Microbial translocation is associated with the increased risk of cardiovascular disease in HIV-infected individuals. There is scarce information regarding the possible associations between the biomarkers of microbial translocation, inflammation and cardiovascular risk that can be evaluated in clinical laboratories using plasma or serum samples. This systematic review was conducted according to the PRISMA protocol in order to verify the most used soluble biomarkers of microbial translocation, inflammation and cardiovascular risk, as well as possible associations between them, in HIV-infected individuals. A search was performed using the Medline, Scopus and Web of Science databases to identify existing studies regarding the relationship between microbial translocation biomarkers, inflammation and cardiovascular risk in HIV-infected patients. Eleven articles that presented soluble biomarkers of microbial translocation (LPS, rDNA, sCD14, LBP and EndoCAb) were selected. The most frequently evaluated soluble biomarker was sCD14, followed by LPS; the latter were associated with some lipid profile parameters. This systematic review considered soluble blood biomarkers that can be utilized in laboratory diagnosis. The aim was to identify the interconnection between microbial translocation, inflammation and cardiovascular risk. Despite the fact that a large number of inflammation and cardiovascular risk biomarkers have been previously reported, it was noted that important markers involved in the pathophysiology of cardiovascular diseases need to be included in future research.

**Keywords:** Microbial translocation. Inflammation. Cardiovascular risk. HIV. Biomarkers.

INTRODUCTION

Cardiovascular disease is classified as a major cause of morbidity and mortality in HIV-infected individuals (Palella, Phair, 2011). Evidence indicates that systemic inflammation and chronic immune activation are related to increased cardiovascular risk (Grinspoon, 2014). Previous studies have suggested that these mechanisms can be triggered by the microbial translocation of products from the gut to the systemic circulation due to damage in the intestinal epithelium during the progression of HIV infection (Brenchley et al., 2006).

Microbial translocation can be evaluated in plasma by the direct quantification of bacterial products such as the presence of lipopolysaccharides (LPS) (components of gram-negative bacterial cell wall), peptidoglycans (components of gram-positive bacterial cell wall), or bacterial DNA fragments (such as rDNA - ribosomal bacterial DNA) (Lichtfuss et al., 2011).

In addition, the presence of LPS in plasma promotes the hepatic synthesis of the LPS-binding protein (LBP) responsible for the increased binding of LPS to the CD14 co-receptor, adjacent to the toll-like receptor 4 (TLR-4), which is expressed on the surface of monocytes and macrophages (Plöciennikowska et al., 2015).
the binding of LPS to the CD14 co-receptor occurs, these blood cells secrete soluble CD14 (sCD14) into the circulation (Płociennikowska et al., 2015). Therefore, the measurement of LBP and sCD14 can indirectly identify the effects of microbial translocation (Lichtfuss et al., 2011).

Another indirect biomarker of microbial translocation is related to the active protection of antibodies (such as EndoCAb/Endotoxin core antibodies) to neutralize LPS and its effects as a potent immunological activation molecule, thus limiting the effects of microbial translocation (Marchetti, Tincati, Silvestri, 2013).

After the activation of TLR-4 receptors by LPS binding, immune system cells trigger a signaling cascade, which leads to the production of proinflammatory cytokines (i.e. interleukin-1β, interleukin-6, tumor necrosis factor and type I interferons) (Meng, Lowell, 1997; Sandler et al., 2011; Zanoni, Granucci, 2013) and may induce chronic inflammatory conditions such as the development of atherosclerosis (Płociennikowska et al., 2015).

Several studies have demonstrated the use of biomarkers of microbial translocation, inflammation and cardiovascular risk (Blodget et al., 2012; Yong et al., 2016; Ballegaard et al., 2017). However, information regarding possible associations between these biomarkers, which could be evaluated in clinical laboratories using plasma or serum samples, are scarce (Kelesidis et al., 2012). Therefore, a systematic review was conducted to verify the most used soluble biomarkers of microbial translocation, inflammation and cardiovascular risk, as well as the possible associations between them in HIV-infected individuals.

MATERIAL AND METHODS

Literature search

This systematic review was performed according to the Preferred reporting items for systematic reviews and meta-analyses - PRISMA (Liberati et al., 2009) checklist. We systematically searched electronic databases, including Medline, Scopus and Web of Science, to identify potential studies that examined the relationship between soluble biomarkers of microbial translocation, inflammation and cardiovascular risk in HIV-infected individuals. The following search terms: (HIV or human immunodeficiency virus or AIDS); and (microbial translocation); and (cardiovascular diseases) were used for the literature search. The search terms were limited to titles and abstracts. Publications were restricted to the following languages: English, Portuguese and Spanish. The databases were searched for studies published until December 2017.

Study selection

The following criteria were applied to identify eligible studies for this systematic review:

Firstly, the studies were screened on the basis of title and abstract. The following inclusion criteria were considered: i) case-control studies, cross-sectional cohort, longitudinal cohort and clinical trials; ii) studies that determined soluble biomarkers for microbial translocation, inflammation and cardiovascular risk (i.e. biomarkers that can be evaluated in plasma or serum). The following exclusion criteria were considered: i) review studies; ii) studies of HIV-infected individuals under the age of 18; iii) animal studies; and iv) in vitro studies.

Secondly, full-text articles were evaluated; those which did not present any relationship between soluble biomarkers of microbial translocation, inflammation and cardiovascular risk were excluded (Figure 1).

Data extraction

Using a standardized data extraction form, the following data were extracted from the retrieved full-text articles: country; year of publication; study design; sample size; gender; age; CD4+ T cell count; percentage of participants in antiretroviral therapy (ART); soluble biomarkers of microbial translocation, inflammation and cardiovascular risk assessed; laboratory methods for the biomarkers; and relationship between the biomarkers.

Critical analysis of the included studies

The selected articles were evaluated regarding the level of scientific evidence according to the Oxford Center for Evidence-Based Medicine Classification (Phillips et al., 2009). Two researchers independently performed all the stages of research and any discrepancies were discussed at a consensus meeting between two reviewers.
Analysis of results

Given the heterogeneity of the studies, especially the evaluation of the biomarkers in different groups and subgroups of HIV-infected individuals, the results were presented using descriptive statistics (mean ± standard deviation, number, and percentage).

The evaluations of possible associations between the biomarkers were divided into groups according to each microbial translocation biomarker identified in the studies. The extraction of the association results between the biomarkers was performed in the following order: i) multivariable regression analysis; ii) univariable regression analysis; and iii) correlation; if they were not reported, data were extracted from the relationship between the presence of microbial translocation and changes in biomarkers of inflammation and cardiovascular risk. The results were reported as follows: positive association; inverse association; and no association, or no data.

RESULTS AND DISCUSSION

The literature search produced 180 articles; 22 articles were screened using full-text, and 11 articles were eligible for data extraction (Figure 1). The characterization of the selected studies is set out in Table I. The results showed that most of the analyzed studies (45.5%) were conducted in the United States of America (Sandler et al., 2011, 2014; Kelesidis et al., 2012; Steele...
et al., 2014; Timmons et al., 2014). Three studies (27.3%) were performed in Denmark (Pedersen et al., 2013, 2014; Haissman et al., 2017); two (18.2%) in Spain (Reus Bañuls et al., 2014; Leon et al., 2017); and one in the Netherlands (9.1%) (van den Dries et al., 2015). All the studies were published between 2011 and 2017.

The most frequent study design was cross-sectional cohort (54.6%) (Pedersen et al., 2013, 2014; Reus Bañuls et al., 2014; Steele et al., 2014; Timmons et al., 2014; Haissman et al., 2017), followed by longitudinal cohort (18.2%) (Kelesidis et al., 2012; van den Dries et al., 2015); case-control (18.2%) (Sandler et al., 2011; León et al., 2017); and only one clinical study (9.1%) (Sandler et al., 2014) (Table I). Therefore, the majority of studies (73%) were classified as Level 2 of scientific evidence (Kelesidis et al., 2012; Pedersen et al., 2013, 2014; Reus Bañuls et al., 2014; Steele et al., 2014; Timmons et al., 2014; van den Dries et al., 2015; Haissman et al., 2017; León et al., 2017) (Table II) according to the Oxford Center for Evidence-Based Medicine Classification (Table I).

**TABLE I** - Metal mass concentrations, in mg·g⁻¹, of dried cell mass at the three groups: Zero-control, M-control, and Gd-Glu for incubation times of 30 and 50 min

<table>
<thead>
<tr>
<th>Group Specification</th>
<th>Incubation time [min]</th>
<th>30</th>
<th>50</th>
</tr>
</thead>
<tbody>
<tr>
<td>Zero-control</td>
<td></td>
<td>0.0 (n.d)</td>
<td>0.0 (n.d)</td>
</tr>
<tr>
<td>M-control</td>
<td></td>
<td>-</td>
<td>2780 ± 440 (Uc)</td>
</tr>
<tr>
<td>Gd-Glu group</td>
<td></td>
<td>13404 ± 2104</td>
<td>11347 ± 2742</td>
</tr>
</tbody>
</table>

A total of 1,769 HIV-infected individuals were included. The demographic characteristics (gender and age), clinical data regarding HIV infection (CD4 + T cell counts, and use of antiretrovirals), and information regarding the biomarkers of microbial translocation, inflammation and cardiovascular risk are set out in Table II.

The majority of the studies showed a prevalence of males; more than 50% of the population consisted of men, with a mean age of 46.50 ± 4.70 years (Table II). The mean CD4 + T cell count was 532 ± 107 cells/mm³ and the use of ART (antiretroviral therapy) was observed in 10 (90.9%) studies (Sandler et al., 2011; Kelesidis et al., 2012; Pedersen et al., 2013, 2014; Reus Bañuls et al., 2014; Steele et al., 2014; Timmons et al., 2014; van den Dries et al., 2015; Haissman et al., 2017; León et al., 2017) (Table II).

Figure 2 shows the number of studies that evaluated biomarkers of microbial translocation, inflammation, and cardiovascular risk. The soluble microbial translocation biomarkers that were studied were LPS, rDNA, sCD14, LBP and EndoCAb. The most frequently evaluated biomarker was sCD14, which was used in 10 (90.9%) studies (Sandler et al., 2011, 2014; Kelesidis et al., 2012; Pedersen et al., 2014; Reus Bañuls et al., 2014; Steele et al., 2014; Timmons et al., 2014; van den Dries et al., 2015; Haissman et al., 2017; León et al., 2017), followed by the detection of LPS in nine (81.8%) studies (Sandler et al., 2011, 2014; Kelesidis et al., 2012; Pedersen et al., 2013, 2014; Steele et al., 2014; Timmons et al., 2014; van den Dries et al., 2015; Haissman et al., 2017; León et al., 2017) (Table II). The biomarker rDNA was reported in three (27.3%) studies (Sandler et al., 2011; Reus Bañuls et al., 2014; León et al., 2017). EndoCArb was reported in two (18.2%) studies (Sandler et al., 2011, 2014), and

**TABLE II** - Attributions of the m/z signals in the spectrum of the Gd-Glu solution, the relative abundance in ESI-MS, the specification of theoretical assignment of the chemical formula, nominal mass (a.m.u) estimation and possible ion species in the complex formation

<table>
<thead>
<tr>
<th>m/z</th>
<th>Relative Abundance (%)</th>
<th>Theoretical assignment</th>
<th>MW (a.m.u)</th>
<th>Proposed species</th>
</tr>
</thead>
<tbody>
<tr>
<td>516</td>
<td>26</td>
<td>C₁₂H₂₀O₁₂Gd</td>
<td>515.54</td>
<td>[Gd(Glu)₂ - 2H]⁺</td>
</tr>
<tr>
<td>552</td>
<td>100</td>
<td>C₁₂H₂₃O₁₂GdCl</td>
<td>552.00</td>
<td>[Gd(Glu)₂Cl - H]⁺</td>
</tr>
<tr>
<td>696</td>
<td>34</td>
<td>C₁₉H₁₆O₁₆Gd</td>
<td>695.69</td>
<td>[Gd(Glu)₂ - 2H]⁺</td>
</tr>
<tr>
<td>923</td>
<td>12</td>
<td>C₁₅H₂₁O₁₆Gd₂Cl₂</td>
<td>922.84</td>
<td>[Gd₂(Glu)₂Cl₂ - 3H]⁺</td>
</tr>
</tbody>
</table>
LBP was reported in two (18.2%) studies (Sandler et al., 2014; van den Dries et al., 2015) (Figure 2).

A large number of biomarkers of inflammation and cardiovascular risk were used. The use of CRP (C-reactive protein) was prominent and it featured in six studies (54.5%) (Sandler et al., 2011, 2014; Kelesidis et al., 2012; Pedersen et al., 2014; Steele et al., 2014; Haissman et al., 2017). The use of IL-6 was reported in five (45.4%) studies (Sandler et al., 2011, 2014; Reus Bañuls et al., 2014; Steele et al., 2014; León et al., 2017).

The results of the present study are in accordance with a previous literature review that highlighted i) LPS and rDNA as the main biomarkers for microbial translocation; ii) LBP, sCD14 and EndoCAb for response to bacterial products; and iii) CRP, IL-6 and D-dimer for inflammation/activation immunity (Lichtfuss et al., 2011). However, the aforementioned review did not demonstrate any association between the biomarkers of microbial translocation, (Lichtfuss et al., 2011).

The associations between sCD14, inflammation biomarkers and cardiovascular risk are presented in Figure 3; sCD14 showed a more frequent positive association with CRP (Sandler et al., 2011, 2014; Kelesidis et al., 2012; Steele et al., 2014) and IL-6 (Sandler et al., 2011, 2014; Reus Bañuls et al., 2014; Steele et al., 2014) in four studies (36.4%), and with triglycerides in two studies (18.2%) (Kelesidis et al., 2012; Timmons et al., 2014). However, there was an inverse association with HDL-C in one study (9.1%) (Timmons et al., 2014) (Figure 3).

The association of sCD14 with CRP, IL-6 and triglycerides, demonstrates the interconnection between microbial translocation, inflammation and CVD, considering that sCD14 is produced by monocytes in response to lipopolysaccharide stimulation (Zanoni, Granucci, 2013); CRP and IL-6 are traditional biomarkers of systemic inflammation and cardiovascular risk (Ridker, 2003; Sarwar et al., 2012), and triglycerides...
are a source of energy for macrophages (Kelesidis et al., 2012), as well as an independent risk factor for CVD (Cullen, 2000).

The associations between LPS and the biomarkers of inflammation and cardiovascular risk are presented in Figure 4. LPS was only positively associated with the lipid profile: triglycerides (18.2%) (Pedersen et al., 2013; Timmons et al., 2014); cholesterol (9.1%) (Pedersen et al., 2013); and LDL-C (9.1%) (Pedersen et al., 2013) (Figure 4).

Regarding rDNA (one of the microbial translocation biomarkers), there was a positive association with IL-6 in two (18.2%) studies (Reus Bañuls et al., 2014; León et al., 2017), and with TNF-α in one study (9.1%) (Reus Bañuls et al., 2014). LBP showed a positive association with CRP and IL-6 (Sandler et al., 2014), whereas EndoCAb had no association with biomarkers of inflammation and cardiovascular risk.

Microbial translocation biomarkers were also evaluated for associations with each other; only one study showed a correlation between LPS and sCD14 (van den Dries et al., 2015). In most of the studies there was no correlation between LPS and sCD4; LBP and sCD14; LPS and LBP; sCD14 and EndoCAb; and LPS and EndoCAb (Kelesidis et al., 2012; Pedersen et al., 2014; Sandler et al., 2014; Steele et al., 2014; van den Dries et al., 2015).

With regard to the methodology that was employed, plasma levels of sCD14 were evaluated by ELISA (enzyme-linked immunosorbent assay) and LPS was evaluated by using limulus amebocyte lysate (LAL) (Table II). The most frequently used method to quantify LPS in plasma is LAL, which utilizes a series of enzymatic reactions that mimic the coagulation cascade (Lichtfuss et al., 2011). However, this assay can easily show high sensitivity and contamination during sample preparation (Lichtfuss et al., 2011). In addition, enzymatic reactions critically depend on time and temperature, and may be affected by numerous inhibitors that are present in plasma (Lichtfuss et al., 2011).
Association between soluble biomarkers - microbial translocation, inflammation and cardiovascular risk in HIV-infected individuals: a systematic review

Furthermore, the heterogeneity present in the structure, solubility, physical state and bioactivity of LPS pose important limitations in the interpretation of plasma endotoxin tests (Munford, 2016). Thus, the association of plasma endotoxin levels with inflammatory markers has been inconsistent (Munford, 2016). Consequently, unlike LPS, which has significant limitations, the quantification of sCD14 is highly reproducible and can be used reliably (Lichtfuss et al., 2011).

Other biomarkers of inflammation and cardiovascular risk that were associated with sCD14 were: tumor necrosis factor-alpha (TNF-α) (Reus Bañuls et al., 2014); asymmetric dimethylarginine (ADMA) and its symmetrical dimethylarginine stereoisomer (SDMA) (Pedersen et al., 2014); trimethylamine-N-oxide (TMAO) (Haissman et al., 2017); and serum amyloid A and D-dimer (Sandler et al., 2011). However, these data were reported only once and should be interpreted with caution (Figure 3).

The only association found by van den Dries et al. (2015) was a correlation between the biomarkers of microbial translocation, sCD14 and LPS \( (r = 0.255; p = 0.003) \); however, there was a weak trend toward positive correlation between plasma levels of sCD14 and von Willebrand factor (vWF) \( (r = 0.184; p = 0.078) \), which is related to increased cardiovascular events (Kato et al., 2018). There was no correlation between the vWF and LPS; vWF and LBP; sCD14 and LBP; and LPS and LBP (van den Dries et al., 2015). TMAO, which is a metabolite of the intestinal microbiota and is considered to be a biomarker for CVD risk independent of the traction risk factors (Bergeron et al., 2016), was evaluated by Haissman et al. (2017), who demonstrated the association of sCD14 with TMAO (univariable regression, \( r = 0.381; p = 0.008 \) ) in untreated HIV-infected individuals, but not in HIV-infected individuals on ART. However, no association between LPS and TMAO was found (Haissman et al., 2017). In the multivariate regression models, sCD14 remained an...
independent predictor of TMAO after adjusting for age, gender, smoking and viral load (Haissman et al., 2017). It should be noted that a recent study demonstrated that TMAO was associated with increased risk of carotid plaques in HIV-infected patients, and also exhibited a correlation with the sCD14 biomarker (Shan et al., 2018).

Kelesidis et al. (2012) observed associations between the levels of sCD14 with hs-CRP levels (p < 0.001) and triglycerides ≥ 150 mg/dL (p = 0.027) using univariable regression analysis. The results for multivariate regression were similar. However, there was no change in LPS levels over time within the study groups, and there was no association with sCD14, which was probably due to the individual variability of the host response to LPS rather than the amount of LPS in the activation of macrophages (Kelesidis et al., 2012).

Nevertheless, when the aforementioned study evaluated atherosclerosis using ultrasonographic measurement of the carotid artery intima-media thickness, it was found that sCD14 and LPS biomarkers were associated with the progression of subclinical atherosclerosis, providing a potential unifying etiology for the increased risk of cardiovascular disease in HIV-infected individuals (Kelesidis et al., 2012).

Leon et al. (2017) used ribosomal bacterial DNA (rDNA) as a microbial translocation biomarker; they demonstrated that the relationship between the presence of rDNA and the level of IL-6. HIV-infected individuals with microbial translocation had significantly (p = 0.001) higher median values [34 (17–51) pg/mL] of IL-6 compared to individuals without microbial translocation [4.9 (2.4–6.2) pg/mL] (León et al., 2017).

Pedersen et al. (2013) presented the results for the biomarkers from 50 HIV-infected individuals divided into tertiles (17, 16 and 17 individuals, respectively) according to the level of LPS [46.1 (43.2 to 49.1) pg/mL, 62.4 (60.0 to 64.7) pg/mL and 84.7 (72.0 to 97.5) pg/mL, respectively]. The highest level of triglycerides was found in the third tertile compared to the first and second tertiles (p = 0.006 and p = 0.046, respectively) (Pedersen et al., 2013). In addition, total cholesterol was higher in the second and third tertiles compared to the first tertile (p = 0.022 and p = 0.016, respectively). LDL-C was higher in the second and third tertiles compared to the first tertile (p = 0.009 and p = 0.002, respectively) (Pedersen et al., 2013). There was no difference in the HDL-C concentrations. Significant associations between LPS and lipids were found: triglycerides (r = 0.450, p = 0.001); total cholesterol (r = 0.147, p = 0.005); and LDL-C (r = 0.110, p = 0.018) (Pedersen et al., 2013).

Another study by Pedersen et al. (2014) demonstrated a correlation between sCD14 and ADMA and SDMA (r = 0.38, p = 0.008 and r = 0.51, p < 0.001, respectively), which are biomarkers of endothelial dysfunction and contribute to the impairment of endothelial function by the inhibition of nitric oxide (NO) synthesis. In contrast, LPS did not correlate with ADMA or SDMA (r = -0.02, p = 0.900 and r = 0.02, p = 0.889, respectively) (Pedersen et al., 2014). Furthermore, this study did not demonstrate associations between sCD14, LPS, hs-CRP and D-dimer (Pedersen et al., 2014).

Reus Bañuls et al. (2014) demonstrated that HIV-infected individuals treated with ART, and with higher values of IL-6 and TNF-α inflammatory markers, had a higher frequency of bacterial translocation and a history of cardiovascular disease. In addition, the aforementioned study demonstrated a correlation between sCD14 and IL-6 and TNF-α (r = 0.28; p = 0.01; r = 0.40, p < 0.001, respectively). This article also demonstrated the association (multivariate and univariate regression model) of high inflammatory markers with rDNA, sCD14 and cardiovascular events (Reus Bañuls et al., 2014). However, in the multivariate analysis, the IL-6 and TNF-α values were only independently associated with the presence of bacterial DNA (Odds Ratio 62, p = 0.0001) and history of cardiovascular events (Odds Ratio 25, p = 0, 01) (Reus Bañuls et al., 2014).

A study by Sandeler et al. (2011) found that a high percentage of HIV-infected individuals undergoing ART presented an undetectable viral load, and the biomarker levels were studied by comparing individuals with HIV RNA levels ≤ 400 copies/mL (n = 420) with those with HIV RNA levels > 400 copies/mL (n=155). In the group of individuals with HIV RNA levels ≤ 400 copies/mL, sCD14 was correlated to IL-6 (r = 0.18, p < 0.001), serum amyloid A (r = 0.16, p < 0.001), hs-CRP (r = 0.10, p = 0.04) and D-dimer (r = 0.11, p = 0.03). In contrast, in the individuals with detectable levels of HIV RNA, sCD14 was correlated to IL-6 (r = 0.26, p < 0.001), serum amyloid A (r = 0.18, p = 0.004) and hs-CRP (r = 0.18, p = 0.005) (Sandler et al., 2011).

This study examined the association between microbial translocation markers and inflammation in the untreated subset (n = 117), with a correlation of sCD14 with IL-6 (r = 0.35, p < 0.001) and D-dimer (r = 0.26, p = 0.006) (Sandler et al., 2011). However, these results should be interpreted with caution because the
number of individuals evaluated for the biomarkers did not represent the sample of the total of individuals enrolled in the study. Furthermore, the effects of ART on intestinal permeability and immune response to microbial products are not well characterized.

Another study by Sandler et al. (2014) showed no correlation between the microbial translocation biomarkers LPS, sCD14, and EndoCAb. However, levels of the acute phase proteins LBP, IL-6 and CRP were significantly correlated with each other (Sandler et al., 2014).

Steele et al. (2014) presented associations between sCD14 and hs-CRP ($r = 0.292, p = 0.008$) and IL-6 ($r = 0.418, p < 0.0001$) in HIV-infected individuals. However, there was no association with the intestinal fatty acid binding protein (iFABP) ($r = -0.019, p = 0.870$) (Steele et al., 2014). Regarding the biomarker of LPS microbial translocation, there was a tendency for a positive correlation with hs-CRP ($r = 0.206, p = 0.076$) and IL-6 ($r = 0.209, p = 0.089$) but none reached statistical significance in this cohort (Steele et al., 2014). In addition, the LPS biomarker did not correlate with sCD14s ($r = 0.186, p = 0.112$) (Steele et al., 2014).

Timmons et al. (2014) evaluated the associations of biomarkers for all HIV-infected individuals included in the study. Moreover, they investigated the markers for each subgroup of the two cohorts that were evaluated. Regarding the total population of HIV-infected individuals, there was a positive correlation between LPS and triglycerides ($n = 167, r = 0.32, p < 0.01$), and a negative correlation between sCD14 and HDL-C ($n = 166, r = -0.21, p < 0.01$) (Timmons et al., 2014). The group of the AIDS clinical trial group cohort, before ($n = 81, r = 0.35, p < 0.01$) and after treatment ($n = 79, r = 0.81, p < 0.01$) presented a correlation between LPS and triglycerides (Timmons et al., 2014). However, the Indiana University cohort presented associations only for the ART group, with a positive correlation for LPS and sCD14 with triglycerides ($n = 40, r = 0.33, p = 0.04$; $n = 42, r = 0.35, p < 0.02$; respectively) and a negative correlation between sCD14 and HDL-C ($n = 41, r = -0.32, p < 0.04$) (Timmons et al., 2014). Although these results are relevant, they should be carefully considered because the number of individuals evaluated for the biomarkers did not represent the sample of the total individuals enrolled in each subgroup of the study.

This systematic review summarized the main biomarkers of microbial translocation, inflammation and cardiovascular risk that are currently used, as well as the possible associations between them in HIV infection. The strong point of this review for clinical practice was the finding that, of all the biomarkers of microbial translocation, sCD14 showed a greater association with the biomarkers of inflammation and cardiovascular risk.

However, it is necessary to consider some of the limitations of this systematic review, such as the methodological differences between the various studies, especially with respect to the assessment of the biomarkers in different groups and subgroups of HIV-infected individuals. It is important to note that the results of the associations between biomarkers may be influenced by differences in the populations of HIV-infected individuals evaluated in the studies. In addition, several studies did not evaluate the biomarkers relative to the total HIV-infected population included in the study.

This systematic review considered the soluble blood biomarkers that can be inserted in clinical laboratory routines for the purpose of diagnosis, as well as their connections with microbial translocation, inflammation and cardiovascular risk. Despite the fact that a large number of inflammation and cardiovascular risk biomarkers have been reported, especially CRP and IL-6, it is clear that important markers involved in the pathophysiology of cardiovascular diseases need to be included in future research.

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