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Temporal variation in the vertical stratification of blubber fatty acids alters diet predictions for lactating Weddell seals

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Abstract

Fatty acid signature analysis of blubber has been used to study the foraging ecology of some marine mammals. However, species-specific information on fatty acid (FA) deposition, distribution and mobilization is required to develop further the application of FA as trophic markers within the marine environment. Blubber samples were collected from adult female Weddell seals post-parturition and end of lactation, and were divided into inner and outer half sections. We determined the degree to which there was vertical stratification in FA composition, and how this changed over the lactation period. Inner and outer layers of post-parturition blubber cores separated into two distinct groups. Sixty-two per cent of the dissimilarity between the two layers was accounted for by a higher abundance of monounsaturated fatty acids (18:1ω9c and 16:1ω7c) in the outer blubber layer, and more saturated fatty acids (16:0 and 14:0) in the inner layer. By end of lactation, the FA composition of the inner layer was different to post-parturition samples, and 20:5ω3 had the highest fractional mobilization of all FA. In contrast, the proportion of FA in the outer layer did not change, and there was more variability in the fractional mobilization of FA indicating mobilization was not uniform across the blubber layer. Dietary predictions changed considerably when highly mobilized FA were removed from analyses, and predictions were more consistent with previous dietary studies. The lack of uniformity in FA mobilization adds problems to the future use of FASA in dietary predictions, highlighting the need for more detailed information on FA mobilization.

Keywords: Blubber; Diet; Fatty acids; Lactation; Mobilization; Stratification

1. Introduction

Marine birds and mammals have been of increasing interest in ecosystem studies because of the premise that temporal shifts in their behaviour and physiology reflect the amplitude and timing of climate variability and change (Croxall, 1992; Hindell et al., 2003). In particular, variation in diet composition is expected to aid in the assessment of abundance and demographic shifts in lower trophic level taxa (*i.e.*, prey). A necessary precursor to this aim is an assessment of the accuracy and reliability of methods to measure diet variation (*e.g.*, Bradshaw et al., 2003) so that

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they can be applied across different taxa and ecosystems. The diet of marine birds and mammals has been determined traditionally through the analysis of stomach contents and prey remains in faeces (Coria et al., 1995; Field et al., 2007; Lake et al., 2003). Several drawbacks occur with these approaches: (1) remains in stomachs and faeces only represent prey consumed over a short period of time (*i.e.*, days to weeks; Hammond and Rothery, 1996), (2) hard parts (*e.g.*, fish otoliths, cephalopod beaks) are more recognizable and therefore, possibly over-represented than partially digested soft tissue (Hyslop, 1980), (3) differential passage rates of different prey species bias estimates of frequency of occurrence (Harvey and Antonelis, 1994), and (4) taxonomic identification can be difficult and time consuming.

To alleviate problems associated with traditional diet analyses, biochemical approaches have been developed. Fatty acid signature analysis (FASA) has been of interest from both nutritional and tropho-dynamic perspectives, with the application of fatty acids (FA) as trophic markers to trace or confirm many different marine predator–prey relationships from secondary producers to upper trophic level predators (Ackman et al., 1970; Auel et al., 2002; Iverson et al., 1997; Lea et al., 2002; Nelson et al., 2001; Ruchonnet et al., 2006). In essence, FASA assumes that base lipid constituents, *i.e.*, fatty acids, are incorporated into the tissues of predators conservatively so that a predator's FA composition will reveal the dietary source of lipids. If the prey-to-predator lipid transfer is traceable, identification of ingested species can enable a description of trophic interactions and food webs (Bradshaw et al., 2003; Iverson et al., 1997).

Using FASA to determine diet composition is not straightforward, because (1) several FA are biosynthesized *de novo*, possibly altering the FA signature of the predator, (2) stratification of FA within the blubber has been observed in many species (Best et al., 2003; Birkeland et al., 2005; Grahl-Nielsen et al., 2003; Olsen and Grahl-Nielsen, 2003), indicating components of blubber are synthesized independently of diet, (3) rates of mobilization and breakdown of FA can vary according to life history stage and environmental context (Iverson et al., 1995; Pierce and McWilliams, 2005; Samuel and Worthy, 2004; Wheatley et al., in

Table 1
Average fatty acid composition (%) of the inner and outer blubber layer of Weddell seals at post-parturition and end-lactation

Fatty acid	Post-partum				End-lactation				Change			
	Inner	$n=19$	Outer	$n=19$	Inner	$n=10$	Outer	$n=10$	Inner	$n=10$	Outer	$n=10$
	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM	Mean	SEM
14:1ω5c	0.9	0.08	1.9	0.12	0.4	0.07	1.1	0.11	0.4	0.14	0.9	0.13
14:0	8.0	0.58	6.3	0.37	3.6	0.47	3.8	0.39	4.9	1.12	3.2	0.45
i15:0	0.3	0.02	0.3	0.01	0.2	0.02	0.2	0.02	0.1	0.04	0.1	0.02
16:1ω9c	0.3	0.01	0.3	0.01	0.1	0.02	0.2	0.02	0.1	0.02	0.1	0.02
16:1ω7c	10.1	0.52	13.0	0.49	3.3	0.54	8.0	1.02	7.2	0.92	5.9	0.95
16:1ω5c	0.3	0.01	0.3	0.01	0.1	0.02	0.2	0.03	0.2	0.03	0.2	0.03
16:0	8.5	0.46	5.7	0.28	3.2	0.44	3.6	0.47	6.0	0.75	2.5	0.45
i17:0	0.2	0.01	0.2	0.01	0.1	0.01	0.1	0.01	0.1	0.01	0.1	0.02
18:4ω3	0.9	0.03	0.9	0.04	0.3	0.05	0.5	0.07	0.6	0.06	0.4	0.06
18:2ω6	1.5	0.06	1.6	0.04	0.8	0.10	1.1	0.12	0.7	0.13	0.6	0.12
18:1ω9c	25.3	1.21	28.5	0.63	12.6	1.72	18.4	2.12	14.1	2.07	10.7	2.15
18:1ω7c	6.0	0.23	6.4	0.22	2.7	0.34	4.0	0.44	3.5	0.46	2.4	0.48
18:1ω5	0.5	0.02	0.5	0.02	0.2	0.03	0.3	0.04	0.3	0.03	0.2	0.04
18:0	1.1	0.04	0.7	0.03	0.6	0.08	0.4	0.05	0.5	0.08	0.3	0.06
20:4ω6	0.3	0.02	0.3	0.02	0.1	0.02	0.2	0.03	0.2	0.03	0.1	0.03
20:5ω3 EPA	3.2	0.18	2.8	0.18	0.6	0.13	1.6	0.26	2.6	0.25	1.3	0.22
20:4ω3	0.2	0.03	0.3	0.03	0.1	0.02	0.2	0.03	0.1	0.02	0.1	0.03
20:2ω6	4.0	0.16	4.1	0.19	1.1	0.04	0.6	0.07	0.5	0.07	0.0	0.07
20:1ω9c	4.5	0.22	3.7	0.14	3.4	0.43	2.5	0.29	1.4	0.37	1.3	0.32
20:1ω7c	0.5	0.02	0.4	0.01	0.4	0.04	0.3	0.02	0.2	0.04	0.1	0.03
22:6ω3 DHA	4.0	0.17	4.1	0.20	2.3	0.28	2.6	0.26	1.8	0.25	1.5	0.32
22:5ω3 DPA	1.2	0.15	1.4	0.14	0.8	0.11	0.8	0.10	0.3	0.07	0.5	0.13
22:1ω11c[a]	0.8	0.05	0.4	0.03	0.6	0.06	0.3	0.03	0.2	0.07	0.1	0.04
22:1ω9c	0.6	0.04	0.4	0.03	0.5	0.07	0.3	0.04	0.0	0.00	0.1	0.05
24:1	0.2	0.02	0.1	0.01	0.2	0.02	0.1	0.01	0.0	0.02	0.0	0.02

SEM = standard error of the mean.
[a] Includes 22:1ω13c.