Minimizing acylation of peptides in PLGA microspheres

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Supporting information

















Figure S1. Morphology of peptide-PLGA microspheres with or without excipients, formulation 1-18, as recorded by scanning electron microscopy.

Table S1. Observed molecular masses by MALTI-TOF analysis of salmon calcitonin
(sCT) and human parathyroid hormone (hPTH) and their impurities recovered from
PLGA millicylinders incubated in 97% RH and 37 $^{\circ}$ C for 21 days.

Observed mass (Da)	Expected Peptide
3434.0	sCT
3456.1	sCT-Na ⁺
3492.6	sCT-GA
3506.1	sCT-LA
3550.0	sCT-2GA
3564.4	sCT-LA-GA
3578.9	sCT-2LA
4118.9, 4118.3	hPTH ₁₋₃₄
4139.0	hPTH ₁₋₃₄ -Na ⁺
4177.2	hPTH ₁₋₃₄ -GA
4191.1	hPTH ₁₋₃₄ -LA
4249.6	hPTH ₁₋₃₄ -LA-GA



Figure S2. MALDI-TOF MS of sCT and its acylation products inside millicylinders incubated for 0 (A) and 21 days (B) at 97% RH and 37 $^{\circ}$ C





Figure S3. MALDI-TOF MS of hPTH and its acylation products inside millicylinders incubated for 0 (A) and 21 days (B, C and D) at 97% RH and 37 $^{\circ}$ C



Figure S4. Proposed potential mechanisms to explain stabilization of peptide by divalent cations and CMCS. Peptide adsorption and acylation (A); acylation is inhibited by blocking peptide from combining with negative sites in PLGA (B); acylation is inhibited by increasing peptide partitioning in a swollen CMCS/divalent cation phase(C)