soon as the infection is eliminated, or at least controlled,
98 mechanisms are activated that act to limit any type of aggression against the host and to initiate the
99 tissue repair process. Such a process aims to reduce the inflammation and is termed resolution.
100 Resolution is now known to be an active process involving the activation of negative feedback
101 mechanisms, such as anti-inflammatory cytokine secretion, a reduction in receptor expression,
102 activation of regulatory cells, and production of pro-resolving lipid mediators [20-22].

103 Histamine, bradykinin, neuropeptides, prostaglandins, thromboxanes, leukotrienes and
104 platelet-activating factor stand out among the non-cytokine/chemokine mediators involved in the
105 inflammatory response. The generation of eicosanoids initially occurs due to activation of
106 phospholipase A2, which hydrolyzes membrane phospholipids to yield a free fatty acid.
107 Arachidonic acid, an ω -6 PUFA, is predominant among the fatty acids released by phospholipase
108 A2. The released fatty acids are used as a substrate by the cyclooxygenase enzymes (COX), which
109 catalyze the synthesis of prostaglandins and thromboxanes, as well as by lipoxygenase (LOX)
110 enzymes, which catalyzes the synthesis of leukotrienes. Such mediators are responsible for many
111 aspects of the inflammatory response, such as vasodilation (prostaglandin E₂) and leukocyte
112 migration (leukotriene B₄) [23-25].

113 Chronic inflammation involves progressive changes in inflammatory cells as well as in
114 tissue destruction and repair due to the on-going inflammatory process. Accordingly, inflammation
115 can become pathologic because of the loss of tolerance or regulatory processes. As a result, there is
116 an increase the plasma concentrations of many inflammatory biomarkers and in the number of
117 activated inflammatory cells in the bloodstream as well as in the primary lesion area. Such changes
118 can be easily observed, for instance, in patients with frank chronic conditions like rheumatoid
119 arthritis and inflammatory bowel diseases [26,27].

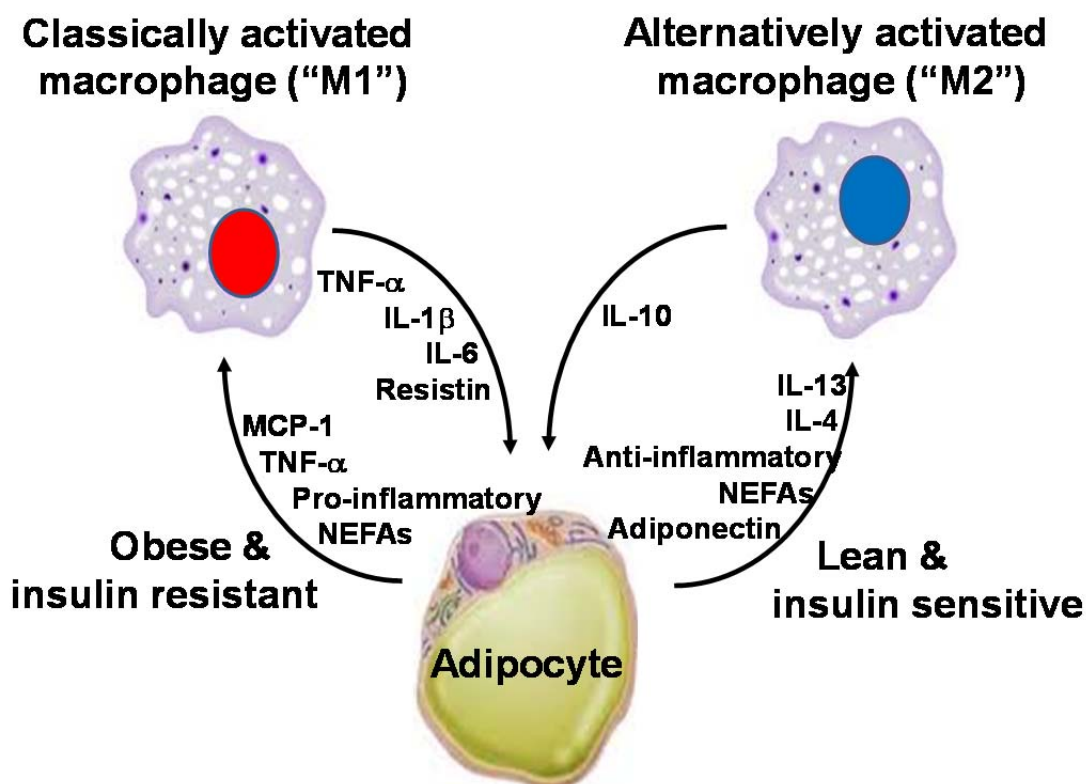
120 Chronic inflammation can also present at lower intensities than seen in the classic
121 inflammatory diseases. Evidence that obesity results in inflammation started emerging in the 1990s.
122 This inflammation is directly involved in the etiology of cardiovascular diseases, DM2 and certain
123 cancer types [28]. Hotamisligil et al. [29] found that genetically obese rodents, such as db/db and
124 ob/ob mice and fa/fa rats, had increased expression of the TNF- α gene in white adipose tissue. They
125 identified that neutralization of TNF by anti-TNF- α antibodies mitigated the resistance of these
126 animals to insulin action, establishing a link between inflammation, insulin resistance and
127 hyperglycemia. Macrophages from the stromal vascular fraction of adipose tissue appear to be the
128 main cell type responsible for TNF- α and IL-6 release from the adipose tissue. The increased
129 concentration of cytokines in this tissue is mostly derived from the infiltration of M1 macrophages,
130 which are activated in the classical way and characterized by the high expression of
131 pro-inflammatory cytokines like TNF- α , IL-1 β and IL-6 [30-32] (Figure 1). It should be noted that
132 macrophages correspond to about 40% of total white adipose tissue cells in obese mice and humans,

133 compared to only 18% in lean controls [33]. In the white adipose tissue, the expression of monocyte
134 chemoattractant protein (MCP)-1 correlates positively with adiposity, and is also higher in visceral
135 adipose tissue compared to subcutaneous adipose tissue [34,35]. The receptor for MCP-1, CCR2 (CC
136 receptor 2), is expressed on monocytes present in peripheral blood and on adipose tissue
137 macrophages. This implies that obesity favors the process of migration of blood monocytes into the
138 visceral adipose tissue of obese individuals, which then differentiate into macrophages. This process
139 is regulated by colony stimulating factors such as macrophage-specific growth factor called CSF -1
140 or M-CSF [36].

141 In mammals, there are two types of adipose tissue: white and brown adipose tissue (BAT). BAT
142 is specialized in the production of heat (thermogenesis) and, therefore, actively participates in the
143 regulation of body temperature. BAT deposits are found in fetuses and newborns. In adult humans,
144 there is a small volume of BAT in the cervical supra-clavicular, supra-adrenal and para-spinal
145 regions [37,38]. Brown and white adipocytes appear to have different physiology and opposing
146 functions [39] Beiging/browning of white adipose tissue promotes energy expenditure by triggering
147 thermogenesis, which suppresses diet-induced weight gain, as well as enhancing the efficiency of
148 BAT activity [40]. In this context, individuals with low amounts of BAT would be prone to the
149 development of obesity. Studies in animals lacking BAT or uncoupling protein 1 (UCP1) have clearly
150 demonstrated the involvement of BAT thermogenesis in protection against diet-induced obesity (DIO)
151 [41]. Decreasing BAT activity or removal of BAT in mice provokes increased glycemia and plasma
152 triglyceride concentration and promotes insulin resistance [42]. Also, in humans, BAT activity was
153 found to be inversely related to BMI and fat mass [43]. Furthermore, visceral adipose tissue
154 inflammation may also be linked to the lower BAT volume since TNF- α has been shown to induce
155 brown adipocyte apoptosis and hamper BAT differentiation [44].

156 Obesity is a relevant causal factor in the etiology of insulin-action resistance. Thus, obese
157 patients present with reduced insulin action in the skeletal muscle due to lower phosphorylation of
158 the tyrosine residues of the insulin receptor substrate (IRS)-1 and the reduced
159 phosphatidylinositol-4,5-bisphosphate 3-kinase (PI3K) activity in this tissue. Such an outcome can
160 cause a further reduction in insulin-induced glucose transport into the muscle tissue [45].

161
162



163

164 **Figure 1.** Interaction between M1 and M2 macrophages and adipocytes. Abbreviations: IL,
 165 interleukin; MCP, monocyte chemotactic protein; NEFAs, non-esterified fatty acids; TNF, tumor
 166 necrosis factor.

167

168 An increased inflammatory response is an important factor in the etiology of insulin-action
 169 resistance in obese patients. Such a response triggers the activation of protein kinases related to Toll
 170 signaling pathways and TNF-α receptors, such as the inhibitor of kappa B kinase (IKK) and c-jun
 171 N-terminal kinase (JNK)-1, which are capable of phosphorylating IRS-1 at the serine 307 residue.
 172 This reduces IRS-1 interaction with the insulin receptor beta subunit and, consequently, causes
 173 decreased insulin signal transduction [46,47]. JNK knockout mice show lower adiposity, enhanced
 174 sensitivity to insulin and an increased capacity for insulin receptor signaling even when they are fed
 175 a lipid-rich feed. These findings suggest that activation through JNK is an important mechanism
 176 linked to insulin resistance in obese patients [48].

177

178 Among the inflammatory biomarkers related to obesity, IL-6 favors insulin-action resistance
 179 in obese individuals due to the induction of the cytokine signaling suppressor protein 3 (SOCS3),
 180 which physically associates itself with tyrosine phosphorylated proteins, such as the insulin
 181 receptor. In addition, SOCS3 decreases the phosphorylation of IRS-1 tyrosine, which weakens the
 182 IRS-1 coupling to the insulin receptor and the subsequent association between IRS-1 and PI3K. These
 183 findings suggest that SOCS3 is a relevant inhibitor of the insulin signaling pathway, as well as
 184 allowing a better understanding of the IL-6 effect on the insulin-action resistance induced by obesity
 [49].

185

186 Understanding that the immune system and different metabolic pathways are closely
 187 related to each other as well as that they are functionally dependent is essential for studies focused
 on obesity and on its possible metabolic repercussions. Thus, signaling pathways responsive to

188 nutrient intake and the presence of pathogens are evolutionarily conserved and greatly integrated
189 [50]. The excessive intake of obesity-associated nutrients can be detected by innate recognition
190 receptors, and this results in the activation of pro-inflammatory signaling pathways as well as in
191 stress responses in many parts of the body. This causes low-intensity chronic inflammation, defined
192 by Hotamisligil et al. [30] as metabolic inflammation or as meta-inflammation, which is different
193 from the classic inflammatory response. Moreover, the genesis of this inflammation is closely related
194 to lifestyle and mainly to the quality of diet and exercise [51].

195 Meta-inflammation development is associated with a wide and integrated network of
196 intracellular signal pathways, among which IKK- β and JNK-1 stand out. These proteins induce the
197 synthesis of inflammatory mediators in different cell types. IKK- β and JNK-1 activation results in
198 activating the transcription factors nuclear factor kappa B (NF- κ B) and activating protein (AP)-1,
199 which translocate to the cell nucleus and activate the transcription of many genes encoding the
200 proteins involved in inflammation including TNF- α and COX-2. This process allows the continuity
201 of the inflammatory reaction, which is associated with conditions such as atherogenesis and
202 insulin-action resistance [52,53].

203 This systemic inflammatory response mainly originates from adipose tissue, which
204 produces a wide variety of pro-inflammatory cytokines and chemokines called adipokines [23].
205 However, currently, it is known that there are other tissues involved in meta-inflammation, such as
206 the liver [54], pancreas [55], hypothalamus [56,57] and skeletal muscle [58]. It seems likely that the
207 chronic low-grade inflammation that develops in adipose tissue with obesity is “transferred” to
208 these other tissues through the appearance of active inflammatory mediators in the bloodstream.

209 In the context of inflammation and obesity, the role of gut microbiota in the development of
210 metabolic disease should be noted. Studies have shown that certain bacteria populations produce
211 enzymes that increase the efficiency of nutrient digestion, leading to improved nutrient supply to
212 the host, therefore, contributing to increased energy storage in the adipose tissue. The resulting
213 increase in body adiposity can trigger the development of insulin resistance. There is also evidence
214 that the gut microbiome can modulate genes involved in energy storage and expenditure [59-62].

215 In 2004, Backhed et al. [61] reported that conventionally reared mice had a 42% increase in
216 body fat and a 47% increases in periepididymal adipose tissue compared to germ-free mice.
217 Furthermore, transfer of the microbiota from the bowel of the conventional mouse to the gut of the
218 germ-free mouse resulted in a 57% increase in body fat in 2 weeks, although feed consumption
219 decreased. This result highlights the important role that the intestinal microbiota plays in energy
220 homeostasis and its potential involvement in the etiology of obesity. Germ-free mice are resistant to
221 diet -induced adiposity, which is associated with increased activity of AMP-activated protein kinase
222 (AMPK) in liver and muscle and increased expression of adipose factor induced by fasting (Fiaf) in
223 the small intestine [62]. On the other hand, the inoculation of the microbiota of conventional mice fed
224 with this diet into germ-free animals results in an increase in adiposity [59].

225 It should also be noted that the dysbiosis associated with consuming a high-fat diet has been
226 shown to increase intestinal permeability, which results in a greater translocation of LPS from the
227 intestinal lumen to the blood circulation. This metabolic endotoxemia is associated with increased
228 body fat, glucose intolerance and increased expression of proinflammatory mediators and
229 macrophage infiltration in white adipose tissue [60].

230

231 3. Toll-Like Receptor 4 and Inflammatory Response

232

233 The innate immune systems of mammals—which encompasses cells such as neutrophils and
234 macrophages—use different strategies to recognize microorganisms. One of these strategies is based
235 on recognizing general aspects of molecules associated with pathogens (*pathogen-associated molecular*
236 *patterns*, or PAMPs) that result from microbial metabolism conserved throughout the evolution of
237 the species. These molecules are widely distributed among pathogens; for instance, the LPS
238 molecule is common in all Gram-negative bacteria, although it is not produced by the host [63-65].

239 Innate immune system receptors capable of recognizing PAMPs are called pattern
240 recognition receptors and these induce the expression of pro-inflammatory cytokines—for example,
241 TNF- α and IL-1 β —as well as activating the host's antimicrobial defense mechanisms, such as the
242 synthesis of reactive oxygen and nitrogen species, including hydrogen peroxide and nitric oxide
243 (NO), respectively [66,67]. PAMP recognition can induce CD80 and CD86 costimulatory molecules
244 on the surface of cells, presenting antigens as well as inducing small antigenic peptides linked to
245 MHC class II molecules in cell membranes that present antigens to CD4⁺ T lymphocytes so activating
246 adaptive immune responses [68].

247 The innate immune system recognizes PAMPs through toll-like receptors (TLRs) that are a
248 family of transmembrane proteins responsible for playing an essential role in the innate immune
249 system [69]. The main function of the TLR protein lies in controlling inflammatory and
250 immunological responses. TLRs can recognize a whole variety of microbial PAMPs. Eleven different
251 TLRs have been identified in humans and thirteen among all mammals [70]. TLRs belong to the IL-1
252 receptor (IL-1R) superfamily, which have a significant homology in their cytoplasmic regions, such
253 as in the Toll/IL-1R (TIR) domain. The TIR domain is needed for the interaction and recruiting of
254 many adaptive molecules involved in the activation of signaling pathways [67].

255 TLRs are expressed in different cell compartments and are recognized by many PAMPs
256 deriving from viruses, pathogenic bacteria, fungi, and protozoa. TLR1, TLR2, TLR4, TLR5, TLR6,
257 and TLR11 are expressed in the cellular membrane, whereas TLR3, TLR7, TLR8 and TLR9 are
258 expressed in intracellular compartments, such as the endosome and the endoplasmic reticulum.
259 Based on the amino acid sequence and on the genomic structure, TLRs can be divided into five
260 subfamilies: TLR2, TLR3, TLR4, TLR5, and TLR9. The subfamily TLR2 comprises TLR1, TLR2, TLR6
261 and TLR10, whereas the subfamily TLR9 encompasses TLR7, TLR8, and TLR9 [71-73].

262 TLR4 was the first TLR reported in humans; it is expressed in innate immune cells, including
263 monocytes, macrophages, and dendritic cells, as well as in other cell types like adipocytes,
264 enterocytes and muscle cells. As indicated above, LPS is the primary agonist for TLR4 [74]. LPS is an
265 integral structural component found in the external membrane of Gram-negative bacteria as well as
266 representing one of the most powerful microbial inflammation indicators. It is a complex glycolipid
267 composed of one hydrophilic polysaccharide and one hydrophobic domain called lipid A [75]. There
268 is some evidence that saturated fatty acids can also bind to TLR4 and activate TLR4-mediated
269 signaling pathways [76,77]. Also, there are other endogenous ligands for TLR4 like heat shock protein
270 (Hsp) 60, Hsp 70, type III repeat extra domain A of fibronectin, oligosaccharides of hyaluronic acid,
271 polysaccharide fragments of heparan sulfate, and fibrinogen [78]. In the context of obesity, the
272 increase in the plasma fibrinogen levels, which represents a positive acute phase protein, acts as a

273 factor involved in the activation of the TLR4 pathway and, consequently, in the amplification of the
274 inflammatory response [79].

275 The interaction between LPS and TLR4 induces the synthesis of pro-inflammatory cytokines
276 such as TNF- α , IL-1 β , IL-6, IL-8, and IL-12, which, in turn, work as endogenous inflammatory
277 mediators by interacting with receptors found in different target cells. In addition to cytokines,
278 macrophages release a whole variety of biological mediators in response to LPS, including platelet
279 activation factor, prostaglandins, enzymes, and reactive oxygen and nitrogen species, such as
280 superoxide anion and NO. The synthesis of these pro-inflammatory mediators by monocytes and
281 macrophages is designed to inhibit the growth and dissemination of pathogens and to eliminate
282 them either directly or through induction of adaptive immune responses [63,80].

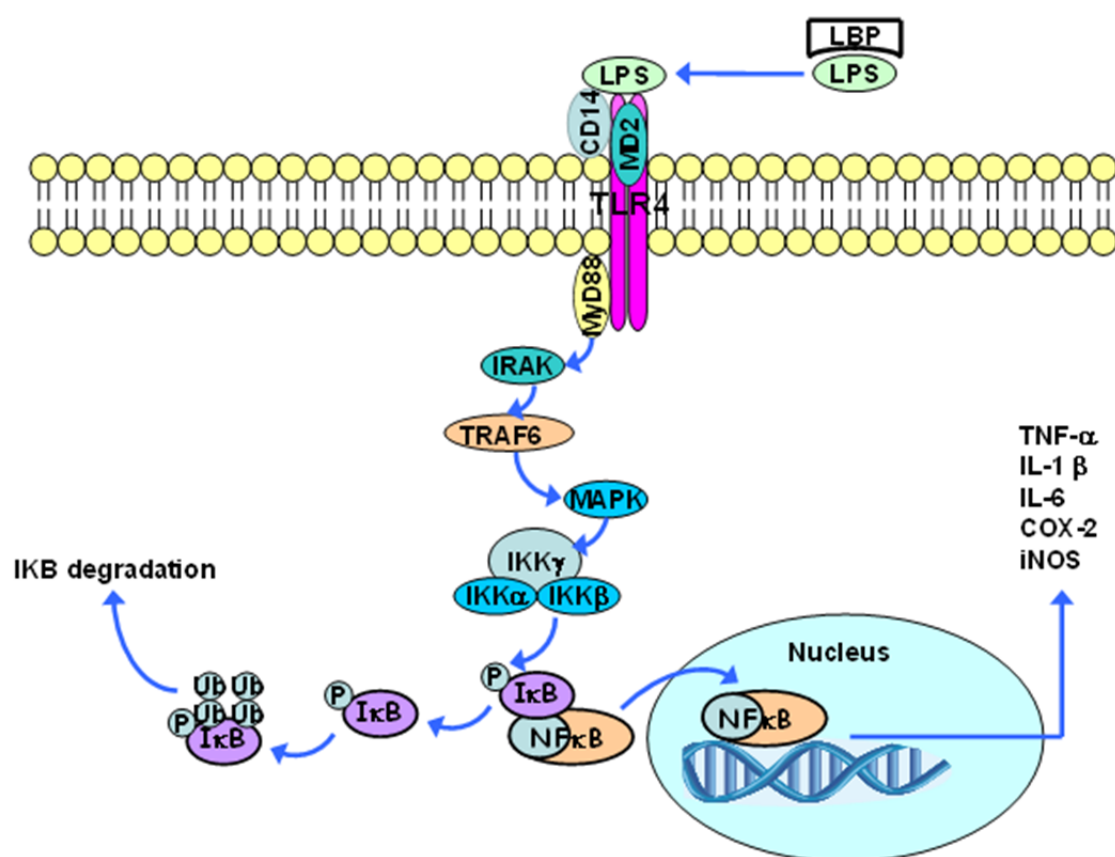
283 LPS initially binds to the LPS-binding protein (LBP), which is found in the blood or in
284 extracellular spaces. This protein promotes LPS binding to the CD14 molecule, which, in turn, is
285 moored to the lipid bilayer by means of a glycosphosphatidylinositol group found in most cells,
286 except for endothelial ones. CD14 can also exist as a soluble protein and, in this case, can lead LPS to
287 the cell surface. The CD14 molecule is not found in transmembrane and intracellular domains; thus,
288 it cannot trigger signal transduction processes on its own. When LPS binds to CD14, LBP dissociates
289 itself and the LPS-CD14 complex physically associates with TLR4. Such a receptor needs an
290 additional molecule, the so-called extracellular accessory protein (MD2), which binds to the TLR4
291 extracellular complex in order to recognize LPS [71].

292 Following ligand binding, TLRs dimerize and undergo conformational changes required for
293 the subsequent recruitment of cytosolic TIR domain-containing adaptor molecules, including the
294 cytoplasmic adapter protein MyD88. The association between TLR4 and MyD88 gathers proteins
295 from the IL-1 receptor associated kinase (IRAK) family. Two members (IRAK4 and IRAK1) are
296 phosphorylated in sequence, and this disrupts them from the receptor complex and promotes their
297 association with TNF receptor associated factor 6 (TRAF6). TRAF6 then activates mitogen activated
298 protein kinase (MAPK) proteins. These kinases can activate the AP-1 transcription factor [81].

299 The transcription factor NF- κ B, which is found in a dimeric form in the cytoplasm of
300 non-stimulated cells, is inactive when associated with κ B inhibitors (I κ B) (**Figure 2**). The family of
301 I κ B proteins includes I κ B α , I κ B β , I κ B ϵ , and Bcl-3, as well as the carboxy-terminal regions of NF- κ B1
302 (p105) and NF- κ B2 (p100). The I κ B proteins bind to different NF- κ B dimers, although they have
303 different affinities and specificities; therefore, besides the different NF- κ B dimers found in a specific
304 cell type, there are a large number of combinations of the I κ B and the NF- κ B dimers [82,83].

305 Via MAPK, TRAF6 activates the I κ B kinase complex (IKK), which is composed of two
306 catalytic subunits (IKK α and IKK β) and one regulatory subunit (IKK γ) and has the capacity to
307 induce I κ B phosphorylation. This phosphorylation results in I κ B dissociation from the NF- κ B
308 complex and its subsequent polyubiquitination, which, in turn, leads to I κ B degradation (mediated
309 by the 26S proteasome) [73,81]. This process allows the NF- κ B dimer to translocate into the nucleus
310 and to activate the transcription of many κ B-dependent genes, such as the genes of
311 pro-inflammatory cytokines, including TNF- α , IL-1 β , IL-6, COX-2 and inducible nitric oxide
312 synthase (iNOS) (**Figure 2**). NF- κ B also stimulates the synthesis of I κ B. Accordingly, the newly
313 synthesized I κ B binds to NF- κ B and suppresses its activity, providing a feedback inhibition
314 mechanism [74,81]. There are five members of the family of NF- κ B transcription factors in mammals:
315 NF- κ B1 (p105/p50), NF- κ B2 (p100/p52), RelA (p65), RelB and c-Rel, which can dimerize to form

316 homodimers and heterodimers that, in turn, are associated with specific transcriptional responses to
 317 different stimuli. NF- κ B1 and NF- κ B2 do not contain transcriptional activation domains and their
 318 homodimers work as repressors. On the other hand, Rel-A, Rel-B and c-Rel drive the transcriptional
 319 activation domain and, except for Rel-B, are capable of forming homodimers and heterodimers
 320 along with other members of this family of proteins. Consequently, the balance between different
 321 NF- κ B homodimers and heterodimers regulates the transcriptional activity level. It is worth
 322 highlighting that these proteins are expressed in a specific cell and tissue pattern, which leads to an
 323 additional level of regulation. NF- κ B1 (p50) and RelA, for example, are broadly expressed and,
 324 therefore, the p50/RelA heterodimer is the most common NF- κ B-binding activity inducer [82,83].
 325



326

327 **Figure 2.** TLR4 induced signaling activates the transcription factor NF κ B.

328

329 Human monocytes express TLR1, TLR2, TLR4, TLR5, TLR6, TLR8 and TLR9; but TLR2 and
 330 TLR4 are the receptors most commonly expressed in these cells. The expression of TLR2 and TLR4 in
 331 the plasma membrane of monocytes has been confirmed by flow cytometry; TLR2 and TLR4-binding
 332 (by peptidoglycan and LPS, respectively) generates pro-inflammatory cytokine secretion in these
 333 cells. Moreover, TLR2 and TLR4 activation recruits monocytes and forms foam cells in murine
 334 models of atherosclerosis [30,84].

335 Studies conducted *in vitro* with cell cultures showed the negative effects of
 336 pro-inflammatory cytokines deriving from TLR4 signal pathway activation on glucose uptake and
 337 on the metabolism of fatty acids [33,85,86]. TLR4 gene deletion in mice has a protective effect against
 338 adipose tissue inflammation and against the resistance to insulin action induced by intake of a high

339 fat diet, a fact that points towards the causal role played by TLR4 in metabolic changes driven by
340 over-eating and obesity [87,88].

341 Humans with type I diabetes exhibit a greater expression of TLR2 and TLR4 in the cellular
342 membrane in monocytes, as well as greater MyD88 protein content and IRAK phosphorylation in
343 monocytes in the peripheral blood than in control groups [89]. Individuals with DM2 show
344 increased cellular membrane levels of TLR2 and TLR4 in blood monocytes, as well as a higher
345 concentration of IL-1 β , IL-6, IL-8 and TNF- α in serum than in controls [90]. Similarly, TLR2, TLR4
346 and MyD88 are more highly expressed in blood mononuclear cells and in the abdominal
347 subcutaneous white adipose tissue in obese and diabetic individuals than in patients with normal
348 weight [63,80]. Also, overweight and obese people showed increased expression of TLR2 and TLR4
349 on peripheral blood mononuclear cells and in adipose tissue in comparison with lean people; the
350 expression levels of TLR2 and TLR4 increased significantly with increasing body mass index [91].

351 Furthermore, insulin-action resistance in obese individuals can increase the expression of
352 TLR4, which depends on the designated PU.1 transcription factor that, in turn, regulates the gene
353 expression related to the activation and differentiation of myeloid cells, including the TLR2, TLR4,
354 and TLR9 receptors [92,93]. Insulin has a suppressive effect on the expression of TLR4 and on the
355 activity of the PU.1 transcription factor; however, the suppressive effect of the hormone would be
356 expected to be reduced due to the insulin-action resistance related to obesity. Such a reduction
357 would increase the expression of TLR4 in peripheral blood monocytes [94]. In view of this, it seems
358 that the increase of the inflammatory response favors the occurrence of resistance to the action of the
359 insulin, through the activation of the IKK- β and JNK kinases that reduce the activation of IRS-1 in
360 the insulin signaling pathway. Conversely, the presence of insulin resistance favors the expression of
361 TLR4, suggesting that insulin resistance promotes inflammation.

362 As described earlier, the TLR4 pathway increases the expression of pro-inflammatory
363 cytokines, such as TNF- α , IL-1 and IL-6, by activating the transcription factors NF- κ B and AP-1.
364 These cytokines, in turn, increase the hepatic synthesis of CRP, the classic positive acute phase
365 reactant and the most studied and accepted inflammatory biomarker. CRP is often used in clinical
366 practice due to its high stability (mean half-life of 19 hours) and its rapid production in response to
367 inflammatory stimuli [95,96]. It is important to note that other inflammatory biomarkers, such as
368 IL-6, TNF- α , the intercellular adhesion molecule (ICAM)-1, P-selectin, E-selectin, the monocyte
369 chemotactic protein (MCP)-1, fibrinogen and soluble CD40, have been characterized as predictors of
370 cardiovascular disease, regardless of other cardiovascular risk factors [19,26].

371 Dietary lipids can cause changes in the expression patterns of TLRs [97]. Ingestion of a high
372 calorie (910 kcal), high lipid (51 g) and high carbohydrate (88 g) meal by normal weight individuals
373 caused significant changes in TLR in the post-prandial period, with TLR2 and TLR4 increasing in
374 blood mononuclear cells. This reinforces the potential importance of postprandial inflammation for
375 obesity, DM2 and cardiovascular disease physiopathology [98,99]. A high-fat meal also leads to
376 increased NF- κ B activation in the post-prandial period as well as increased leucocyte activation, as
377 assessed by surface expression of CD11a, CD11b and CD62L [100], and metabolic endotoxemia (i.e.
378 increased plasma LPS levels) [101].

379

380 4. Fatty Acids, Toll-Like Receptors and Inflammation

381

382 4. 1 Saturated Fatty Acids

383 Saturated fatty acids, particularly lauric acid and palmitic acid, are capable of stimulating an
384 inflammatory response through the TLR4 signaling pathway [102]. Lee et al. [103] published the first
385 study that demonstrated the effect of different fatty acids on the TLR4 signaling pathway. In this
386 study, it was verified that lauric, palmitic, and stearic acids could induce COX-2 expression through
387 an NF- κ B-dependent mechanism in a macrophage cell line. Among the saturated fatty acids tested,
388 lauric acid (C12:0) had the greatest activation capacity through TLR4. Different from saturated fatty
389 acids, monounsaturated and polyunsaturated acids did not lead to TLR4 signal activation.
390 Moreover, cell pretreatment *in vitro* for three hours with different polyunsaturated fatty acids,
391 particularly the ω -3 fatty acid docosahexaenoic acid (DHA: 22: 6 ω -3), or oleic acid (ω -9)
392 significantly reduced the subsequent pro-inflammatory effect induced by lauric acid [103].

393 Saturated fatty acids represent an essential component of bacterial endotoxins. The lipid A
394 portion of LPS has six saturated fatty acids coupled to this structure through ester or amide bonds.
395 The carbon chain length of these fatty acids in lipid A varies from 12 to 16 carbons. Interestingly, the
396 replacement of these saturated fatty acids by monounsaturated or polyunsaturated fatty acids stops
397 the pro-inflammatory activity of the LPS [104].

398 Saturated fatty acids can also induce an inflammatory response through activation of TLR2,
399 which forms heterodimers in the plasma membrane along with TLR1 or TLR6. Diacylated and
400 triacylated lipoproteins, peptidoglycans and lipoteichoic acid are among this receptor's agonists
401 [676,105,106]. Lee et al. [107] reported that lauric acid induced activation through NF- κ B when TLR2
402 was cotransfected with TLR1 or TLR6; however, this did not occur when TLR1, 2, 3, 5, 6, or 9 were
403 individually transfected. On the other hand, the omega-3 polyunsaturated fatty DHA suppresses
404 activation through the NF- κ B signaling pathway, whether this is induced by LPS or by lauric acid
405 [108]. Furthermore, inhibition of TLR2 expression enhances the sensitivity to insulin action in the
406 skeletal muscle and in the white adipose tissue of mice fed on a high fat diet as well as inhibiting the
407 expression of this receptor. This process results in partial reversal of palmitic acid-induced insulin
408 resistance [23,109].

409 Erridge and Samani [110] suggested that saturated fatty acids would not directly stimulate
410 TLR2 and TLR4 but that this effect could result from the contamination of the bovine serum albumin
411 used to solubilize the saturated fatty acids in the studies conducted *in vitro*. However, Huang et al.
412 [76] demonstrated that saturated fatty acids activate the inflammatory response *in vitro* through
413 TLR2 and TLR4. Lauric acid—which was not solubilized in bovine serum albumin—induced the
414 activation of the NF- κ B signaling pathway through TLR2—which was dimerized with TLR1 or
415 TLR6—and TLR4. In addition, there are current propositions addressing TLR4 activation by
416 saturated fatty acids that depend on fetuin A, which is produced in the liver and works through
417 endogenous TLR4-binding [77].

418 Palmitate acid bound to TLR4 activates the kinase proteins JNK and IKK- β and increases the
419 expression and secretion of pro-inflammatory cytokines [86]. Palmitic acid also impairs insulin
420 signaling pathways by inducing IRS-1 phosphorylation at serine residue position 307 [111]. This
421 process reduces its interactions with the insulin receptor and, consequently, diminishes
422 insulin-induced signal transduction. Moreover, saturated fatty acids induce insulin-action resistance
423 due to the antagonistic action of the peroxisome proliferator-activated receptor-gamma coactivator

424 (PGC)-1 alpha. Such a process induces the expression of mitochondrial genes involved with
425 oxidative phosphorylation and with glucose capture, which is mediated by insulin [112,113].
426

427 4.2 Polyunsaturated Fatty Acids

428 Polyunsaturated fatty acids consist of two families (ω -3 and ω -6) characterized by the
429 double bond locations defined by the first double bond in relation to the methyl terminal group in
430 the fatty acid molecule. α -Linolenic and linoleic acids are examples of polyunsaturated fatty acids
431 belonging to the ω -3 and ω -6 families, respectively. These two fatty acids are not synthesized in
432 humans, and the lack of ω -3 and ω -6 intake causes signaling and symptom deficits, indicating that
433 such nutrients are essential to humans; therefore, they must be consumed through the diet
434 [24,25,114,115]. However, studies have shown that the ratio of ω -6 to ω -3 fatty acids in the diet has
435 implications for health since increased ratios are associated with an increased risk of chronic disease
436 incidence and progression [116,117].

437 α -Linolenic acid is the precursor of the ω -3 polyunsaturated fatty acids with a longer chain
438 and a high degree of unsaturation, such as eicosapentaenoic acid (EPA: 20: 5 ω -3) and DHA, which
439 are found in seafood, especially fatty fish, and in fish oil supplements. It is important to note that the
440 α -linolenic concentration in the blood, cells, and tissues is significantly lower than that of the EPA
441 and DHA. This suggests that the primary biological function of α -linolenic is as a substrate in EPA
442 and DHA synthesis [118]. However, evidence shows that α -linolenic conversion into EPA and DHA
443 in humans is relatively low: conversion into EPA is estimated to only be around 8%–12% and
444 conversion into DHA is lower than 1% [119,120].

445 The beneficial effects resulting from an increased intake of ω -3 fatty acids were originally
446 associated with suppression of thrombosis. However, epidemiologic evidence suggests that the
447 intake of ω -3 fatty acids reduces the morbidity and mortality rates due to cardiovascular diseases, as
448 well as reducing systemic blood pressure, triacylglycerol concentrations and the risk of endothelial
449 dysfunction [27,121–126]. The capacity to lower triacylglycerol concentrations, which is related to
450 diminished hepatic VLDL secretion, stands out among the aforementioned possible metabolic effects
451 resulting from the intake of ω -3 fatty acids. This effect is partially dependent on mechanisms related
452 to nuclear receptors, particularly the peroxisome proliferator activated receptor (PPAR)- α [127].

453 An increased intake of ω -3 fatty acids results in the corresponding accumulation of these
454 fatty acids in cell membranes and circulating lipids. They replace ω -6 fatty acids (such as linoleic and
455 arachidonic acids) in blood lipids and in cell membranes and also modulate/activate different
456 signaling pathways [128].

457 The ω -3 and ω -6 polyunsaturated fatty acids generate relevant modulations in the
458 inflammatory response because they are precursors to different series of eicosanoids, which have
459 different effects on the intensity of the inflammatory response. Accordingly, ω -6 arachidonic acid
460 generates even-series eicosanoids, such as prostaglandin E₂ and leukotriene B₄. These eicosanoids
461 induce pro-inflammatory effects, such as increased vascular permeability, vasodilation, fever and
462 chemotaxis. It is important to note that prostaglandin E₂ also has anti-inflammatory effects, such as
463 reduced IL-1 and TNF- α production. EPA is the precursor for odd-series eicosanoids, such as
464 prostaglandin E₃, thromboxane A₃ and leukotriene B₅, which induce lower-intensity inflammatory
465 responses. Leukotriene B₅, for example, is 10 to 100 times less potent as a chemotactic agent in
466 neutrophils than leukotriene B₄ [23,27,129]. EPA also competes with arachidonic acid for COX-2 and

467 5-LOX; therefore, EPA reduces the synthesis of even-series eicosanoids [130]. In addition, higher
468 EPA and DHA concentrations in the plasma membrane favor the production of mediators such as
469 resolvins, maresins and protectins, which are involved in resolution of inflammation and healing
470 [21,25,131].

471 The ingestion of alpha-linolenic acid can also modulate on the inflammatory response in
472 humans. For example, Caughey et al. [132] observed a significant reduction of TNF- α , IL-1 β , TXB₂
473 and PGE₂ production by LPS-stimulated mononuclear cell cultures obtained from healthy subjects
474 who consumed approximately 14 g/d alpha-linolenic acid for 4 weeks compared to baseline and to a
475 control group. The effect of α -linolenic acid may have been mediated through its conversion to EPA.

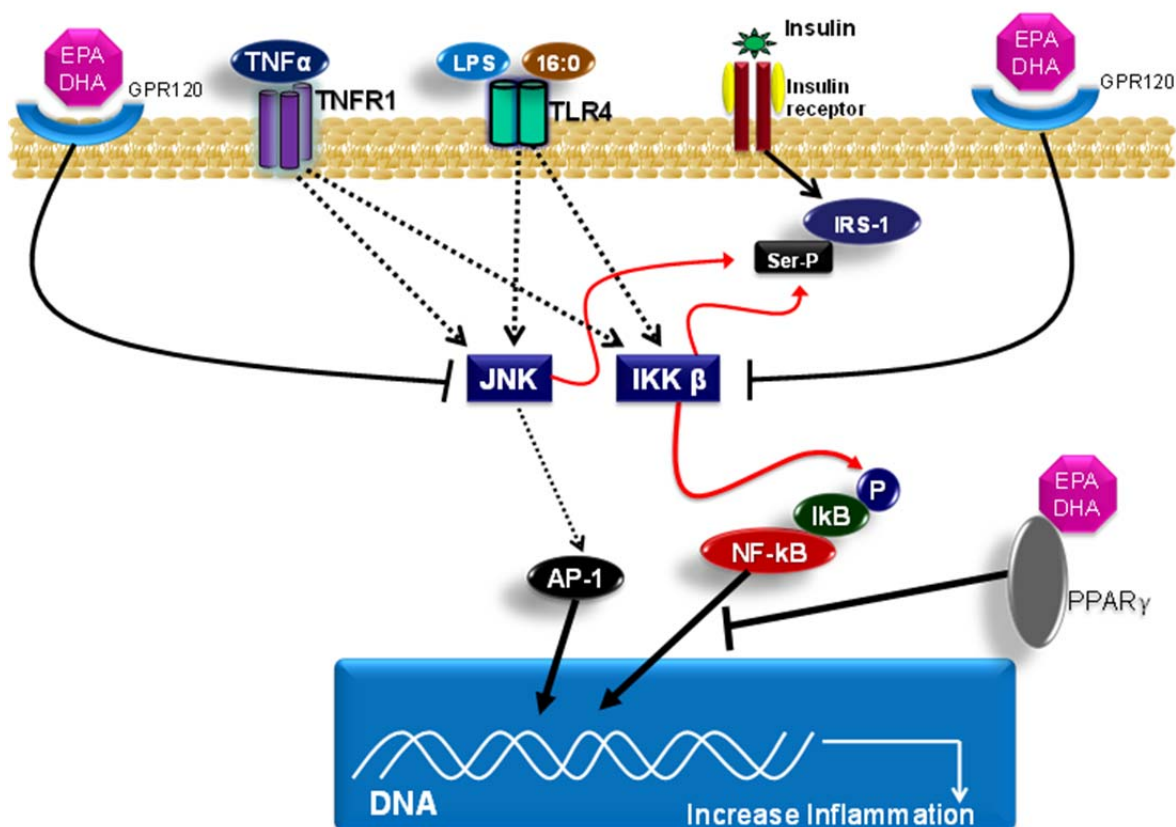
476 With regard to the molecular effects of EPA and DHA on inflammatory-response modulation,
477 studies have shown that these fatty acids inhibit the expression of inflammatory genes, such as
478 COX-2, iNOS and IL-1 in macrophages [103,108]. In contrast to the stimulating effect of saturated
479 fatty acids on TLR2 and TLR4 activation, EPA and DHA are capable of mitigating the activation of
480 the NF- κ B transcription factor pathway induced by various agonists [103,133,134]. Thus, DHA
481 reduces NF- κ B pathway activation and the expression of cytokines and COX-2 induced by TLR
482 agonists, such as lipopeptides (TLR2) and LPS (TLR4) in macrophages [89]. In addition, there is
483 reduced gene expression of COX-2 induced by LPS in monocytes from the peripheral blood of
484 individuals who use fish oil supplements [103,108]. The synthesis of the cytokines IL-1, IL-2 and
485 TNF- α was also mitigated after stimulation with LPS *in vitro* by mononuclear cells from the peripheral
486 blood from individuals supplemented with 18 g of fish oil per day for six weeks [135].

487 In addition, EPA and DHA present another mechanism to modulate the inflammatory
488 response by binding to G-protein coupled receptor 120 (GPR120) which is also known as free fatty
489 acid receptor 4 (FFA4). GPR120 activation induced by EPA or DHA leads to β -arrestin 2 recruitment
490 to the plasma membrane, where this protein binds to GPR120. Subsequently, the GPR120/ β -arrestin
491 2 complex is internalized into the cytoplasmic compartment, where this complex binds to the
492 TAK1-binding protein (TAB1). This process impairs the association between TAB1 and the kinase
493 activated by the growth factor beta (TAK1) and, consequently, results in reduced TAK1 activation
494 and in reduced activity of the IKK- β /NF- κ B and JNK/AP-1 signaling pathways. Accordingly, the
495 TAB1/TAK1 binding is a convergence point of stimuli induced by the TLR4 signaling pathway and
496 of the TNF receptor (TNFR). The mitigation of TAK-1 activation by DHA leads to reduced
497 expression of genes with pro-inflammatory actions, such as TNF- α and IL-6 [136,137].

498 Other mechanisms related to the EPA and DHA effects concern their capacities to bind to
499 peroxisome proliferator activated receptors (PPARs), including the isoforms PPAR-alpha,
500 PPAR-gamma and PPAR-beta/delta. PPARs are a group of nuclear receptors coded for by different
501 genes. PPAR isoforms form heterodimers with the retinoid X receptor (RXR) and bind to peroxisome
502 proliferator response elements (PPRE) in the region responsible for promoting the target genes
503 involved in lipid metabolism and in the inflammatory response; subsequently, they modulate the
504 expression of these genes [138]. PPAR-alpha and PPAR-gamma activations reduce the expression of
505 genes that code for proteins presenting pro-inflammatory actions through inhibition of NF- κ B
506 activation. It is worth emphasizing that EPA and DHA directly interact with PPARs and, therefore,
507 modulate the expression of genes involved in lipid metabolism and the inflammatory response
508 [139]. Furthermore, the anti-inflammatory effects of EPA and DHA on this signaling pathway can
509 occur due to diminished nicotinamide adenine dinucleotide phosphate (NADPH) oxidase activity,

510 which leads to lower TLR4 recruitment for lipid rafts and TLR4 dimerization [102]. Moreover, the
 511 lower NADPH oxidase activity also decreases the production of reactive oxygen species, which, in
 512 turn, are necessary to activate the TLR4 signaling pathway. Another possible mechanism of action of
 513 the ω -3 fatty acids concerns the capacity of incorporating DHA into the plasma membrane, which
 514 can lead to reduced TLR4 translocation for lipid rafts formation. This decreases TLR4 pathway
 515 activation and, consequently, decreases NF- κ B activation [102,140,141].

516 **Figure 3** shows the main molecular mechanisms related to the effects of saturated and
 517 omega-3 fatty acids on the TLR4 pathway.



518

519 **Figure 3.** Molecular mechanism of the effects of saturated (16:0) and omega-3 polyunsaturated fatty acids (EPA,
 520 DHA) on the TLR4 and NF κ B pathways. The arrows \rightarrow indicate activation and the arrows \vdash indicate inhibition.
 521 Abbreviations: TNF α , Tumor necrosis factor; TNFR1, Tumor necrosis factor receptor 1; LPS,
 522 Lipopolysaccharides; 16:0, palmitic acid; TLR4, Toll-like receptor 4; GPR120, G-protein coupled receptor 120;
 523 EPA, eicosapentaenoic acid; DHA, Docosahexaenoic acid; IRS-1, Insulin receptor substrate 1; Ser-P,
 524 phosphorylated *serine* residues; PPAR γ , Peroxisome proliferator-activated receptor gamma; JNK, c-Jun
 525 N-terminal kinases; IKK β , inhibitor of nuclear factor kappa-B kinase subunit beta; I κ B, NFKB Inhibitor; P,
 526 phosphate; AP-1, Activator protein 1.

527

528 5. Conclusions

529

530 The inflammatory process that occurs in obese people differs from the classical
 531 inflammatory response in certain respects. This inflammatory process manifests itself systemically
 532 and is characterized by a chronic low-intensity reaction. In this context, the TLR4 signaling pathway

533 has been recognized as one of the main triggers in increasing the obesity-induced inflammatory
534 response. This pathway responds to increased exposure to saturated fatty acids and to LPS. Both of
535 these are relevant in the context of obesity, with saturated fatty acids arising from within the adipose
536 tissue triglyceride stores and the LPS arising from increased intestinal permeability perhaps due to
537 an altered gut microbiota. Adipose tissue driven inflammation increases insulin resistance both
538 locally and systemically, so contributing to the co-morbidities of obesity like DM2. Studies indicate
539 that omega-3 fatty acids, namely EPA and DHA, have an anti-inflammatory effect, which involves
540 attenuating the activation of the TLR4 signaling pathway. This has relevant implications for
541 reducing meta-inflammation and, consequently, resistance to insulin action and risk of DM2 and
542 cardiovascular disease in obese individuals. The omega-3 fatty acids can oppose the action of both
543 classic TLR agonists (e.g. LPS) and saturated fatty acids in this regard.
544

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550

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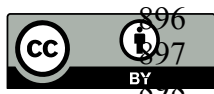
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