

Modulation of protein release from penta-block copolymer microspheres

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4	MODULATION OF PROTEIN RELEASE FROM PENTA-
5	BLOCK COPOLYMER MICROSPHERES
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25 ABSTRACT

Releasing a protein according to a zero-order profile without protein denaturation during 26 the polymeric microparticle degradation process is very challenging. The aim of the 27 current study was to develop protein-loaded microspheres with new PLGA based penta-28 block copolymers for a linear sustained protein release. Lysozyme was chosen as model 29 protein and 40 µm microspheres were prepared using the solid-in-oil-in-water solvent 30 extraction/evaporation process. Two types of PLGA-P188-PLGA penta-block copolymers 31 were synthetized with two PLGA-segments molecular weight (20 kDa or 40 kDa). The 32 resulting microspheres (50P20-MS and 50P40-MS) had the same size, an encapsulation 33 efficiency around 50-60% but different porosities. Their protein release profiles were 34 complementary: linear but non complete for 50P40-MS, non linear but complete for 35 50P20-MS. Two strategies, polymer blending and microsphere mixing, were considered to 36 37 match the release to the desired profile. The (1:1) microsphere mixture was successful. It induced a bi-phasic release with a moderate initial burst (around 15%) followed by a 38 nearly complete linear release for 8 weeks. This study highlighted the potential of this 39 penta-block polymer where the PEO block mass ratio influence clearly the Tg and 40 consequently the microsphere structure and the release behavior at 37°C. The (1:1) 41 mixture was a starting point but could be finely tuned to control the protein release. 42

43 Keywords: protein sustained release, penta-block copolymer, microsphere,

44 microencapsulation, release modulation.

Abbreviations: PLGA, poly(D,L-lactic-co-glycolic acid); PLA, Polylactic acid; MS, 45 microsphere; PEO, poly(ethylene oxyde); PPO, poly(propylene oxyde); S/O/W, solid-in-46 oil-in-water emulsion; DMF, dimethylformamide; DCM, methylene chloride; Tris, 47 trizmabase; P188, Poloxamer 188; THF, tetrahydrofuran; CHCl₃, chloroform; DMSO, 48 Dimethyl sulfoxide; NMR, nuclear magnetic resonance; PVA, Poly(vinyl alcohol); SEM, 49 scanning electron microscopy; DSC, differential scanning calorimetry; Tg, glass transition 50 temperature; EE, encapsulation efficiency; BSA, Bovine serum albumin; IQR, 51 interquartile range; PEO, polyethylene oxyde. 52

53

54 **1. INTRODUCTION**

55 During the past two decades, there has been a great interest in controlled release of drugs 56 particularly for therapeutic proteins. Proteins are usually injected so it is crucial to reduce 57 the frequency of the injections, to increase the confort and patient compliance [1][2][3]. 58 Many approaches have been proposed to carry and deliver protein following continuous 59 and sustained manners. Among those, protein encapsulation in microspheres using 50 biodegradable and biocompatible polymers such as poly(D,L lactide-co-glycolide) 61 (PLGA) [4] were often used to control the release over several weeks.

However protein sustained delivery from PLGA-based microspheres (MS) is still a 62 challenge due to the variety of protein native structures, their instability particularly during 63 the polymer degradation [5], and their very low diffusivity into PLGA matrixes [6]. To 64 limit this drawback, a central hydrophilic segment such as poly(ethylene oxyde) (PEO) 65 was polymerized with PLGA to obtain a polymer triblock [7][8][9][10][11]. The protein 66 release from A-B-A type triblock was enhanced as the presence of hydrophilic segments in 67 multi-block copolymers facilitated the microsphere swelling during the release and 68 provided protein diffusion pathways [7][16]. But an incomplete release was still observed 69 due to the degradation of the entrapped protein into the microsphere core [12]. In addition, 70 it was shown that by adding free poloxamer in the formulation, the protein degradation 71 [Ref to add] and its adsorption on PLGA were reduced [14][15]. In that respect, to 72 modulate both the hydrophilic/hydrophobic balance of the polymer and improve the 73 protein stability, a penta-block was synthetized by copolymerizing PLGA with 74 amphiphilic triblock polymers such as poloxamers [13][17]. 75

In the literature, many efforts have been made to develop different strategies to modulate the protein release profile. Most of them relied on polymer blend strategies [18][19][20][21], whereas the strategy of mixing different types of PLGA-based microspheres was rarely addressed. Nevertheless, releasing a protein according to a zeroorder profile without protein denaturation during the polymer degradation process is still very challenging. 82 The aim of the current study was to modulate the protein release from the penta-block copolymer microspheres. Lysozyme was chosen as a model protein [22] and 40 µm 83 prepared using the solid-in-oil-in-water (S/O/W) 84 microspheres were solvent extraction/evaporation process [13]. Penta-block copolymers were synthetized with two 85 PLGA-segments molecular weight (20 kDa or 40 kDa). Various strategies (i.e. polymer 86 blending, microsphere mixing) were also considered to modify the release profile while 87 maintaining the completion of the protein release over 8 weeks. The proposal of a strategy 88 to achieve a complete active protein release from microspheres with the desired profile 89 was the main contribution of this study. 90

91

92 2. MATERIALS AND METHODS

93

94 **2.1. Materials**

Lysozyme (chicken egg white) and its substrate *Micrococcus lysodeikticus*, glycofurol,
dimethylformamide (DMF), methylene chloride (DCM), acetone, and trizmabase (Tris)
were purchased from Sigma-Aldrich (Saint-Quentin Fallavier, France). Poloxamer (P188,
Pluronic[®] F68) was obtained from BASF (Levallois-Perret, France). D,L-lactide and
glycolide were purchased from Corbion (Gorinchem, The Netherlands). Polyvinyl alcohol
(Mowiol[®] 4-88) was supplied by Kuraray Specialities Europe (Frankfurt, Germany).

101 Tin(II) 2-ethylhexanoate (Sn(Oct)₂, 95%), dichloromethane (DCM), diethyl ether,
102 tetrahydrofuran (THF), chloroform (CHCl₃) were purchased from Sigma-Aldrich (St103 Quentin Fallavier, France).

104 The poloxamer 188 (P188) is a commercial tri-block copolymer of PEO and 105 poly(propylene oxyde) (PPO) with general formula $HO(C_2H_4O)_{80}(C_3H_6O)_{27}(C_2H_4O)_{80}H$ 106 [23]. Two penta-block copolymers (named 50P20 and 50P40) were synthesized by ring-107 opening polymerization of D,L lactide and glycolide from P188 as initiator. Typically, 5g 108 of P188 and various amounts of D,L-lactide and glycolide (respectively 25 and 20.1 g for

the 50P40 and 13 and 10.1 g for the 50P20) were introduced into two flasks, then were 109 vacuum dried for 24h. Tin (II)-2 ethylhexanoate (0.1% of the number of hydroxyl 110 functions of P188) was added in dried polymerization flasks. After degassing, the flask 111 was sealed under vacuum and polymerization was carried out at 130°C for 5 days. The 112 copolymers were recovered by dissolution in dichloromethane and precipitated in cold 113 ethanol. The precipitated copolymers were filtered and dried under reduced pressure up to 114 constant weight. The composition of copolymers was investigated by nuclear magnetic 115 resonance spectroscopy (1H-NMR spectroscopy) at room temperature with an AMX300 116 Bruker[®] spectrometer (300 MHz), using DMSO as a solvent and trimethylsilane as the 117 internal standard. The dispersity (D) was determined by size exclusion chromatography 118 (SEC, Shimadzu[®], Japan) using two mixed medium columns PLgel 5 µm MIXED-C (300 119 \times 7.8 mm), a Shimadzu[®] RI detector 20-A and a Shimadzu[®] UV detector SPD-20A (270 120 nm) (40°C thermostatic analysis cells). Tetrahydrofuran (THF) was the mobile phase with 121 1 mL/mn flow at 30°C (column temperature). 122

123 The general formula of the resulting penta-block copolymer is (PLGA-PEO-PPO-PEO-124 PLGA). The PLGA segments contained 25% D-lactic units, 25% L-lactic units and 50% glycolic units. The penta-block copolymer 50P40 was composed of one central segment of 125 P188 (Mn=8,400 g/mol) and two segments of PLGA (Mn=40,000 g/mol each) at the ends, 126 the copolymer average molecular mass (Mn) was 88,400 g/mol (Đ=1.72). The penta-block 127 copolymer 50P20 was composed of one central segment of P188 (Mn=8,400 g/mol) and 128 two segments of PLGA (Mn=20,000 g/mol each) at the ends, the copolymer average 129 molecular mass was (Mn) 48,400 g/mol (Đ=1.51). 130

131

132 **2.2. Microsphere preparation**

133 **2.2.1. Preparation of 50P40-MS or 50P20-MS**

Copolymer microspheres (50P40-MS and 50P20-MS) were prepared as described previously (called thereafter the standard procedure) [12]. The theoretical protein loading was 0.6% (w/w). Briefly, lysozyme and P188 (ratio lysozyme/P188 1/10 (w/w)) were

dissolved in water. Then 3.12 g of glycofurol were introduced in the solution to form a 137 suspension. After an incubation at 4°C for 30 min, the nanoprecipitated protein was 138 recovered by centrifugation (10,000 g, 4°C, 30 min). The precipitated protein was 139 dispersed in 2 mL solution of dichloromethane/acetone 3/1 (v/v) containing 150 mg of 140 penta-block copolymer. The suspension was emulsified in 90 mL PVA (6% w/v) at 1°C 141 and mechanically stirred at 1,000 rpm for 1 min in a glass vessel (4.5 cm inside diameter) 142 with a dual wall to control the temperature. 100 mL of cold deionized water were then 143 added and the emulsion was stirred for 10 min more. Then, the emulsion was poured into a 144 second glass vessel (10 cm inside diameter, with a dual wall) containing 500 mL of 145 deionized water (1°C) and stirred continuously at 550 rpm during 20 min to extract the 146 solvent. In all steps, an overhead stirrer with a 4 blades propeller was used (Heidolph[®]) 147 RZR 2041, Schwabach, Germany). Finally, microspheres were recovered by filtration on a 148 5 µm filter (HVLP type, Millipore SA, Guyancourt, France), washed, freeze-dried and 149 stored at -20°C. 150

151 2.2.2. Preparation of microspheres using polymer blend

The formulation process was similar to the standard procedure describe above. The mixture of lysozyme and P188 was nanoprecipitated in glycofurol using the same protocol. In this case, a physical blend of 50P40 and 50P20 copolymers (with a weight ratio 1/1) was dissolved in DCM/acetone (3/1, v/v). The nanoprecipitated protein was dispersed in a 2 mL solvent mixture containing 150 mg of the copolymer blend. Later on, the emulsification and solvent extraction/evaporation steps were performed using the standard procedure described above.

159 2.2.3. Strategy of batch mixing following the preparation of microspheres

The 50P40-MS and 50P20-MS were prepared separately following the standard procedure. Then, equal amounts of 50P40-MS and 50P20-MS (15 mg) were suspended in 1 mL of water. The mixture was gently mixed using the vortex prior to be freeze-dried. The resulting microsphere mixture (50P40-MS/50P20-MS 1/1, w/w) was stored at -20°C for further study.

165 2.3. Microsphere characterization

166 2.3.1. Microsphere morphology and mean size

The microsphere mean size was measured using a Coulter[®] Multisizer (Coultronics,
Margency, France). Microspheres were dispersed in an isotonic saline solution prior to be
analyzed (Isoton[®] II solution, Coultronics, Margency, France).

Microsphere surface morphology was observed using scanning electron microscopy -170 SEM (JSM 6310F, JEOL, Paris, France). Freeze-dried microspheres were mounted onto 171 metal stubs using double-sided adhesive tape, vacuum-coated with a film of carbon using 172 a MED 020 (Bal-Tec, Balzers, Lichtenstein) before being analyzed. The microsphere 173 internal morphology was studied using the following process [13]. An appropriate amount 174 of microspheres was dispersed into 1 mL of Tissue-Tek® (Sakura Finetek, USA) and 175 freezed (-20°C, 1 hour). Resulting blocks were cut into slices (20 µm-thickness) at -15°C 176 using a micro-cutting device (Leica, Nanterre, France). Slices were rinsed three times with 177 178 cold water (1°C) before being freeze-dried. Samples were then analyzed by SEM as described above. 179

180 2.3.2. Glass transition temperature of the copolymers

To measure the glass transition of raw copolymers and microspheres, differential scanning calorimetry (DSC) analysis was carried out. DSC measurements were performed under nitrogen on a Perkin-Elmer Instrument DSC 6000 thermal analyzer. Samples were subject to a first heating ramp from -50°C to 200°C (<u>10°C/min</u>), followed by a cooling step (<u>10°C/min</u>) and finally a second heating ramp from -50°C to 200°C (<u>10°C/min</u>) was performed to measure the glass transition temperature (Tg).

187 **2.3.3. Protein encapsulation efficiency**

The amount of entrapped lysozyme was determined by dissolving 5 mg of microspheres in 0.9 mL DMF in a silanized glass tube at room temperature under agitation (1 hour). Then, 3 mL of a Tris solution (Tris 0.05 M buffer and 0.09% w/v NaCl, pH 7.4) was added and the agitation was carried on for 1 hour more. The resulting solution was introduced into a *Micrococcus lysodeikticus* test for active lysozyme quantification as described previously
 [13]. The protein encapsulation efficiency (EE) was determined in triplicate.

194 2.3.4. *In vitro* release of active lysozyme from microspheres

5 mg of lysozyme-loaded microspheres were dispersed in 375 µL of buffer solution (Tris 195 0.05 M buffer, pH 7.4, containing 0.1% w/v BSA and 0.09% w/v NaCl) [24] using 1.5 mL 196 polyethylene microtubes (Eppendorf type). The suspension was incubated in a water bath 197 at 37°C and oscillated on a rack at 125 rpm. At defined time intervals, tubes were removed 198 199 and centrifuged for 5 min at 3,000 g. The supernatant was collected, tested for active lysozyme quantification and replaced by fresh buffer. Release profiles were determined on 200 at least 3 different microsphere batches and for each one, at least 3 experiments were 201 carried out. 202

To investigate the effect of the release temperature on the microsphere morphology, release tests were carried out in a similar way but the water bath was controlled at 22°C or placed in a 4°C cold chamber.

206 2.3.5. Microsphere morphology change during the release test

15 mg of lysozyme-loaded microspheres were dispersed into 1,050 µL of buffer solution 207 (Tris 0.05 M buffer, pH 7.4, containing 0.1% w/v BSA and 0.09% w/v NaCl) in 1.5 mL 208 polyethylene microtubes (Eppendorf type). The suspension was incubated in a water bath 209 at 37°C and oscillated on a rack at 125 rpm. After a defined duration, tubes were 210 centrifuged for 5 min at 3,000 g. The supernatant was removed and the remaining particles 211 were washed 3 times with cold water (1°C) before being freeze-dried. For microsphere 212 cross-sectional observations, microspheres were cut and analysed with SEM as described 213 214 above.

215

216 **2.4. Statistical Analysis**

The quantitative variables were described using the mean +/- 95% confident interval when
variable distribution was normal, and otherwise using median and Inter-Quartile Range.

- 219 Both batches and samples were taken into account to assess the global variability of the
- 220 process. In view of the observation, a non-parametric Mann-Whitney test was performed
- 221 <u>when necessary.</u>

222

223 3. RESULTS AND DISCUSSION

224

225 **<u>3.1 Glass transition temperature</u>**

- 226 The glass transition temperature (Tg) of raw copolymers (table 1) was 24.3°C for 50P40
- 227 and 9.6°C for 50P20. Both values were smaller than the ones reported in the literature for
- bulk PLGA where Tg varies from around 50°C for 40kDa to around 40°C for 20kDa
- 229 PLGA [25]. In a previous study, it was shown that when PLGA blocks were
- 230 copolymerized with a central PEO blocks, the resulting triblock Tg decreased noticeably
- as the relative amount of the hydrophilic block was increased [12]. This was also observed
- in the present study where the relative amount of PEO increased from 9.5% (w/w) in
- 50P40 to 17% (w/w) in 50P20. Decreases of Tg were mainly due to plasticizing effects
- 234 provided by the PEO block [26].
- 235 Besides, Tg values of uncharged lyophilized microspheres were very closed to those of
- 236 raw copolymers. It is known from the literature that the surfactant, especially PVA due to
- its hydroxyl groups [27], and residual solvents like DCM [28] can significantly impact Tg
- 238 values. Then, it can be assumed a good elimination of PVA and residual solvents during
- the process.
- 240 On the other hand, the co-encapsulated poloxamer lowered the Tg values of microspheres,
- the effect being more pronounced for 50P20-MS where Tg fell from 9.1°C to 5.5°C.
- 242 Incorporating the lysozyme enhanced these phenomena. Plasticizing effects of additives
- 243 <u>like pegylated compounds or proteins have been widely reported in the literature [29][30].</u>
- 244 <u>These observations were important to explain the morphology of microspheres formulated</u> 245 at 1°C and their behaviors during the protein release process at 37°C. In this work, Tg

246 were measured on dry (lyophilized) products. But it is known that hydrated products,

247 especially porous ones, display lower Tg [31]. Any how it was reasonable to assume that

248 hydration should not modify our conclusions as the Tg of hydrated 50P20-MS should still

- 249 <u>be lower than the one of hydrated 50P40-MS.</u>
- **[Table 1]** Glass transition temperatures of different copolymers.
- 251

252 **<u>3.2. Morphology, mean size and encapsulation efficiency</u>**

- Both types of microspheres were formulated below the glass transition temperature of 253 their constitutive copolymer. For 50P40, the microsphere formation took place at 5% 254 below Tg. They exhibited smooth surface with no visible pores. Their internal structure 255 was porous with closed small pores distributed uniformly in the volume (Figure 1A). For 256 50P20, the microsphere formation took place at 1% below Tg. They were highly porous 257 with numerous interconnected pores visible on the surface as well as in the interior (Figure 258 1B). 259 During the solvent/cosolvent extraction step, the phase separation occurs into the initial 260 polymer solution droplets with coexisting polymer rich and polymer poor phases. The 261 further removal of solvent induces the glass transition in the polymer rich phase, and the 262 microsphere solidification comes to an end. The phase transition kinetics becomes arrested 263 as the glassy state is reached in the dense polymer phase while the polymer poor phase 264 will form the future pores in the microsphere structure. The competition between the 265 ongoing phase separation and the appearance of the glassy state has been described and 266 modeled in the literature [32][33] and could explain the structural differences observed. 267
- ²⁶⁸ 50P40-MS reached the glassy state faster than 50P20-MS and consequently developed less
- 269 porous structures compared to 50P20-MS.
- 270

The median particle size and the interquartile range [IQR] of 50P40-MS were respectively 39.0 μ m [38.7, 41.2] and 38.3 μ m [37.6, 41.5] for 50P20-MS (Figure 1C). Encapsulation efficiency (EE) values ranged from 52 to 61% regardless the copolymers used (Figure

1C). Both types of microspheres were not significantly different considering their size (p =

0.4681) and their encapsulation efficiency (p = 0.6501). <u>This result may be due to a</u>

276 <u>statistical lack of power (the sampling was too small) or to the absence of real differences</u>

in the size or EE of 50P20-MS and 50P40-MS.

The rather low encapsulation yield can be attributed to the leakage of the protein into the external aqueous phase during the microparticle formation [34][35].

[Figure 1] Characterisation of MS produced using copolymers: (A) external/internal 280 structure of 50P40-MS; (B) external/internal structure of 50P20-MS. In both cases, white 281 scale bars represents 10 μ m; (C) particle mean size (n=5) and encapsulation efficiency 282 (n=5 for 50P40-MS and n=10 for 50P20-MS) as function of copolymers. Grey plot aims 283 to compare the distribution of both interest variable as function of copolymers types. The 284 boxes indicate the 75th percentile (upper horizontal line), median (black bold horizontal 285 line), and the 25th (lower horizontal line) percentiles of the distribution. Surrounding the 286 287 boxed (shaded area) on each side is a rotated kernel density plot.

288

289 **3.3. Protein release profiles**

Drug release from PLGA-based microspheres can follow mono-, bi- or tri-phasic profiles 290 depending on various factors including the hydrophilic balance or their morphology [29]. 291 Polymer characteristics (Tg), porosity and mean particle size are recognized as critical 292 factors for the protein release profile from PLGA-based microspheres [37][38]. In the 293 present study, the microsphere diameter was kept constant to avoid its impact on the 294 profile. The active protein release from 50P40-MS (dense surface/porous interior; Figure 295 1A) was carried out during 8 weeks and compare to 50P20-MS (porous surface/porous 296 interior; Figure 1B). 297

[Figure 2] Average protein release profiles from microspheres of copolymer 50P20 (triangles) and copolymer 50P40 (squares). Error bars represent 95% confident intervals of mean values (n=24 for 50P20 and n=10 for 50P40). The dashed line is a guide to the eyes, it figures out the ideal desired profile.

Figure 2 shows release profiles for both 50P40-MS and 50P20-MS. Lysozyme release 302 from 50P40-MS complied with a bi-phasic profile with a moderate burst (11.2% \pm 1.3% 303 released after 24 hours). The release was then sustained and linear until Day 56 but the 304 cumulated amount was $53.8\% \pm 6.2\%$ only. Despite a highly porous surface and a porous 305 internal structure, 50P20-MS exhibited a biphasic protein release with also a moderate 306 burst after 24 hours (15.2% \pm 1.1%), followed by a sustained and complete release 307 (ending-up with 93.4% \pm 3.1% of active lysozyme released) but not linear as emphasized 308 by the dashed line in figure 2. 309

For protein loaded microspheres, a bi-phasic release profile is commonly achieved with porous microspheres [38][39] or with microspheres having non-porous surface but porous internal structure [40]. The mechanism of drug release from PLGA is impacted by both the diffusion process and the polymer erosion [41][42]. However, due to the very low diffusion coefficient of a protein embedded in a PLGA matrix, its transport through the pores was proposed as the main release mechanism [6].

316

317 **3.4.** Microsphere size and morphology change during the release test

To clarify involved mechanisms, particle sizes and morphologies were monitored during the release (Figure 3 and Figure 4). After 2 days, 50P40-MS showed the appearance of few pores on their surface with an increase of the pore density in the peripheral structure (Figure 4-A2). These morphology changes were along with a 12% size increase (Figure 3). This phenomena was more marked on Day 10 with a stabilised size until Day 28 (Figure 4-A3).

[Figure 3] Evolution of microsphere mean sizes as a function of the release time for 50P20 (triangles) and 50P40 (squares). Error bars represent 95% confident intervals of the mean value (n=6 for 50P20 and 50P40).

A delayed polymer degradation and erosion were previously observed for porous PLGAbased microspheres and have been explained by facilitated interchanges between the internal environment and the external buffer medium. This reduced the acidification and
autocatalysis phenomena [43][44] prolonging the drug release duration [45].

[Figure 4] Morphological changes of 50P40-MS (left column) and 50P20-MS (right
 column) during the release test (white scale bars represent 10 µm). After Day 28 MS could
 not be observed by SEM.

The active protein release was incomplete and a plateau around 54% was observed from Day 56 up to Day 70 (data not shown, n=3). This phenomenon has already been observed for 60 µm PLGA-PEG-PLGA microspheres and it was demonstrated that the protein was entrapped and degradated within the dense microsphere core [12].

The scenario was totally different for 50P20-MS which contained a higher amount of hydrophilic segments than 50P40-MS (17% vs 9.5% w/w respectively) with a lower Tg (3.5°C vs 15.9°C respectively, see Table 1).

The 50P20-MS size decreased continuously from the beginning to Day 28 (Figure 3). It appeared clearly from the SEM images that a pore-closing process occurred during the first 2 days. It was accompanied by a complete reorganization of the internal structure. Microsphere structure became homogeneous with no visible pores neither on the surface nor in the interior. This phenomenon could explain the reduced burst while a significant one is classically expected for microsphere showing an initial porous surface [46][47].

From Day 10, microspheres were no longer spherical and became brittle due to the polymer degradation/erosion.

To explain the drastic change observed at Day 2 for 50P20-MS, their morphology was investigated for various temperature of the release media, 3°C, 22°C, 37°C (Figure 5). These temperatures corresponded to three different relative distances to the <u>dry</u> microsphere Tg (-0.2%, +6.7%, +12,1% respectively). From figure 5, it was clearly evidenced that no reorganisation occurred at 3°C. A moderate one can be seen at 22°C and a complete one with, a pore closing process, was observed at 37°C. This demonstrated that the mobility of the polymer chains was a key parameter to explain this reorganization. **[Figure 5]** Internal structure at day 2 of 50P20-MS incubated into the release medium at different temperature : (A): 3° C; (B): 22° C; (C): 37° C. White scale bars represent 10 μ m.

50P20-MS have shown a nearly complete active protein release after 8 weeks $(93 \pm 3\%)$ with a moderate burst but a non constant release rate (See the ideal expected profile in figure 2), while 50P40-MS had a constante rate after a moderate burst, but did not achieve a complete release $(54 \pm 7\%)$.

Both kinds of delivery system were good candidates for further optimizations using combination strategies. Indeed, a complete protein release with a moderate burst and a constant rate could ideally be wanted for some given therapeutic applications.

365

366 **3.5. Adjustment of protein release profile**

We have tried to design an optimal protein delivery system using two strategies: either a polymer blending or a microsphere mixing.

369 **3.5.1. Release profile from polymer blending microspheres**

370 The mean size $(39.9 \pm 3.4 \,\mu\text{m})$ and encapsulation yield $(45.9 \pm 1.9\%)$ (n=3) of microsphere from polymer blending (hereafter called blend-microspheres) were rather 371 similar to those of 50P40-MS and 50P20-MS. Blend-microspheres exhibited numerous 372 pores on the surface and in the internal structure (Figure 6-A1). Regarding the release of 373 the protein (Figure 6-A2), the initial burst $(20.4 \pm 1.0\%)$ was higher than previously 374 observed. Then the subsequent protein release was rather linear from Day 1 to Day 42 375 $(R^2 = 0.9026)$ and reached a plateau (69.1 ± 4.9% on Day 56). This kind of strategy has 376 already been used with more or less success for PLA and PLGA microspheres [18][21]. 377

In the present study, the polymer blend strategy was not an improvement.

[Figure 6] (A1) Initial morphology of blend-MS (white scale bars represent 10 μ m); (A2) average protein release profile from microspheres of a copolymer blend 50P20 and 50P40 (see text for details). Error bars represent 95% confident intervals of mean values (*n*=13); (B1) Initial morphology of mix-MS, porous particles represent 50P20-MS while nonporous surface particles correspond to 50P40-MS (white scale bar represents 10 μ m); (B2) Average protein release profile from a mixture of microspheres of copolymer 50P20 and 50P40 (see text for details). Error bars represent 95% confident intervals of mean values (*n*=8). The red straight line represents a linear fit to the data (R² = 0.9795) from Day 1 to Day 56.

388 **3.5.2. Release profile from a mixture of microspheres**

Concerning the microsphere mixing strategy, SEM picture (Figure 6 - B1) clearly revealed the two different types of microspheres (hereafter called Mix-microspheres). The initial burst was not significantly modified $(15.2 \pm 4.0\%)$. Then the subsequent protein release was linear from Day 1 to Day 49 (R² = 0.9915) and reached a plateau (82.3 ± 2.6% on Day 56) (Figure 6 - B2). This was an improvement in the protein release control compared to the non linear profile of 50P20-MS.

Hickey and co-workers [48] developed PLGA-MS for continuous delivery of 395 dexamethasone over a month. Authors proposed to use a physical mixture of fresh and 396 predegraded PLGA-MS. The resultant mixture exhibited an interesting profile with a 397 moderated initial burst (from 15% to 20%) followed by a linear release but end up at 398 around 60% after Day 3. Duvvuri and co-workers [49] prepared a physical mixture of two 399 types of microspheres (containing ganciclovir) and dispersed the mixture into a 400 thermogelling polymer. The resultant mixture exhibited an intermediate release profile 401 compared to individual ones. In spite of a nearly 100% ganciclovir released after 25 days, 402 the profile was tri-phasic with an initial massive burst. Herein, we successfully prepared a 403 mixture of protein-loaded microspheres with the desired release profile: bi-phasic with a 404 moderate burst, followed by a nearly complete linear release. The current achievement 405 could be considered as a promising protein sustained release system. 406

407

408 4. CONCLUSION

The protein release profile from penta-block copolymer microspheres was successfully modulated using a mixture strategy based on 50P20-MS and 50P40-MS. Both had the

same size, a moderate burst and complementary profiles (linear but non complete for 411 50P40-MS; non linear but complete for 50P20-MS) The microsphere mixture (1/1, w/w) 412 induced a bi-phasic protein release profile with a moderate initial release followed by a 413 nearly complete linear protein release over 8 weeks. This study highlighted the potential of 414 this kind of penta-block polymers where the mass ratio of PEO blocks influenced clearly 415 the Tg and consequently the release behavior at 37°C associated with the microsphere 416 mixture strategy. The 1:1 mass ratio was used as a starting point but could be finely tune 417 to control the protein release. 418

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426 **Declaration of Interest**

427 The authors declare no conflict of interest.

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