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Effects of bovine colostrum supplementation on upper respiratory illness in active males

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Conflict of Interest Statement

All authors declare that there are no conflicts of interest.

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Bovine colostrum (COL) has been advocated as a nutritional countermeasure to exercise-induced immune dysfunction and increased risk of upper respiratory illness (URI) in athletic populations, however, the mechanisms remain unclear. During winter months, under double-blind procedures, 53 males (mean training load ± SD, 50.5 ± 28.9 MET-h·week\(^{-1}\)) were randomized to daily supplementation of 20 g of COL (N = 25) or an isoenergetic/isomacronutrient placebo (PLA) (N = 28) for 12 weeks. Venous blood was collected at baseline and at 12 weeks and unstimulated saliva samples at 4-week intervals. There was a significantly lower proportion of URI days and number of URI episodes with COL compared to PLA over the 12 weeks (p < 0.05). There was no effect of COL on in vitro neutrophil oxidative burst, salivary secretory IgA or salivary antimicrobial peptides (p > 0.05), which does not support previously suggested mechanisms. In a subset of participants (COL = 14, PLA = 17), real-time quantitative PCR, targeting the 16S rRNA gene showed there was an increase in salivary bacterial load over the 12-week period with PLA (p < 0.05) which was not as evident with COL. Discriminant function analysis of outputs received from serum metabolomics showed changes across time but not between groups. This is the first study to demonstrate that COL limits the increased salivary bacterial load in physically active males during the winter months which may provide a novel mechanism of immune-modulation with COL and a relevant marker of in vivo (innate) immunity and risk of URI.

Keywords: URTI, innate immunity, mucosal immunity, microbiome, 16S rRNA, metabolomics
1. Introduction

It is now well established that exercise of a strenuous and/or prolonged nature can lead to significant transient perturbations of immune function (commonly referred to as immunodepression) which includes, but is not limited to, decreases in both cell-mediated and mucosal parameters (Nieman, 2007). This may result in an ‘open window’ during which risk of illness is increased (Nieman, 2000). Hence, if such exercise is performed on a regular basis, as with endurance athletes, and particularly in combination with other life stressors (e.g. inadequate nutrition, psychological stress) the overall risk can be substantially higher (Gleeson, 2007). The increase in the frequency and severity of symptoms of upper respiratory illness (URI) in athletes (e.g. sore throat, runny nose) has been attributed to such periods of heavy exertion (Walsh et al., 2011).

Bovine colostrum (COL) may be effective at alleviating recurrent URI in situations of immune deficiency (Patel and Rana, 2006). Previous evidence has shown that 8-10 weeks of COL supplementation can reduce the incidence of URI in physically active populations but the mechanism(s) behind such effects remains unclear (Brinkworth and Buckley, 2003; Crooks et al., 2010). Animal and in-vitro culture studies demonstrate that COL has a mediating effect on cell-mediated immunity by influencing the production of cytokines (Biswas et al., 2007; Boudry et al., 2007; Shing et al., 2009). Increasing concentrations of COL, in-vitro, has been shown to modulate cytokine production in peripheral blood mononuclear cells from resting, healthy individuals, to promote a Th1 profile (cell-mediated immunity) (Shing et al., 2009), which may suppress the binding of pathogens (e.g. rhinovirus) (Sethi et al., 1997). Direct effects of COL on leukocyte capacity are also supported by evidence of an
enhancement of phagocytosis and oxidative burst of polymorphonuclear cells (i.e. neutrophils) following short term culture with COL (Sugisawa et al., 2001, 2002, 2003). Sugisawa et al. (2003) proposed that in the presence of COL leukocytes become primed for subsequent activation by low-molecular weight substances (< 10 kDa) such as protease peptones.

Given the aforementioned effects of COL within inflammatory in vitro culture conditions, it may be expected that COL can act as a nutritional countermeasure to exercise-induced immunodepression. Our previous work suggests that 4 weeks of COL (20 g·day⁻¹) supplementation can limit the immunodepressive effects of an acute physical stressor (2 h of cycling) by enhancing neutrophil function (stimulated degranulation/elastase release) post-exercise (Davison and Diment, 2010). Within this study the modulatory effects of COL also extended to innate mucosal immunity by preventing the exercise-induced decrease of salivary lysozyme concentration and secretion.

Such findings may provide support to proposed mechanisms that some of the immune-modulatory effects of COL are due to bioactive components that become biologically available upon digestion of COL and prime leukocyte capacity (Davison, 2013). It is currently unclear whether longer term supplementation of COL and exposure to these priming agents also leads to changes in innate markers in athletes at rest. Crooks et al. (2006) demonstrated that longer periods of COL supplementation (i.e. 12 weeks) may be associated with significant increases in resting concentrations of salivary secretory IgA (sIgA), which is the only immune measure to date that has been consistently related to risk of URI in exercising populations (Walsh et al., 2011). Other studies have also seen improvements in resting sIgA concentrations with COL supplementation but have not monitored URI (Appukutty et al., 2010; Mero et al.,
To date, the majority of both longitudinal and cross-sectional exercise training studies have focused on changes in salivary slgA (Walsh et al., 2011). Although the importance of other salivary antimicrobial peptides (AMPs) (e.g. lysozyme, lactoferrin) for host defense have been recognized, they have received limited attention (West et al., 2006).

In addition to the presence of inducible factors such as AMPs at mucosal surfaces, protection from invading microorganisms is also provided by the diverse community of commensal microbes which colonize the upper respiratory tract (Blaser and Falkow, 2009; Bosch et al., 2013). Subsequently, disturbance of this respiratory microbial community can contribute to acquisition of new pathogens which may result in respiratory illness, particularly if host immunity is compromised (Murphy et al., 2009).

However, the effects of exercise and nutritional interventions on changes in the salivary microbiome have not previously been investigated.

The aims of this study were to investigate the effects of 12 weeks of COL supplementation on innate and mucosal immunity as well as the salivary microbiome in a population of males who engage in exercise training during the winter months. The study also aimed to determine whether any effects of COL on these parameters would also lead to a change in the incidence of URI. Given the potential involvement of a diverse array of biological pathways, we also undertook a metabolomic profiling approach on serum in an attempt to gain a more detailed understanding of any modulation of the immune system by COL.
2. Methods

2.1. Participants

Following both verbal and written details of the procedures, 57 male participants provided written informed consent for their inclusion within the study. The study was conducted in accordance with the Declaration of Helsinki principles and all procedures were approved by the Research Ethics Committee of Aberystwyth University. Participants were non-smokers, not taking medication or other supplements, free from any infectious illness for 4 weeks prior to the study and completing at least 3 h of moderate-vigorous endurance exercise per week. Participants were not limited in their use of mouthwash before and during the study period.

2.2. Supplementation

All 57 participants were randomly allocated into COL or placebo (PLA) groups with stratification by age and type of exercise training only. In a double blind manner, participants were asked to consume 20 g·day\(^{-1}\) (10 g prior to morning and evening meal) of COL (Neovite UK, London) or an isoenergetic/isomacronutrient PLA (as used in Davison and Diment, 2010) for 12 weeks. Four participants (COL = 3, PLA = 1) were lost due to lack of compliance with the study protocol (e.g. lack of training or supplement consumption due to injury, family bereavement or air travel). All participants who successfully completed the study (COL group, n = 25, age: 30.5 ± 13.8 years, height: 179.9 ± 6.4 cm, body mass: 77.2 ± 8.9 kg); PLA group, n = 28, age: 31.5 ± 13.2 years, height 178.4 ± 6.6 cm, body mass 74.5 ± 8.7 kg) commenced the study between September and December.
2.3. Monitoring of upper respiratory illness and training volume

Participants completed a health questionnaire (Gleeson et al., 2011, 2012) on a daily basis. This involved participants indicating if they were suffering from any of the illness symptoms listed on the questionnaire: sore throat, catarrh in the throat, runny nose, cough, repetitive sneezing, fever, persistent muscle soreness, joint aches and pains, weakness, headache, and loss of sleep. Upon reporting of any of the above symptoms, participants were asked to provide a subjective rating of the severity of symptoms (light, moderate, severe). As used previously (Fricker et al., 2005; Gleeson et al., 2011, 2012), these ratings of light, moderate and severe were given numerical scores of 1, 2 and 3 respectively for data analysis. At any given point during the 12 weeks, a total symptom score of ≥12 was used to indicate that an URI was present.

Each week, participants were asked to complete a standard short-form International Physical Activity Questionnaire (http://www.ipaq.ki.se/downloads.htm) to provide quantitative data of training loads in metabolic-equivalent (MET)-h week\(^{-1}\) (Craig et al., 2003). Participants were allowed unrestricted use of medication during episodes of URI but were asked to report such use and report how their training was affected by the URI (1 – training maintained, 2 – training reduced, 3 – training discontinued).

2.4. Blood sampling

Blood samples were drawn from an antecubital vein into 4 ml K\(_3\)EDTA (BD, Oxford, UK) and 6 ml plain (BD, Oxford, UK) vacutainers at baseline and 12 weeks following COL or PLA supplementation. All participants avoided strenuous exercise for 24 h prior to each visit and arrived at the laboratory following an overnight fast of at least 10 h. Blood collected in the K\(_3\)EDTA vacutainer was used for determination of total and differential leukocyte counts (Pentra 60C+, Horiba, Montpellier, France) and
neutrophil function. Blood collected in the 6 mL plain vacutainers was allowed to clot at room temperature for 1 h 20 min. Following centrifugation (1300 g for 10 min at 4°C), serum was stored at -80°C for later metabolomic analysis.

2.5. Neutrophil function

Whole blood from the EDTA vacutainers was stored at room temperature (no longer than 2 h) prior to measurement of in-vitro stimulated neutrophil oxidative burst activity response to formyl-leucyl-methionyl-phenylalanine (fMLP) using a commercially available chemiluminescence (CL) kit (ABEL, Knight Scientific Ltd, Plymouth, UK). The CL per well was measured by a microplate luminometer (FLUOstar OPTIMA, BMG Labtech, Aylesbury, UK). The contents of each microplate well that contained an fMLP stimulated sample were as follows: 20 µL of diluted whole blood (blood and Hank’s balanced salt solution; HBSS, without calcium and magnesium, at ratio of 1:100), 90 µL assay buffer (HBSS with calcium and magnesium), 50 µL Pholasin and 20 µL adjuvant K (substance that enhances the luminescence of Pholasin).

These mixtures were gently shaken and incubated at 37°C for 30 s in the luminometer, prior to the addition of 20 µL fMLP (10 µM) to provide an end total volume of 200 µL per well, a 1:1010 final blood dilution and a fMLP concentration of 1µM respectively. The unstimulated state was calculated as the mean CL of the well prior to addition of fMLP (45 s). Following addition of fMLP, area under the curve (over 300 s), above the stable unstimulated state was used to determine stimulated CL. To calculate responses on a per cell basis, it was assumed that the stimulated CL is entirely from neutrophils (Morozov et al., 2003). Thus, fMLP-stimulated area under the CL curve was divided by the number of neutrophils present in each well to give CL in RLU (i.e. oxidative burst) per neutrophil.
2.6. Serum metabolomics

To remove proteins before mass spectrometry, 20 µL of each serum sample was mixed with 30 µL of ice-cold ultrapure water and vortexed. 50 µL of ice-cold HPLC grade acetone (Fisher Scientific UK Ltd, Loughborough, UK) was then added and the mixture vortexed. Samples were left on ice for 30 min to allow protein precipitation, after which, they were centrifuged at 16 000 g for 10 min in a micro-centrifuge. After centrifugation, 50 µL of the supernatant was removed and transferred to a glass insert placed in a glass auto-sampling vial, to which 250 µL of ice-cold 70% (v/v) methanol (made up using HPLC grade methanol (Fisher Scientific UK Ltd.) and ultrapure water) was added. Seven control serum samples, from human male AB plasma (Sigma-Aldrich, Dorset, UK), were run simultaneously using the same protocol to act as machine and protocol controls.

Analysis was carried out using Direct Injection Electrospray Ionisation Mass-Spectrometry (DI-ESI-MS) on a Micromass LCT mass-spectrometer (Micromass/Waters Ltd., UK) in negative ionization mode where metabolites are singly ionized by the loss of H+. The polar extracts were reconstituted in 0.25 mL 30% [v/v] methanol: H₂O and 50 µL added to 200 µL inserts in 2 mL (Waters Ltd. UK) and introduced by direct-infusion (DI) at a flow rate of 0.05 mL min⁻¹ in 30% [v/v] methanol: H₂O running solvent. Data were acquired over the m/z range 100-1400 Th and were imported into MATLAB, binned to unit mass and then normalized to percentage total ion as stated in Johnson et al. (2007). Tentative identification of metabolites of interest was achieved through interrogation of the HMDB Serum Metabolome database (Psychogios et al., 2011).
### 2.7. Saliva sampling

Participants reported to the laboratory for a saliva sample at baseline and 4, 8 and 12 weeks following supplementation. All participants avoided strenuous exercise 24 h prior to each visit and arrived at the laboratory after an overnight fast of at least 10 h. For all saliva samples the mouth was rinsed with plain water at least 10 min before the collection period. To obtain the sample, the participant remained seated with the head tilted slightly forward and passively dribbling into a pre weighed 7 mL sterile bijou tube while keeping orofacial movement to a minimum. The final duration of collection was recorded and the tube was weighed again to allow for estimation of saliva flow rate when the density of saliva was assumed to be 1.0 g·mL⁻¹ as used in previous studies (Chicharro et al., 1998; Davison et al., 2009). With the use of a freezing point depression osmometer (Osmomat 030, Gonotec, GbBH, Berlin, Germany), saliva osmolality was determined to allow for concentration of salivary immunological parameters to be expressed relative to saliva osmolality and flow rate. Saliva samples were centrifuged for 5 min at 16000 g to allow separate storage (at -80°C) of the pellet and supernatant for later microbiome analysis and enzyme-linked immunosorbent assay (ELISA) respectively. Aliquots of saliva samples were thawed at room temperature only once prior to each ELISA. Following the thawing of saliva, samples were again centrifuged for 5 min at 16000 g to precipitate mucins and other debris and allow for the resulting clear supernatant to be analyzed.

### 2.8. Blood contamination

Aliquots of saliva were screened for blood contamination by the determination of salivary transferrin concentration using an ELISA kit (Salimetrics, State College, Pennsylvania, USA). If salivary transferrin concentration was greater than 1 mg·dL⁻¹,
the sample was considered to be contaminated with blood. If a sample at any timepoint was found to be contaminated, all salivary lysozyme (s-Lys) and lactoferrin (s-Lys) data for that participant were excluded from the study (this was not done for IgA as the ELISA was specific to sIgA, see below).

2.9. **Saliva sIgA**

The concentration of s-IgA (mg L\(^{-1}\)) was determined in all saliva supernatants following the protocol of Leicht et al. (2011). The sandwich ELISA approach was slightly modified to include a capture antibody specific to the secretory component of human IgA (Mouse anti-human IgA secretory, Merck Millipore, Darmstadt, Germany).

2.10. **Saliva antimicrobial peptides**

All participants who were free from any contaminated samples (COL = 22, PLA = 24) were assessed for changes in s-Lys and s-Lac. Measurements were performed according to manufacturer’s instructions using commercial available ELISA kits (Assaypro LLC, St-Louis, MO).

2.11. **Extraction of microbial DNA**

Microbial DNA was extracted from 200 µL of the salivary pellet at baseline and 12 weeks of 31 participants (COL = 14, PLA = 17) who all commenced the study late September/early October and completed the study late December/early January. Extraction was performed using a FastDNA SPIN Kit (MP Biomedical, Santa Ana, USA) following the manufacturer’s guidelines, except that bead beating was carried out using a FastPrep24 (MP Biomedical) machine with three cycles at speed setting 6.0 for 30 s, with cooling on ice for 60 s between each cycle. Extracted DNA was quantified using Epoch (BioTek, Winooski, USA) spectrophotometry. All extractions
were confirmed to have a 260/280 nm ratio of between 1.8 and 2.0 for quality control purposes.

2.12. 16S rRNA gene terminal restriction fragment length polymorphisms (T-RFLP)

Amplification of the 16S rRNA gene was accomplished through PCR using primers 27f (5’-AGA GTT TGA TCC TGG CTC AG-3’ with FAM labelled on 5’ end) and 1389r (5’-ACG GGC GGT GTG TAC AAG-3’) as described by Huws et al. (2011). All PCR products were verified using a 1.0% agarose gel. Triplicate reactions for each sample were pooled and purified using a QIAquick PCR purification kit (Qiagen, West Sussex, UK) following the manufacturer’s guidelines. 25 ng of purified PCR product for each sample was digested for 5 h at 37°C with restriction enzymes HaeIII and MspI (Promega, Madison, USA), in separate reactions. Restriction products were separated through size using an ABI PRISM1 377 Automated DNA Sequencer (Applied Biosystems, Warrington, UK). As there was an inability to sequence the 16S rRNA genes at one of the timepoints for 2 participants, peak profiles and Shannon Diversity Indexes were determined on 29 participants only (COL= 12, PLA= 17). Peak profiles were examined using Genemapper software (Version 3.7, Applied Biosystems). Those peaks with an estimated fragment size below 50 nucleotides were removed and the remaining data were modelled using FingerPrinting II software (BioRad, Hercules, USA). Shannon Diversity Indexes were determined using Fingerprint Analysis with Missing Data software (Version 1.2) (Schluter and Harris, 2006).

2.13. 16S rRNA Gene Quantitative PCR

Quantitative PCR was carried out on neat extracted DNA against standards created by amplifying the 16S rRNA gene of 5 randomly selected baseline samples. This used
1 µl of each sample in a PCR reaction using 27f and 1389r primers, as detailed above, except that the 27f primer did not have FAM on the 5’ end, to amplify the gene. The resulting PCR product was purified and quantified, as previously detailed, to estimate the total number of 16S rRNA gene copies and serial dilutions made to a $10^{-10}$ level. Serial dilutions of $10^{-0}$, $10^{-2}$, $10^{-4}$, $10^{-6}$, $10^{-8}$, and $10^{-10}$ were used in subsequent qPCR reactions using a C100 thermal cycler (BioRad) and CFX96 optical detector (BioRad), with data captured using CFX Manager software (BioRad). qPCR reactions were completed in 25 µl volumes consisting of 1X SYBR Green Mastermix (Applied Biosystems), 400 nM of each of the EubF forward (5’-GTG STG CAY GGT TGT CGT CA-3’) and EubR reverse (5’-ACG TCR TCC MCA CCT TCC TC-3’) primers, as detailed by Kim et al. (2008) and 3 µl of neat DNA. The final volume was made up with PCR grade water (Roche, Hertfordshire, UK).

2.14. Microbial Growth Curve Analysis

To ascertain the antimicrobial properties of each supplement, 10 µl of a 50 g L$^{-1}$ (w/v) solution of COL or PLA (made using autoclaved ultrapure water), were cultured with 200 µL of artificial saliva medium and 10 µL of a salivary microbial culture as previously described by McBain et al. (2003). In addition, 10 µL of the COL and PLA solutions were incubated with 200 µL of artificial saliva medium, without the addition of the salivary microbial culture, to determine the level of microbial load for each solution. These cultures, alongside appropriate positive and negative growth controls, were incubated in a CellStar tissue culture 96 well plate with flat bottom and lid (Greiner Bio-one, Nürtingen, Germany) in a BioTek ELx808 microplate reader (BioTek Instruments, Winooski, USA) set at 37°C for 72 h. An optical density reading was taken every 20 min at a 630 nm wavelength, before which, the plate was shaken for 5 s.
Kinetic read data was exported from the Gen5 software package (BioTek Instruments) and corrected to a baseline (the first reading taken for each of the 96 wells). To allow for log transformation of the raw data, all data points, after baseline correction, were added to 10. The $\log_{10}$ value for each data point was then calculated. After 3 replicate 96 well plates were completed, the mean and standard deviation for each growth condition, across all 3 plates, was calculated.

2.15. Statistical analyses

Data shown in the text, tables and figures are presented as mean values and standard deviation unless stated otherwise. Statistical analysis of all data were performed via the statistical computer software package SPSS (v20.00; SPSS Inc., Chicago, IL, USA) unless stated otherwise. Statistical significance was accepted at $P < 0.05$. All immunological parameters were checked for normal distribution using the Shapiro-Wilk test. Data not normally distributed (leukocyte counts, stimulated neutrophil oxidative burst, sIgA and sLys) were normalized with log transformation before further analysis. Initially, a 2 factor mixed model ANOVA (group × time) was carried out on all immunological measures, 16S rRNA (salivary bacterial load) and total peak number for HaeIII and MspI (salivary bacterial diversity) to determine if the effect of time was different between COL or PLA groups. Any significant main effects identified in the ANOVA were further analyzed by post-hoc paired t-tests with Holm-Bonferroni correction. Independent t-tests were used to determine differences between groups at baseline and 12 weeks in Shannon Diversity Indexes for TFRLP (HaeIII and MspI). Data for the proportion of reported URI days and proportion of participants who suffered URI over the 12 weeks between the COL and PLA groups were assessed by
chi-squared test. To also examine the time-course of any effect of COL, chi-squared analyses of URI at 4 week intervals were performed, in accordance with the timing of saliva collections in the current study and the methods of Crooks et al. (2006, 2010). Chi-squared analysis was also used to assess proportion of participants within COL or PLA who reported use of medication or a negative effect on training load (reduced or prevented) during URI episodes. Comparisons between COL and PLA groups for mean number of self-reported URI episodes, mean duration of URI, mean severity of URI and mean weekly training loads were performed with an independent \( t \)-test.

Metabolite data was analyzed through multivariate statistics, including principal component analysis and discriminant function analysis (DFA), using PyChem software (Jarvis et al., 2006) and following accepted Metabolomics Standard Initiative procedures (Sansone et al., 2007). Those whole mass unit bins which had a DFA loading of more than 2 standard deviations from the mean were selected for tentative identification. Determination of change from baseline for each whole mass unit bins was determined using 1-way ANOVA.

3. Results

3.1. Training load

Analysis of IPAQ questionnaires showed no significant differences between COL (53.1 ± 6.0 MET·h·week\(^{-1}\)) and PLA (48.2 ± 5.4 MET·h·week\(^{-1}\)) groups for weekly training volume at moderate-vigorous intensity \((t (51) = -0.61, p = .546)\).

3.2. Upper respiratory illness

Chi-squared analysis showed a significantly lower proportion of days with URI during the 12 weeks in the COL group (5%) compared to the PLA group (9%) \((\chi^2(1) = 40.52, p = .0001)\).
Further chi-squared analyses of URI at 4 weeks intervals showed a significantly lower proportion of days with URI in the COL group at 1-4 weeks (COL = 6 %, PLA = 8%; $\chi^2 (1) = 4.56, p = .021$) and 5-8 weeks (COL = 2 %, PLA = 13%; $\chi^2 (1) = 64.12, p < .001$) but not 9-12 weeks (COL = 6 %, PLA = 7%; $\chi^2 (1) = 0.29, p = .348$) (Figure 1). Independent t-test showed a significantly lower mean number of URI episodes in the COL group compared to PLA group over the 12 weeks (COL, 0.4 ± 0.7; PLA, 0.8 ± 0.7; t (51) = 1.88, p = .033). The proportion of participants who reported URI during the study period (all 12 weeks combined) was not lower in the COL group (40%) than PLA group (64%) ($\chi^2 (1) = 3.13, p = .067$). There were, however, a significantly lower proportion of participants who reported URI in the COL group (12%) compared to PLA (36%) at 5-8 weeks ($\chi^2 (1) = 0.29, p = .044$) which was not evident at 1-4 weeks (COL = 16 %, PLA = 25%; $\chi^2 (1) = 0.65, p = .322$) or 9-12 weeks (COL = 20 %, PLA = 18%; $\chi^2 (1) = 0.04, p = .559$) (Figure 1). When URI episodes were reported by participants, the severity (COL, 35.3 ± 26.9; PLA, 42.0 ± 27.4; t (32) = 0.68, p = .250) and duration of symptoms (COL, 7.9 ± 4.4 days; PLA, 9.9 ± 5.6; t (32) = 1.02, p = .159) were similar between groups. During episodes of URI, there were no differences between groups for the proportion of participants who used medication (COL = 50%, PLA = 78%; $\chi^2 (1) = 2.27, p = .139$) or had training negatively affected (i.e. reduced or prevented) (COL = 60%, PLA = 54%; $\chi^2 (1) = 1.15, p = .249$). All of the above patterns/effects were similar in the subset of participants used for microbiome analysis (see section 2.11).
3.3. Cell counts and neutrophil function

Results for total and differential leukocyte counts, and stimulated neutrophil oxidative burst, at baseline and 12 weeks following supplementation in COL and PLA groups are shown in Table 1.

3.4. Salivary sIgA and antimicrobial peptides

The analyses of salivary antimicrobial peptides across the 12 week period are shown in Table 2 and 3. One participant was removed from sIgA analysis due to a lack of clear supernatant upon centrifugation of saliva samples. Final comparison for sIgA was conducted on 52 participants (COL = 25, PLA = 27). This participant had been excluded from sLac and sLys for contamination purposes as previously mentioned (see above). There were no significant differences between groups in salivary measures during the 12 weeks (P > .05) (Table 2 and 3).

3.5. Salivary bacterial load and diversity

The ANOVA to analyze log of estimated copy number of 16S rRNA gene revealed a significant time ($F (1,29)= 15.38, p < .001$) and interaction effect ($F (1,29)= 4.90, p = 0.035$) but no group effect ($F (1,29)= 0.28, p = .602$) (Figure 2). Post-hoc analysis of interaction revealed a significant increase in bacterial load over the 12 weeks in the PLA group ($t (16)= -6.64, p < .001$) that was not present in COL group ($t (16)= -0.90, p = 0.386$) (Figure 2). ANOVA on total TRFLP peak number obtained from the restriction enzymeMspI revealed a main time effect ($F (1,27)= 21.80, p < .001$), with decreased bacterial diversity at 12 weeks, but no interaction ($F (1,27) = 0.43, p = .515$) or group effect ($F (1,27) = 0.01, p = .917$). However, analysis of total TRFLP peak number using HaeIII revealed no time ($F (1,27)= 2.54, p = .123$), interaction ($F (1,27)$
Analysis of Shannon Diversity Indexes for TFRLP using *MspI* showed no differences between groups at baseline \( t(29) = 0.27, p = .789 \) or at 12 weeks \( t(28) = 0.33, p = .746 \). There were also no differences at baseline \( t(28) = 0.41, p = .683 \) or 12 weeks \( t(28) = 0.23, p = .823 \) in Shannon Diversity Indexes for TFRLP using *HaeIII*. Microbial growth analysis, shown in Supplementary Figure 1, showed no indication of a direct antimicrobial effect of either the COL or PLA supplement.

### 3.6. Metabolomics

Sugisawa et al. (2003) have suggested that low molecular weight (< 10 kDa) substances may be responsible for the immunological effects of COL. We therefore used a metabolomics approach to determine whether COL increased the concentration of compounds at the lower end of this range (<1.4 kDa) with the expectation that any such effects would be due to bioactive metabolites. Thus, metabolite profiles of serum derived using DI-ESI-MS were analysed using multivariate approaches. DFA of serum profiles at baseline and at 12 weeks (Figure 3), showed no separation, at either time point, between the COL and PLA groups. However, there was clear separation between the two time points. Interrogation of the loading vectors selected by the algorithm to derive DF1 suggested that 13 m/z were calculated to be the major sources of variation. Interrogation of the HMDB Serum Metabolome database allowed the tentative identification of these 13 metabolites (Table 4). Within the tentative identifications, there are several possibilities for each m/z but no particular biochemical pathways or immunological metabolite markers appeared to have been targeted.
4. Discussion

This study aimed to determine the effects of COL on innate and mucosal markers of immunity and the subsequent incidence of URI in regularly exercising males. Compared to the PLA group, there was a significantly lower number of URI episodes and subsequently less proportion of URI days in the COL group over the 12 weeks. This supports previous evidence in studies of both active and immune-deficient populations (Brinkworth and Buckley, 2003; Crooks et al., 2010; Patel and Rana, 2006). Beneficial effects of COL were most evident during periods of greater prevalence of URI within the study population by reducing the proportion of participants who report URI (hence a greater scope for intervention). As not all participants commenced the study at the same time of year, it is important to recognize that these findings reflect the effects of COL within the timeframe and the incidence of illness in participants of the current study rather than proposing a specific seasonal window where COL affects URI. There was, however, no effect of COL on severity and duration of URI episodes, which supports some previous studies (Brinkworth and Buckley, 2003; Crooks et al., 2006, 2010) but not the beneficial effects reported by Patiroglu and Kondolot (2011).

In contrast to the effect of COL on URI, there was no significant effect of COL on salivary sIgA and AMPs or fMLP-stimulated blood neutrophil oxidative burst. The lack of effect on immune parameters despite differences in URI is in accordance with previous evidence (Crooks et al., 2006; Shing et al., 2007). Although previous studies have found beneficial effects in mucosal protection (sIgA/AMPs) following COL supplementation, either a blunting of the exercise-induced immune dysfunction (Davison and Diment, 2010) or increased resting salivary sIgA (Crooks et al., 2006),
they did not measure URI (Davison and Diment, 2010) or failed to see simultaneous effects of COL on URI (Crooks et al., 2006). This has led to proposals that the effect of COL occurs through a combination of mechanisms (Shing et al., 2007). In the current study we proposed the use of a novel in-vivo marker (salivary microbiome) that may have greater sensitivity to changes in innate mucosal defense following an intervention. This study shows for the first time that during regular training in the winter months, COL limits the increase in salivary bacterial load that was observed in the PLA group. However it is currently unclear whether the significant increase in bacterial load in the PLA group played a role in the greater episodes of URI observed in this group or whether the increased bacterial load occurred as result of a greater number of illnesses, or compromised immunity (due to training and/or seasonal effects).

Future studies should investigate salivary bacterial load at the taxonomic level with next generation sequencing methods to determine whether changes reflect predisposed interactions with viruses which are the common cause of URI (Bosch et al., 2013).

Evidence from respiratory health research has suggested that bacterial colonization of tissues contiguous to the oral cavity (e.g. airway) can trigger an increase in the frequency of disease exacerbations (Wedzicha and Donaldson, 2003). Furthermore, the interaction between viruses and bacteria which colonize the upper respiratory tract has been highlighted to affect the risk of illness (Bosch et al., 2013). Of relevance to this study are suggestions that the balance of microbes involved in colonization can be perturbed when host immunity is compromised (Murphy et al., 2009). It is apparent that the magnitude of change in immunity immediately following each bout of strenuous exercise may have more clinical significance than training-induced alterations in resting immunity (Abhassi et al., 2013; Nieman et al., 1994; Pedersen
and Bruunsgaard, 1995). It is reasonable to suggest that over the course of the 12 weeks the COL group suffered fewer incidences of transient immune perturbations, and/or smaller or shorter disturbance, (in response to training and/or seasonal variation) which may have limited conditions for changes in the salivary microbiome to occur. COL has been shown to prevent exercise-induced decreases in salivary AMPs and improve recovery of the capacity of neutrophils (a source of AMPs) following strenuous exercise (Davison and Diment, 2010). Deficiencies or decreases in AMPs expressed in mucosal secretions have been shown to be related to greater bacterial invasion and/or cases of infection (Bals et al., 1998, 1999; Daele and Zicot, 2000; Smith et al., 1996; Goldman et al., 1997). It is worthy to note, however, that the present study has only investigated a narrow range of AMPs that are present in mucosal secretions. Therefore, the effects of COL on the resting concentrations of other AMPs such as cathelicidins, which have broad anti-bactericidal effects (Bals, 2000), remain unclear and cannot be excluded. In addition, there were no apparent effects of COL on in-vitro microbial culture in this study which supports that the aforementioned effects on bacterial load are not due to components of COL having direct anti-microbial effects in the oral cavity during consumption.

Of particular note was the lack of simultaneous increase in bacterial diversity within the PLA group during the study. This suggests that it was not the acquisition of new bacteria that caused the significant increase in bacterial load in the PLA group but rather amplification of bacteria resident at baseline. The oral cavity is exposed to a constant array of exogenous and endogenous factors, thus measurement via saliva has been recognized to provide a ‘fingerprint’ of the whole oral microbiota (Dewhirst et al., 2010; Fabian et al., 2008; Li et al., 2005; Boutaga et al., 2007). We propose that, rather than causing URI per se, an increase in bacterial load is indicative of
compromised innate immune status, and as such is a relevant marker of in-vivo (innate) immune status. Furthermore, if COL supplementation does limit increases in salivary bacterial load, it will be important to determine whether this is a general reduction in bacteria, or whether it is biased towards certain bacterial taxonomies.

A further aim of this study was to determine any metabolomic changes as a result of COL supplementation. Metabolomics provides an unbiased biochemical “snap shot” of samples which due to the use of high resolution MS-based (as here) or nuclear magnetic resonance (NMR)-based approaches simultaneously and accurately measure hundreds of metabolites. Exercise immunologists view that high throughput laboratory methods such as metabolomics will provide greater understanding of the mechanisms behind modulations of the immune system with exercise and/or nutrition (Walsh et al., 2011). Crucially, in this study, we did not observe any changes in serum metabolome linked to COL supplementation, indicating that either no major changes were occurring or that these were occurring below the detection limits of the Mass Spectrometer (<10^{-12} mol, Sumner et al., 2003). There was, however, a clear separation of metabolome profiles obtained at baseline and at the 12 week timepoint of the study. The timepoint effect could reflect a combination of a seasonal effect and accumulation of training stress. As seasonal and/or exercise effects alone on the immune system were not a primary aim of the study, future studies should investigate whether changes in metabolome are involved in the greater incidence of URI seen in the winter months. Confirmatory identifications of the 13 m/z which appear to be responsible for the majority of the temporal separation were not accomplished as changes in the serum metabolome were not as a result of COL supplementation and thus fell outside of the scope of this project.
Previous *in-vitro* culture studies suggested that low molecular weight (≤ 10 kDa) components of COL (e.g. proteose peptones) rather than larger growth factors or cytokines may be responsible for the effects on human immune function (e.g. leukocyte capacity) (Sugiswa et al., 2003). Given that our metabolomics approach provides data on (<1.4 kDa) metabolites involved in biological pathways (Holmes et al., 2008), it may have been expected to identify traces of such bioactive metabolites in the circulation following 12 weeks of supplementation. Future studies could additionally examine components between 1.4-10 kDa to identify whether the above mentioned components of COL investigated within *in-vitro* culture become bioavailable to affect human immune function following periods of supplementation. Such studies will help identify the bioactive components and eradicate discrepancies found between studies of COL that are due to the source/quality of the supplement (Davison, 2013). It is plausible, however, to suggest that in the present study the proposed priming effects may have been localised to immune parameters in the mucosae rather than having systemic effects. Another proposed mechanism behind the effects on URI is the ability of COL to truncate the increase in gut permeability following strenuous exercise (Marchbank et al., 2011). This effect on intestinal integrity may prevent additional stress on the immune system via the translocation of luminal bacteria into systemic circulation. This hypothesis, however, requires further study in relation to episodes of URI.

Although previous studies have shown inconsistencies in isolated immune markers at rest, the present study suggests that the effects of COL are apparent when an integrated and interactive holistic immune marker is taken (e.g. salivary bacterial load). It should be noted that participants in this study were not limited in their use, either before or during the study, of mouthwash. This could be considered a potential
limitation of the study and an important consideration for future studies using the salivary bacterial load as an in-vivo marker. Given the presence of null findings in the present study compared to previous studies of investigated immune parameters (e.g. sIgA), it is important to acknowledge methodological limitations not yet considered. The present study involved participants who were involved in a range of sports training. Although these were all endurance based activities, previous studies have reported that effects of COL on sIgA may not be universal in all groups of regular exercisers (Crooks et al., 2010). In addition, it is unclear whether the use of participants who had a higher mean weekly training load and hence potentially a greater number of immunodepressive bouts would have produced different findings for these measures. Indeed, when highly trained cyclists completed 5 consecutive days of high-intensity training, COL supplementation was found to prevent the decreases in cytotoxic/suppressor T cells observed at the end and in the recovery period from the training in the PLA group (Shing et al., 2007).

In summary, we have shown for the first time that COL supplementation can limit microbial changes in the oral cavity during the winter months. This may be due to COL acting as a nutritional countermeasure to seasonal effects on salivary microbiome or immune perturbations following acute exercise. The clinical implications of this may be a reduction in the number of URI episodes. Future research should include responses to acute training during the monitoring period to determine the effects on the salivary microbiome and whether COL influences these (and other, e.g. AMPs) responses.

Acknowledgements
We acknowledge the assistance of Kirsten Skøt and Sharon Huws with the T-RFLP sequencing and T-RFLP technique/creation of artificial saliva media respectively. Arwel W. Jones' PhD was supported by a Knowledge Economy Skills Scholarship which was a collaborative project with an external partner, The Golden Dairy Ltd (supplier for Neovite UK). This project was part-funded by the European Social Fund through the European Union's Convergence Programme (West Wales and the Valleys) and administered by the Welsh Government.
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molecular-weight fraction of bovine colostrum and milk enhances the oxidative burst

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Green, C., Pedersen, B.K., Hoffman-Goetz, L., Rogers, C.J., Northoff, H., Abbasi, A.,


Fig. 1. URI during 4 week intervals in bovine colostrum (COL)/placebo (PLA) groups. Columns reflect proportion of participants in each group who report URI. Line and symbol represent proportion of URI days in each group during 4 week intervals. **Significantly lower proportion of URI days in COL group at 1-4 weeks and 5-8 weeks (p<.05). * Significantly lower proportion of participants in the COL group who report URI at 5-8 weeks (p<.05).

Fig. 2. Salivary bacterial load in bovine colostrum (COL)/placebo (PLA) groups. Standard deviation as error bars. *Significant increase in salivary bacterial load from baseline to 12 weeks in PLA group (p<.001).

Fig. 3. Discriminant Function analysis (DFA) plot of metabolomic profiles before and at end of 12 weeks of bovine colostrum (COL)/placebo (PLA) supplementation. ● - PLA group at baseline; ■ - COL group at baseline; ● - PLA group at 12 weeks; ■ - COL group at 12 weeks. A satisfactory separation was obtained between time points but not groups. Rings on figure display 95% confidence intervals for DFA separation.

Table 1. Blood leukocytes and neutrophil function in bovine colostrum (COL)/placebo (PLA) groups. Statistically significant difference between baseline and 12 week measures (main effect of time) indicated by * p <.05. Values are mean ± SD.

Table 2. sIgA before, during and at the end of 12 weeks of bovine colostrum (COL)/placebo (PLA) supplementation. Values are mean ± SD.
Table 3. sLac and sLys before, during and at end of 12 weeks of bovine colostrum (COL)/placebo (PLA) supplementation. Values are mean ± SD. Main effect of time indicated by * $p < .05$. Post hoc analysis could not reveal any significant differences between timepoints for sLac concentration. There was a significant increase in sLac secretion rate (at 8 and 12 weeks) and sLys secretion rate (at 8 weeks) from baseline ($p < .05$). Values are mean ± SD.

Table 4. Tentative identifications of metabolites which may be responsible for the separation between the 2 timepoints visible in DF1 of Figure 3. For some of the whole number molecular weight bins there are multiple tentative IDs which may or may not contribute to the DF1 loading. Change from the baseline and subsequent ANOVA $P$ values are detailed alongside the tentative IDs.
Fig. 1
**Fig. 2**

The figure shows a bar graph comparing the Log10 of estimated copy number of 16S RNA gene at baseline and 12 weeks. The bars represent two groups: COL and PLA. The graph indicates a significant increase in the PLA group at 12 weeks compared to baseline, as marked by an asterisk (*).
Fig. 3
<table>
<thead>
<tr>
<th>Immune measure</th>
<th>Baseline</th>
<th>12 weeks</th>
<th>( F(df) )</th>
<th>( P )</th>
<th>time</th>
<th>( F(df) )</th>
<th>( P )</th>
<th>trial</th>
<th>( F(df) )</th>
<th>( P )</th>
<th>interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>Total leukocytes (cells ×10^9.L^-1)</td>
<td></td>
<td></td>
<td>1.74 (1,51)</td>
<td>.193</td>
<td></td>
<td></td>
<td></td>
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<td></td>
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<tr>
<td>COL</td>
<td>4.74 ± 1.02</td>
<td>4.90 ± 1.01</td>
<td>0.78 (1,51)</td>
<td>.382</td>
<td></td>
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<tr>
<td>PLA</td>
<td>5.20 ± 1.68</td>
<td>5.27 ± 1.63</td>
<td>0.17 (1,51)</td>
<td>.687</td>
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<tr>
<td>Neutrophils (cells ×10^9.L^-1)</td>
<td></td>
<td></td>
<td>0.86 (1,51)</td>
<td>.359</td>
<td></td>
<td></td>
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<tr>
<td>COL</td>
<td>2.31 ± 0.61</td>
<td>2.31 ± 0.59</td>
<td>0.51 (1,51)</td>
<td>.268</td>
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<tr>
<td>PLA</td>
<td>2.58 ± 1.18</td>
<td>2.74 ± 1.28</td>
<td>1.26 (1,51)</td>
<td>.480</td>
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<tr>
<td>Monocytes (cells ×10^9.L^-1)</td>
<td></td>
<td></td>
<td>0.33 (1,51)</td>
<td>.567</td>
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<tr>
<td>COL</td>
<td>0.46 ± 0.11</td>
<td>0.46 ± 0.12</td>
<td>0.09 (1,51)</td>
<td>.766</td>
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<tr>
<td>PLA</td>
<td>0.46 ± 0.13</td>
<td>0.47 ± 0.20</td>
<td>0.63 (1,51)</td>
<td>.431</td>
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<tr>
<td>Total lymphocytes (cells ×10^9.L^-1)</td>
<td></td>
<td></td>
<td>0.26 (1,51)</td>
<td>.619</td>
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<tr>
<td>COL</td>
<td>1.77 ± 0.50</td>
<td>1.91 ± 0.67</td>
<td>&lt;0.01 (1,51)</td>
<td>.970</td>
<td></td>
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<tr>
<td>PLA</td>
<td>1.90 ± 0.61</td>
<td>1.79 ± 0.47</td>
<td>3.21 (1,51)</td>
<td>.079</td>
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<tr>
<td>Atypical lymphocytes (cells ×10^9.L^-1)</td>
<td></td>
<td></td>
<td>2.92 (1,51)</td>
<td>.093</td>
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<tr>
<td>COL</td>
<td>0.04 ± 0.01</td>
<td>0.04 ± 0.02</td>
<td>0.56 (1,51)</td>
<td>.458</td>
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<tr>
<td>PLA</td>
<td>0.05 ± 0.02</td>
<td>0.05 ± 0.02</td>
<td>2.44 (1,51)</td>
<td>.124</td>
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<tr>
<td>Large immature cells (cells ×10^9.L^-1)</td>
<td></td>
<td></td>
<td>0.05 (1,51)</td>
<td>.832</td>
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<tr>
<td>COL</td>
<td>0.03 ± 0.01</td>
<td>0.03 ± 0.02</td>
<td>1.08 (1,51)</td>
<td>.305</td>
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<tr>
<td>PLA</td>
<td>0.05 ± 0.04</td>
<td>0.04 ± 0.03</td>
<td>0.27 (1,51)</td>
<td>.605</td>
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<td></td>
<td>fMLP-stimulated CL per neutrophil (RLU per s⁻¹ per cell⁻¹)</td>
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<tr>
<td></td>
<td>5.31 (1,51) .025*</td>
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<tr>
<td>COL</td>
<td>43.65 ± 27.44 53.99 ± 26.51</td>
<td>0.68 (1,51) .413</td>
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<tr>
<td>PLA</td>
<td>42.79 ± 25.58 44.52 ± 24.91</td>
<td>0.84 (1,51) .365</td>
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</tbody>
</table>

Table 1. Blood leukocytes and neutrophil function in bovine colostrum (COL)/placebo (PLA) groups. Statistically significant difference between baseline and 12 week measures (main effect of time) indicated by * p <.05. Values are mean ± SD.
Table 2. sIgA before, during and at the end of 12 weeks of bovine colostrum (COL)/placebo (PLA) supplementation. Values are mean ± SD.

<table>
<thead>
<tr>
<th>Immune measure</th>
<th>Baseline</th>
<th>4 weeks</th>
<th>8 weeks</th>
<th>12 weeks</th>
<th>$F$ (df)</th>
<th>$P$ time</th>
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<tr>
<td>slgA concentration (mg L$^{-1}$)</td>
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<tr>
<td>COL</td>
<td>267.0 ± 126.5</td>
<td>252.9 ± 119.7</td>
<td>256.0 ± 142.8</td>
<td>272.2 ± 152.5</td>
<td>0.71 (1,50)</td>
<td>0.404</td>
</tr>
<tr>
<td>PLA</td>
<td>259.9 ± 202.9</td>
<td>217.1 ± 124.4</td>
<td>230.4 ± 132.3</td>
<td>215.0 ± 98.5</td>
<td>0.37 (1,50)</td>
<td>0.546</td>
</tr>
<tr>
<td>slgA secretion rate (µg·min$^{-1}$)</td>
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<tr>
<td>COL</td>
<td>116.5 ± 89.3</td>
<td>125.6 ± 105.6</td>
<td>129.5 ± 89.6</td>
<td>143.9 ± 96.8</td>
<td>1.65 (1,50)</td>
<td>0.733</td>
</tr>
<tr>
<td>PLA</td>
<td>121.1 ± 125.9</td>
<td>104.7 ± 51.5</td>
<td>114.3 ± 63.0</td>
<td>108.1 ± 57.3</td>
<td>0.12 (1,50)</td>
<td>0.180</td>
</tr>
<tr>
<td>slgA:osmolality (mg·mOsmol$^{-1}$)</td>
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<tr>
<td>COL</td>
<td>3.8 ± 1.5</td>
<td>3.6 ± 1.4</td>
<td>3.5 ± 1.4</td>
<td>3.8 ± 1.8</td>
<td>1.19 (1,50)</td>
<td>0.280</td>
</tr>
<tr>
<td>PLA</td>
<td>3.6 ± 2.0</td>
<td>3.2 ± 1.4</td>
<td>3.4 ± 1.5</td>
<td>3.1 ± 1.2</td>
<td>0.75 (1,50)</td>
<td>0.525</td>
</tr>
</tbody>
</table>
Table 3. sLac and sLys before, during and at end of 12 weeks of bovine colostrum (COL)/placebo (PLA) supplementation. Main effect of time indicated by * p < .05. Post hoc analysis could not reveal any significant differences between timepoints for sLac concentration.

There was a significant increase in sLac secretion rate (at 8 and 12 weeks) and sLys secretion rate (at 8 weeks) from baseline (p < .05). Values are mean ± SD.
<table>
<thead>
<tr>
<th>Immune measure</th>
<th>Group</th>
<th>Baseline</th>
<th>4 weeks</th>
<th>8 weeks</th>
<th>12 weeks</th>
<th>$F$ (df) $P$ time</th>
<th>$F$ (df) $P$ trial</th>
<th>$F$ (df) $P$ interaction</th>
</tr>
</thead>
<tbody>
<tr>
<td>sLac concentration</td>
<td>COL</td>
<td>3.3 ± 0.8</td>
<td>3.7 ± 0.8</td>
<td>3.7 ± 0.8</td>
<td>3.8 ± 0.8</td>
<td>3.02 (1,44) .032*</td>
<td>0.63 (1,44) .431</td>
<td></td>
</tr>
<tr>
<td>(mg $L^{-1}$)</td>
<td>PLA</td>
<td>3.8 ± 1.2</td>
<td>3.8 ± 1.0</td>
<td>4.0 ± 1.0</td>
<td>3.8 ± 1.0</td>
<td>1.58 (1,44) .198</td>
<td></td>
<td></td>
</tr>
<tr>
<td>sLac secretion rate</td>
<td>COL</td>
<td>1.6 ± 1.0</td>
<td>1.9 ± 1.2</td>
<td>2.0 ± 0.9</td>
<td>2.1 ± 0.8</td>
<td>6.29 (1,44) .001*</td>
<td>0.84 (1,44) .365</td>
<td></td>
</tr>
<tr>
<td>(µg·min$^{-1}$)</td>
<td>PLA</td>
<td>1.9 ± 1.0</td>
<td>2.1 ± 1.2</td>
<td>2.3 ± 1.4</td>
<td>2.3 ± 1.3</td>
<td>0.29 (1,44) .829</td>
<td></td>
<td></td>
</tr>
<tr>
<td>sLac:osmolality</td>
<td>COL</td>
<td>0.05 ± 0.02</td>
<td>0.06 ± 0.02</td>
<td>0.06 ± 0.02</td>
<td>0.06 ± 0.02</td>
<td>2.04 (1,44) .111</td>
<td>0.36 (1,44) .549</td>
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<tr>
<td>(mg·mOsmol$^{-1}$)</td>
<td>PLA</td>
<td>0.06 ± 0.02</td>
<td>0.06 ± 0.02</td>
<td>0.06 ± 0.02</td>
<td>0.06 ± 0.02</td>
<td>1.29 (1,44) .282</td>
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<tr>
<td>sLys concentration</td>
<td>COL</td>
<td>21.5 ± 13.3</td>
<td>23.0 ± 13.5</td>
<td>22.3 ± 12.6</td>
<td>20.1 ± 12.8</td>
<td>0.57 (1,44) .636</td>
<td>0.04 (1,44) .837</td>
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<tr>
<td>(mg$L^{-1}$)</td>
<td>PLA</td>
<td>22.0 ± 14.6</td>
<td>20.1 ± 12.1</td>
<td>21.3 ± 11.5</td>
<td>21.1 ± 12.1</td>
<td>1.25 (1,44) .295</td>
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<tr>
<td>sLys secretion rate</td>
<td>COL</td>
<td>9.9 ± 8.3</td>
<td>10.5 ± 6.5</td>
<td>11.4 ± 8.4</td>
<td>10.0 ± 5.1</td>
<td>2.91 (1,44) .037*</td>
<td>0.09 (1,44) .764</td>
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</tr>
<tr>
<td>(µg·min$^{-1}$)</td>
<td>PLA</td>
<td>10.8 ± 8.8</td>
<td>10.7 ± 8.4</td>
<td>11.7 ± 7.4</td>
<td>11.6 ± 8.8</td>
<td>0.58 (1,44) .627</td>
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<tr>
<td>sLys:osmolality</td>
<td>COL</td>
<td>0.34 ± 0.23</td>
<td>0.36 ± 0.25</td>
<td>0.33 ± 0.17</td>
<td>0.30 ± 0.18</td>
<td>0.59 (1,44) .622</td>
<td>0.01 (1,44) .941</td>
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</tr>
<tr>
<td>(mg·mOsmol$^{-1}$)</td>
<td>PLA</td>
<td>0.33 ± 0.22</td>
<td>0.31 ± 0.20</td>
<td>0.33 ± 0.19</td>
<td>0.33 ± 0.19</td>
<td>0.95 (1,44) .420</td>
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</table>
Table 4. Tentative identifications of metabolites which may be responsible for the separation between the 2 timepoints visible in DF1 of Figure 3. For some of the whole number molecular weight bins there are multiple tentative IDs which may or may not contribute to the DF1 loading. Change from the baseline and subsequent ANOVA $P$ values are detailed alongside the tentative IDs.

<table>
<thead>
<tr>
<th>MW</th>
<th>Tentative ID</th>
<th>Change from Baseline</th>
<th>$F$ (df) $P$</th>
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<tbody>
<tr>
<td>108</td>
<td>Cresol</td>
<td>Decrease</td>
<td>5.31 (3,100) .002</td>
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<tr>
<td>154</td>
<td>Gentisic acid</td>
<td>Decrease</td>
<td>84.70 (3,100) &lt; .001</td>
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<tr>
<td></td>
<td>2-Pyrocatechuic acid</td>
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</tr>
<tr>
<td></td>
<td>Protocatechuic acid</td>
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<td></td>
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<tr>
<td></td>
<td>Hydroxytyrosol</td>
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<td></td>
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<tr>
<td>155</td>
<td>L-Histidine</td>
<td>Increase</td>
<td>94.18 (3,100) &lt; .001</td>
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<tr>
<td>157</td>
<td>Unknown</td>
<td>Increase</td>
<td>53.65 (3,100) &lt; .001</td>
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<tr>
<td>168</td>
<td>Uric acid</td>
<td>Decrease</td>
<td>16.11 (3,100) &lt; .001</td>
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<tr>
<td></td>
<td>Homogentisic acid</td>
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<tr>
<td></td>
<td>3-Hydroxymandelic acid</td>
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<tr>
<td></td>
<td>3,4-Dihydroxybenzeneacetic acid</td>
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<tr>
<td></td>
<td>Pyridoxamine</td>
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<td></td>
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<tr>
<td>169</td>
<td>Norepinephrine</td>
<td>Increase</td>
<td>11.13 (3,100) &lt; .001</td>
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<tr>
<td></td>
<td>Pyridoxine</td>
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<tr>
<td></td>
<td>3-Methylhistidine</td>
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<td></td>
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<tr>
<td></td>
<td>D-Glyceraldehyde 3-phosphate</td>
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<tr>
<td></td>
<td>Dihydroxyacetone phosphate</td>
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<tr>
<td>170</td>
<td>Gallic acid</td>
<td>Increase</td>
<td>36.68 (3,100) &lt; .001</td>
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<td></td>
<td>3,4-Dihydroxyphenylglycol</td>
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<tr>
<td></td>
<td>cis-4-Decenoic acid</td>
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<tr>
<td>172</td>
<td>Glycerol 3-phosphate</td>
<td>Decrease</td>
<td>6.57 (3,100) &lt; .001</td>
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<tr>
<td></td>
<td>Glycyrlproline</td>
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<tr>
<td>173</td>
<td>2-Oxoarginine</td>
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<td>Pyroprophosphate</td>
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<td>174</td>
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<td>Increase</td>
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<td>Suberic acid</td>
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<td>N-Acetylornithine</td>
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<td>L-Arginine</td>
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<td>Decrease</td>
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<tr>
<td>285</td>
<td>Unknown</td>
<td>Increase</td>
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<td>325</td>
<td>10-Nitrolinoleic acid</td>
<td>Decrease</td>
<td>11.86 (3,100) &lt; .001</td>
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<tr>
<td></td>
<td>N-Oleoylethanolamine</td>
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