Long term dietary supplementation with microalgae increases plasma docosahexaenoic acid in milk and plasma but does not affect plasma 13, 14-dihydro-15-keto $PGF_{2\alpha}$ concentration in dairy cows

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SUPPLEMENTARY FILE

Supplementary Material and Methods

The FA content of the TMR was determined according to Jenkins (2010), whilst milk FA analysis followed the method described by Feng et al. (2004) for lipid extraction, with the methylation of the lipids conducted as described by Lock et al. (2006). Individual FAME were determined by GLC (Hewlett Packard 7820, Wokingham, UK) fitted with a CP-Sil 88 column (100 m×0.25 mm i.d.×0.2 µm film, Agilent Technologies, Santa Clara, California, USA) as described previously (Lock et al. 2006). Total lipid was extracted from plasma samples and methylated using the method of Burdge et al. (2005). Resulting FA methyl esters were resolved on a CP-Sil 88 column using a gas chromatograph (GC; Bruker 350, Bruker, Germany) equipped with a flame ionisation detector. The GC conditions were as previously described (Kliem et al., 2013), and plasma FAME were identified based on retention time comparisons with an authentic standard (GLC463, Nu-Chek Prep Inc., Elysian, MN), and cross-referencing with previously published chromatograms (Kliem et al., 2013). Carbon deficiency in the detector response was accounted for using a combined correction factor (Ulberth et al., 1999), and results were expressed as g/100 g total FA.

References

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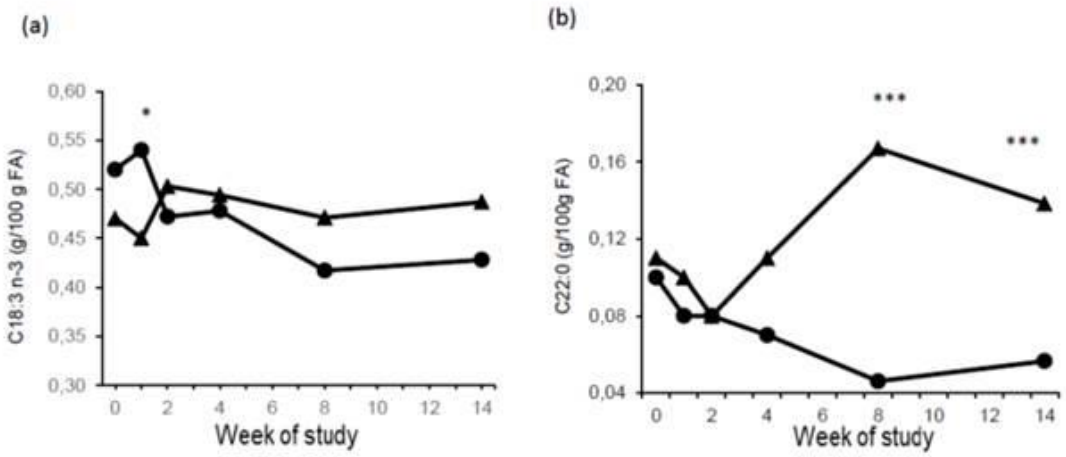
Supplementary Fig. 1. Milk fat concentration of (a) C18:3 n-3 and (b) C20:0. SED = 0.034, 0.022 respectively. Within time points, treatments that differ at P < 0.05 or P < 0.001 are denoted by * , or *** respectively.



Supplementary Fig. 2. Blood plasma fat concentration of (a) C18:0 (b) C18:1 *trans*-10 (c) C18:3 n-3, (d) C20:4 n-6 (e) C20:0 (f) total saturated fatty FA and (g) total n-3 PUFA in dairy cows fed no SCIM (Control ●) or 100 g per cow per day of microalgae (SCIM ▲). SED = 0.44, 0.066, 0.19, 0.09, 0.05, 0.68 and 0.34 respectively. Within time points, treatments that differ at P < 0.05, P< 0.01 or P < 0.001 are denoted by * , ** or *** respectively.