

Amino Acids

Radiopharmacological characterization of ⁶⁴Cu-labeled α-MSH analogs for potential use in imaging of malignant melanoma --Manuscript Draft--

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Abstract:	<p>The melanocortin-1 receptor (MC1R) plays an important role in melanoma growth, angiogenesis and metastasis, and is overexpressed in melanoma cells. α-Melanocyte stimulating hormone (α-MSH) and derivatives are known to bind with high affinity at this receptor that provides the potential for selective targeting of melanoma. In this study, one linear α-MSH-derived peptide Nle-Asp-His-D-Phe-Arg-Trp-Gly-NH₂ (NAP-NS1) without linker and with εAhx-β-Ala linker, and a cyclic α-MSH derivative, [Lys-Glu-His-D-Phe-Arg-Trp-Glu]-Arg-Pro-Val-NH₂ (NAP-NS2) with εAhx-β-Ala linker were conjugated with p-SCN-Bn-NOTA and labeled with ⁶⁴Cu. Radiochemical and radiopharmacological investigations were performed with regard to transchelation, stability, lipophilicity and in vitro binding assays as well as biodistribution in healthy rats. No transchelation reactions, but high metabolic stability and water solubility were</p>	

	<p>demonstrated. The linear derivatives showed higher affinity than the cyclic one. [64Cu]Cu-NOTA-εAhx-β-Ala-NAP-NS1 ([64Cu]Cu-2) displayed rapid cellular association and dissociation in murine B16F10 cell homogenate. All [64Cu]Cu-labeled conjugates exhibited affinities in the low nanomolar range in B16F10. [64Cu]Cu-2 showed also high affinity in human MeWo and TXM13 cell homogenate. In vivo studies suggested that [64Cu]Cu-2 was stable, with about 85% of intact peptide in rat plasma at 2 h p.i. Biodistribution confirmed the renal pathway as major elimination route. The uptake of [64Cu]Cu-2 in the kidney was 5.9% ID/g at 5 min p.i. and decreased to 2.0% ID/g at 60 min p.i.</p> <p>Due to the prospective radiochemical and radiopharmacological properties of the linear α-MSH derivative [64Cu]Cu-2 this conjugate is a promising candidate for tracer development in human melanoma imaging.</p>
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1
2 **Abstract**
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7 targeting of melanoma.
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13 without linker and with ϵ Ahx- β -Ala linker, and a cyclic α -MSH derivative,
14 [Lys-Glu-His-D-Phe-Arg-Trp-Glu]-Arg-Pro-Val-NH₂ (NAP-NS2) with ϵ Ahx- β -Ala linker were
15 conjugated with p-SCN-Bn-NOTA and labeled with ⁶⁴Cu. Radiochemical and radiopharmacological
16 investigations were performed with regard to transchelation, stability, lipophilicity and in vitro binding
17 assays as well as biodistribution in healthy rats.
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26 No transchelation reactions, but high metabolic stability and water solubility were demonstrated. The
27 linear derivatives showed higher affinity than the cyclic one. [⁶⁴Cu]Cu-NOTA- ϵ Ahx- β -Ala-NAP-NS1
28 ([⁶⁴Cu]Cu-2) displayed rapid cellular association and dissociation in murine B16F10 cell homogenate.
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30 showed also high affinity in human MeWo and TXM13 cell homogenate. In vivo studies suggested that
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44 derivative [⁶⁴Cu]Cu-2 this conjugate is a promising candidate for tracer development in human
45 melanoma imaging.
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Introduction

Melanoma accounts for less than 2% of skin cancer but it causes a large majority of skin cancer death. If melanoma can be detected in an early stage to be removed surgically, the overall 5-year survival rate is 98%. However, it dramatically falls to 63% when lymph nodes were affected and even to 16% when metastases occur (American Cancer Society 2015).

Current clinical diagnosis of melanoma relies on the morphology of melanoma, but the diagnostic accuracy of melanoma differs from more than 77% for the superficial-spreading type down to 41% for nodular type, or only 21% for desmoplastic melanomas (Tandler et al. 2012; Lin et al. 2014).

Therefore, it is highly desired to develop effective imaging tracers for precise detection of melanoma, especially for primary metastatic melanoma. The melanocortin type 1 receptor (MC1R) is overexpressed in melanoma cells (Loir et al. 1999; Salazar-Onfray et al. 2002; López et al. 2007), and represents a distinct molecular target for malignant melanoma imaging.

Wild type α -melanocyte stimulating hormone (α -MSH) is a potent naturally occurring melanotropic peptide to activate MC1Rs, but it displays a short half-life in culture medium (Sawyer et al. 1980) and blood serum (Ashton et al. 1977; Rudman et al. 1983; Eberle 1988). The replacement of Met⁴ and Phe⁷ by Nle and D-Phe, respectively, in α -MSH prolonged the half-life, leading to [Nle⁴,D-Phe⁷]- α -MSH (NDP-MSH) that has even higher affinity than α -MSH and is more stable (Sawyer et al. 1980; Siegrist et al. 1988; Lunec et al. 1992). Even shorter linear peptides [Ac-Nle⁴, Asp⁵, D-Phe⁷]- α -MSH₄₋₁₁ (NAPamides) also show high affinities in the low nanomolar range at MC1R (Froidevaux et al. 2004; Cheng et al. 2007; Bapst et al. 2007). In this regard, Froidevaux et al. (2004) conjugated the metal chelator DOTA to the ϵ -amino group of the C-terminal lysine (Lys¹¹) of NAPamide (DOTA-NAPamide) and radiolabeled with ¹¹¹In and ⁶⁷Ga/⁶⁸Ga. Both ¹¹¹In-DOTA-NAPamide and ⁶⁷Ga-DOTA-NAPamide exhibited high tumor accumulation, indicating that modification to the terminal Lys¹¹ did not compromise receptor affinity, and low kidney uptake leading to high tumor-to-kidney ratios (Froidevaux et al. 2004, 2005). In another study, Cheng et al. (2007) radiolabeled DOTA-NAPamide with ⁶⁴Cu and found that [⁶⁴Cu]Cu-DOTA-NAPamide showed high accumulation in tumors, but the radioactivity levels in liver and kidney were relatively high. It is suggested that the high hepatobiliary radioactivity accumulation was primarily caused by instability of [⁶⁴Cu]Cu-DOTA coordination in vivo (Cheng et al. 2007). Nevertheless, NAPamides are proposed to be interesting agents for targeting melanoma. Besides, it has been shown that cyclic α -MSH peptides also have high binding affinity to

1 MC1Rs and better resistance to proteolysis (Castruciet al. 1984; Giblin et al. 1998; Cheng et al. 2004;
2 Fung and Hruby 2005; Guo et al. 2009). There are several cyclization methods: cyclization via
3 disulfide bonds (Chen et al. 2001), cyclization via metal coordination (Giblin et al. 1998; Chen et al.
4 2000) and cyclization via lactam bridges (Chen et al. 2001; Chen et al. 2002; Raposinho et al. 2008;
5 Miao et al. 2008). Lactam cyclized peptides are of great interest since an improvement of both, in vivo
6 stability and melanoma tumor uptake has been demonstrated. A lactam-cyclized α -MSH analog, based
7 on the sequence of melanotan II has been prepared and conjugated with a pyrazolyldiamine backbone
8 chelator. The conjugate was radiolabeled with ^{99m}Tc -tricarbonyl and the radiolabeled complex
9 displayed higher tumor uptake than its linear counterpart in the B16F1 melanoma mouse model.
10 However, the clearance from the liver and kidney as well as the overall excretion rate were negatively
11 affected by cyclization (Raposinho et al. 2008).

12 A different order of amino acids in receptor-targeting peptides can alter lipophilicity, radiolabeling
13 chemistry, and linkers could affect the pharmacokinetic profiles (Schottelius and Wester 2009). The
14 introduction of a linker between a radionuclide in a bifunctional chelator (BFC) complex and a peptide
15 also can influence the physicochemical properties of the radiolabeled peptide, causing steric effects of
16 the chelator on the binding affinity to the receptors and thus modifying the pharmacokinetic profile
17 such as clearance rate from the kidney (Yang et al. 2010; Fani and Maecke 2012).

18 In the present study, NAPamide analogs with and without ϵ -Ahx- β -Ala linker (indicated as β -Ala)
19 NAP-NS1 (no linker) and NAP-NS1- β -Ala were used. These two linear peptides together with the
20 cyclic peptide NAP-NS2- β -Ala were studied as agents to target the MC1R. p-SCN-Bn-NOTA was the
21 chelator coupled to the peptides because it forms a stable complex with copper(II) (Cooper et al. 2012).
22 The radiopharmacological behavior of these ^{64}Cu -labeled peptides was investigated, and the most
23 promising one was selected for studies on human melanoma cells with regard to further investigations
24 on appropriate mouse xenograft models.

Materials and Methods

Chemicals and reagents

⁶⁴Cu was produced at the Helmholtz-Zentrum Dresden-Rossendorf by a biomedical cyclotron (Cyclone 18/9, IBA, Louvain la Neuve, Belgium). Two linear peptides NAP-NS1 (no linker; Nle-Asp-His-D-Phe-Arg-Trp-Gly-NH₂) and NAP-NS1-β-Ala (with β-Ala linker; ε-Ahx-β-Ala-Nle-Asp-His-D-Phe-Arg-Trp-Gly-NH₂) as well as one cyclic peptide NAP-NS2-β-Ala (with β-Ala linker; ε-Ahx-β-Ala-Lys-Glu-His-D-Phe-Arg-Trp-Glu-Arg-Pro-Val-NH₂, cyclized from Lys³ to Glu⁹) were custom made by GL Biochem, Shanghai, Ltd following the previously reported procedure from Biondi et al. (2010). p-NOTA-Bn-SCN (NOTA) was purchased from Macrocyclics, Inc., USA. (Nle⁴, D-Phe⁷)-α-MSH (NDP-MSH) was purchased from Bachem AG, Switzerland. [¹²⁵I]-NDP-MSH was obtained from Biotrend Chemikalien GmbH, Germany. All other chemical and biological reagents were purchased from Sigma Aldrich, USA, and Biochrom AG, Germany, respectively. Semi-preparative high-performance liquid chromatography (HPLC) was carried out on a chromatography system equipped with a Perkin Elmer UVIVIS LC290 UV detector and a flow-through radioactivity detector (Raytest Ramona) to purify and analyze the conjugates. Zorbax C18 column with inner diameter of 8 mm was used. The mobile phase was solvent A: water with 0.1% trifluoroacetic acid (TFA) and solvent B: acetonitrile with 0.1% TFA. The HPLC gradient was 0-30 min 95%-50% solvent A, 30-35 min 50% A, 35-36 min 50%-95% A, 36-41 min 95% A with a flow rate of 3 mL/min. Radioactive samples were counted using 1480 WIZARD 3" automatic gamma counter (PerkinElmer, Inc., USA). Electrospray ionization-mass spectrometry (ESI-MS) was carried out with micromass tandem quadrupole mass spectrometer (Waters Corporation, USA).

Preparation and (radio)chemical characterization of [⁶⁴Cu]Cu-NOTA-peptide conjugates

NOTA peptides conjugates 10 nmol of p-SCN-Bn-NOTA, 10 nmol of the native peptides (NAP-NS1, NAP-NS1-β-Ala and NAP-NS2-β-Ala) and 100-150 nmol triethylamine (TEA) in dimethylformamide (DMF) was mixed and incubated at 20°C overnight. Afterwards, 100 μL water was added to quench the reaction. The products NOTA-NAP-NS1 (**1**), NOTA-NAP-NS1-β-Ala (**2**) and NOTA-NAP-NS2-β-Ala (**3**) were purified by semi-preparative HPLC and identified by ESI-MS.

⁶⁴Cu-labeling of the NOTA-peptides 1-2 nmol of **1**, **2** or **3**, dissolved in 100 μL H₂O, was mixed with [⁶⁴Cu]CuCl₂ (40-80 MBq) in 400 μL 0.2 M 2-(N-morpholino) ethanesulfonic acid (MES) buffer (pH 6.2) and incubated at 50°C for 20 min. Thereafter, the mixture was separated by semi-preparative

1 HPLC to get purified radiotracers with high specific activity. [⁶⁴Cu]Cu-NOTA-peptides isolated from
2 semi-preparative HPLC were concentrated with a RP-18 cartridge and washed with 2 mL ethanol/H₂O
3 (v/v 1/1). The ethanol was removed by N₂. The radiochemical purities (RCPs) of
4 [⁶⁴Cu]Cu-NOTA-peptides were also monitored by semi-preparative HPLC.
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7 **Preparation of non-radioactive ^{nat}Cu-NOTA-peptide conjugates** 5-7.5 μmol Cu(NO₃)₂ x 2 H₂O in 300
8 μL water was mixed with 5 μmol **1**, **2** or **3** in 500 μL 0.2 M MES buffer (pH 6.2) (ratio of Cu(NO₃)₂ x 2
9 H₂O to NOTA-peptides 1-1.5/1) and shaken under 1000 rpm at 50°C for 60 min. Thereafter,
10 ^{nat}Cu-NOTA-NAP-NS1 (^{nat}Cu-**1**), ^{nat}Cu-NOTA-NAP-NS1-β-Ala (^{nat}Cu-**2**) and
11 ^{nat}Cu-NOTA-NAP-NS2-β-Ala (^{nat}Cu-**3**), were purified by semi-preparative HPLC and characterized by
12 ESI-MS or Maldi-MS.
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20 **Challenge experiments** 100 μL of [⁶⁴Cu]Cu-**1**/MES ([⁶⁴Cu]Cu-**2**/MES or [⁶⁴Cu]Cu-**3**/MES) was added
21 to 400 μL histidine or cysteine solution (final concentration 2 nM and 0.2 nM). The mixture was
22 vortexed and incubated at 37°C for 1 h and 24 h. Aliquots of the reaction mixture were taken and
23 analyzed by semi-preparative HPLC.
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28 **Stability measurements in phosphate buffer and human serum** 100 μL of [⁶⁴Cu]Cu-**1**/MES
29 ([⁶⁴Cu]Cu-**2**/MES or [⁶⁴Cu]Cu-**3**/MES) was mixed in 300 μL phosphate buffer (pH 7.4) or 300 μL
30 human serum. After 1 h or 24 h of incubation at 37°C, the buffer samples were analyzed by
31 semi-preparative HPLC. The serum samples were first treated with ethanol (twice the volume of the
32 mixture) and centrifuged at 4°C for 30 min (13,200 rpm). The liquid phase was filtrated with the filter
33 (VWR sterile syringe filter, 0.2 μm PES) and the filtrate was analyzed by semi-preparative HPLC.
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41 **Determination of lipophilicity.** 20μL of [⁶⁴Cu]Cu-**1**/MES ([⁶⁴Cu]Cu-**2**/MES or [⁶⁴Cu]Cu-**3**/MES) (0.2
42 MBq) was diluted in 500 μL of 1 M HEPES buffer (pH=7.4). 500 μL of n-octanol was added and the
43 mixture stirred vigorously at 23°C for 30 min. Subsequently, the mixture was centrifuged at 23°C for
44 30 min (14,000 g) 450 μL of both water and n-octanol phases were taken and centrifuged again. The
45 radioactivity of 100 μL of both the HEPES buffer phase and the octanol phase was measured in a
46 gamma counter and the octanol/water partition coefficient (Log D_{o/w}) was calculated. The experiments
47 were performed three times.
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56 **Radiopharmacological assays**

57 Binding assays were assessed using cell homogenate of murine melanoma cell line B16F10 (ATCC®
58 CRL-6475™), and two human melanoma cell lines MeWo (ATCC® HTB-65™) and TXM13
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(University of Texas, M.D. Anderson Cancer Center, Houston, USA), as well as the MC1-receptor negative control human embryonic kidney cell line HEK-293 (ATCC® CRL-1573™). The cells were grown as monolayer at 37°C in a humidified atmosphere comprising 5% CO₂ and 95% air in DMEM medium including 10% FCS (Biochrom AG). After washing the confluent cells twice with phosphate buffered saline (PBS) and detaching them with trypsin/EDTA (0.05%/0.02%), the cells were suspended in DMEM and homogenized (Potter-Elvehjem) by forcing 20 times the pestle up and down the rounded vessel on ice. The assays were performed in a final volume of 200 µL.

Competition assay In vitro binding affinity of the non-radiolabeled peptides was assessed in competition binding assays using B16F10 and MeWo cell homogenate and [¹²⁵I]-NDP-MSH as standard radioligand. Homogenized cells were incubated with 40 µL [¹²⁵I]-NDP-MSH (final concentration 0.2 nM) in the presence of increasing concentrations of the three native peptides, **1**, **2**, **3** and ^{nat}Cu-**1**, ^{nat}Cu-**2**, ^{nat}Cu-**3** (final concentrations 5.01×10⁻¹⁴ to 2.45×10⁻⁶ M for B16F10; 5.01×10⁻¹⁴ to 1.23×10⁻⁶ M for MeWo), as well as for comparison NDP-MSH (10⁻¹⁴ to 2.45×10⁻⁵ M) at 23°C for 90 min.

Kinetic assay [⁶⁴Cu]Cu-**2** was selected to conduct a kinetic study in homogenized B16F10 cells. The association rate was evaluated starting the incubation with [⁶⁴Cu]Cu-**2** (final concentration 8 nM) in reverse order (120, 90, 60, 30, 20, 10 and 5 min) at 23°C and simultaneously terminating the incubation of all samples at time 0. In adjacent samples dissociation was initiated by adding 610 µM of NDP-MSH.

Saturation binding assay B16F10 and HEK-293 cell homogenate was incubated with increasing concentrations of [⁶⁴Cu]Cu-**1**, [⁶⁴Cu]Cu-**2** and [⁶⁴Cu]Cu-**3** (0.1 nM to 10 nM for [⁶⁴Cu]Cu-**2** on B16F10 and TXM13 cells, for [⁶⁴Cu]Cu-**1** on B16F10 cells; 0.2 nM to 20 nM for [⁶⁴Cu]Cu-**3** on B16F10 cells, for [⁶⁴Cu]Cu-**2** on MeWo cells; 0.01 nM to 1 nM for [¹²⁵I]-NDP-MSH on B16F10 and TXM13 cells; 0.02 nM to 2 nM for [¹²⁵I]-NDP-MSH on MeWo cells). Thus, MeWo and TXM13 cell homogenate was incubated only with [⁶⁴Cu]Cu-**2**. The three cell lines were incubated with [¹²⁵I]-NDP-MSH (0.016 to 2 nM) for comparison at 23°C for 90 min; adjacent samples received additionally 610 µM of NDP-MSH to obtain the nonspecific binding.

The incubation of all samples was stopped by washing the homogenate with cold PBS four times using a filter (Whatman GF/C, 90 min presoaked in 0.3% polyethyleneimine) in a cell harvester (Brandel, USA). The radioactivity bound to the filter was measured in a gamma counter. In adjacent samples

1 without cell homogenate the pure filter binding was determined. The experiments were performed three
2 times in triplicates. Pharmacological parameters as association and dissociation half time, inhibitory
3 constants (K_i), dissociation constants (K_d) and maximal binding capacities (B_{max}) were calculated by
4 fitting the data using a nonlinear curve fitting program (GraphPad Prism 5.02). The data fitted best to a
5 one-binding-site-model. Determination of protein content of the cell samples from the saturation assays
6 with the bicinchoninic acid (BCA) protein assay kit (Pierce, Thermo Scientific) was used to calculate
7 B_{max} in fmol/mg.
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10 ***In vivo metabolic assay and biodistribution***

11 The animal experiments were performed in accordance to the guidelines of the German Regulationsofr
12 Animal Welfare. The protocol was approved by the local Ethical Committee for Animal Experiments
13 (reference number 24-9168.21-4/2004-1).
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16 Wistar rats (Wistar Unilever, HsdCpb: Wu, Harlan Winkelmann GmbH, Borchon, Germany) were
17 housed under standard conditions with free access to standard food and tap water.
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20 For biodistribution of [^{64}Cu]Cu-2 two groups of rats ($n = 8$ each) were sacrificed under desflurane
21 anesthesia at 5 and 60 min, respectively, after injection of 0.30 ± 0.03 MBq (500 μL). Organs and
22 tissues of interest were removed, and weighed, and the radioactivity was measured in a cross-calibrated
23 well counter (WIZARD, Automatic Gamma Counter, Perkin Elmer, Waltham, MA, USA) or dose
24 calibrator (Aktivimeter Isomed 2000; MED-Nuklear-Medizintechnik, Dresden, Germany). The decay
25 corrected data were normalized to the amount of injected activity calculated from the activity of
26 injection syringes before and after injection and expressed as percentage of injected activity (%ID) or
27 standardized uptake values ($\text{SUV} = \text{ratio of radioactivity per weight of tissue to injected radioactivity}$
28 per rat body weight). Values are quoted as mean \pm standard deviation (mean \pm SD) for one group of
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47 For metabolite studies male Wistar rats ($n = 4$; body weight 180 ± 20 g) were anesthetized with
48 desflurane (9-10%, 30% oxygen/air). The threshold value for breathing frequency was 65 breaths/min.
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Tullamore, Ireland) was introduced into the right femoral artery for arterial blood sampling. A second needle catheter (35G) was placed into a tail vein and was used for [⁶⁴Cu]Cu-2 injection (15 MBq in 500 μL of infusions solution with 5 % ethanol). For metabolic analysis, arterial blood samples were taken 2.5, 5, 10, 20, 30, 60 and 120 min after injection. Arterial plasma was separated by centrifugation (10 min at 1,300 × g) followed by precipitation of the proteins with methanol (2 volumes to 1 volume plasma) followed by 5 min storage at -60°C. The clear supernatant separated by centrifugation was used for analysis. The radio-HPLC system (Agilent 1100 series) applied for metabolite analysis was equipped with UV detection (254 nm) and an external radiochemical detector (RAMONA, Raytest GmbH, Straubenhardt, Germany). Analysis was performed on a Zorbax C18 300SB (250 × 9.4 mm; 4 μm) column with an eluent system A (H₂O + 0.1% TFA) and B (acetonitrile + 0.1% TFA).

Results

Preparation and (radio)chemical characterization of the NOTA-peptide conjugates

Preparation and characterization of NOTA-peptides conjugates The NOTA-peptides **1**, **2** and **3** were synthesized with chemical yields of 42%, 35% and 21%, respectively. They were characterized by ESI-MS or Maldi-TOF-MS. **1**: 1380.44 [M+H]⁺ (measured data), 1379.54 (calculated data); **2**: 1564.38 [M+H]⁺, 782.64 [M+2H]²⁺ (measured data), 1563.78 (calculated data); **3**: 1001.83 [M+2H]²⁺, 667.38 [M+3H]³⁺ (measured data), 1999.30 (calculated data).

Radiochemistry NOTA-conjugated peptides were readily labeled with ⁶⁴Cu at 50°C for 20 min. The chemical structures of the [⁶⁴Cu]Cu-labeled peptides are sketched in **Fig. 1**. In each case, the reaction was followed by RP-HPLC with sequential UV and radiodetection.

After purification, the radiochemical purities of [⁶⁴Cu]Cu-**1** and [⁶⁴Cu]Cu-**2** were over 95%, and the specific activities ranged from 14-30 GBq/μmol.

Fig. 1 Chemical structures of the [⁶⁴Cu]Cu-NOTA-conjugates. **a)** [⁶⁴Cu]Cu-**1**; **b)** [⁶⁴Cu]Cu-**2**; **c)** [⁶⁴Cu]Cu-**3**

To confirm the chemical identity of the radiolabeled compounds, the corresponding ^{nat}Cu-compounds were prepared at millimolar level by reacting in MES buffer at 50°C for 60 min, Cu(NO₃)₂ × 2 H₂O with the selected NOTA-peptide in 1-1.5/1 ratio. Compounds were purified by semi-preparative HPLC and characterized by ESI-MS or Maldi-TOF-MS analyses. After purification the yields for ^{nat}Cu-**1**,

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$^{nat}\text{Cu-2}$ and $^{nat}\text{Cu-3}$ were 41%, 33% and 19%, respectively. The mass spectra showed the expected signals consistent with the formula referable to the complexes: $^{nat}\text{Cu-1}$: 1440.63/1442.78 $[\text{M}+\text{H}]^+$, 721.79/720.89 $[\text{M}+2\text{H}]^{2+}$ (measured data), 1440.07 (calculated data); $^{nat}\text{Cu-2}$: 1625.72 $[\text{M}+\text{H}]^+$, 813.09/814.63 $[\text{M}+2\text{H}]^{2+}$ (measured data), 1624.69 (calculated data); $^{nat}\text{Cu-3}$: 2063.69 $[\text{M}+\text{H}]^+$ (measured data), 2061.84 (calculated data). were used to confirm the $^{64}\text{Cu}\text{Cu-1}$, $^{64}\text{Cu}\text{Cu-2}$ and $^{64}\text{Cu}\text{Cu-3}$. **Fig. 2** shows HPLC analyses of the ^{nat}Cu -compounds (UV) compared with those of the corresponding ^{64}Cu labeled peptides (radiometric). The chromatographic profile displayed superimposable UV and radiometric peaks. Notably, at tracer level, upon the ^{64}Cu -coordination two distinct isomers were observed for ^{64}Cu -labeled linear NOTA-peptides (**Fig. 2** ^{64}Cu Cu-1 and $^{64}\text{Cu}\text{Cu-2}$) (Schlesinger et al. 2011).

For both $^{64}\text{Cu}\text{Cu-1}$ and $^{64}\text{Cu}\text{Cu-2}$ peptides, in HPLC analysis the first isomer appeared about 1.5 ± 0.5 min earlier than the second one, major isomer. On $^{64}\text{Cu}\text{Cu-2}$, the conversion of the isomers was investigated. The second isomer was isolated and immediately analyzed by HPLC. Only one peak corresponding to the major isomer was observed. Injecting 10 min later two isomers were found, in a 1:10 ratio. Since the isomers equilibrate so fast they were not separated from each other.

Fig. 2 Chromatograms of ^{64}Cu -labeled NOTA-peptides (radioactivity detection) and corresponding non-radioactive reference compounds (UV detection). All HPLC runs are performed under the same condition with the same HPLC device

Challenge study An excess of free histidine or cysteine to the ^{64}Cu -labeled peptides yielded in nearly no transchelation reaction. Detection of 94% (histidine) and 93% (cysteine) of intact ^{64}Cu -labeled peptides after 24 h challenge with 1 mM and 10 mM histidine or cysteine, respectively, might imply negligible transchelation.

Stability study in buffer and human serum The stability in phosphate buffer was >99% for $^{64}\text{Cu}\text{Cu-2}$ and $^{64}\text{Cu}\text{Cu-3}$ after 24 h, and for $^{64}\text{Cu}\text{Cu-1}$ about 98% after 24 h. In serum >98% of the ^{64}Cu -labeled peptides was measured, only for $^{64}\text{Cu}\text{Cu-1}$ about 97% after 24h, indicating that $^{64}\text{Cu}\text{Cu-1}$, $^{64}\text{Cu}\text{Cu-2}$ and $^{64}\text{Cu}\text{Cu-3}$ were sufficiently stable both in buffer and serum.

Determination of lipophilicity. The log $D_{o/w}$ values for $^{64}\text{Cu}\text{Cu-1}$, $^{64}\text{Cu}\text{Cu-2}$ and $^{64}\text{Cu}\text{Cu-3}$ obtained by the “shake flask” method under physiological conditions resulted in -2.55 ± 0.035 , -2.30 ± 0.00 and -3.39 ± 0.04 , respectively, demonstrating the hydrophilic nature of the three radiolabeled

peptides. The cyclic conjugate [⁶⁴Cu]Cu-3 displayed a little higher hydrophilic character compared to [⁶⁴Cu]Cu-1 and [⁶⁴Cu]Cu-2.

It is worth noting that despite the high hydrophilicity the labeled peptides showed a high tendency to stick to the wall of vials or injection syringes. To avoid the adsorption phenomenon, after evaporation of the elution solvent [⁶⁴Cu]Cu-1, [⁶⁴Cu]Cu-2 and [⁶⁴Cu]Cu-3 were dissolved in MES buffer (pH=7.0) containing 10% ethanol.

Radiopharmacological assays

Competition In B16F10 cell homogenate, the K_i values for the three native peptides, **1**, **2**, **3** and ^{nat}Cu-1, ^{nat}Cu-2, ^{nat}Cu-3, and in MeWo cell homogenate the K_i values for NAP-NS1-β-Ala, **2** and ^{nat}Cu-2, each in relation to the standard NDP-MSH, were evaluated by competition binding assays using [¹²⁵I]I-NDP-MSH. Applying the K_d values of saturation assays with [¹²⁵I]I-NDP-MSH of 0.19 ± 0.01 nM and 0.23 ± 0.03 nM in B16F10 and MeWo homogenate, respectively, into the Cheng-Prusoff equation, the K_i values were determined (**Table 1**).

Table 1 K_i values of the three native peptides, **1**, **2**, **3** and ^{nat}Cu-1, ^{nat}Cu-2, ^{nat}Cu-3 and NDP-MSH on B16F10 and MeWo cell homogenate (mean ± SEM of three assays)

B16F10						
		K _i (nM)	NOTA	K _i (nM)	^{nat} Cu-NOTA	K _i (nM)
Linear no linker	NAP-NS1	0.5 ± 0.1	1	0.7 ± 0.2	^{nat} Cu-1	0.5 ± 0.02
Linear β-Ala	NAP-NS1-β-Ala	0.5 ± 0.1	2	1.2 ± 0.1	^{nat} Cu-2	3.5 ± 0.5
Cyclic β-Ala	NAP-NS2-β-Ala	12 ± 1	3	81 ± 4	^{nat} Cu-3	138 ± 9
	NDP-MSH	0.01 ± 0.00				
MeWo						
Linear β-Ala	NAP-NS1-β-Ala	1.2 ± 0.1	2	1.5 ± 0.1	^{nat} Cu-2	4.6 ± 0.2
	NDP-MSH	0.7 ± 0.1				

In general, the affinity of the standard compound NDP-MSH (K_i 0.01 ± 0.00 nM) to MCR1 was considerably higher than that of the investigated peptides.

In B16F10 cells, the linear peptides (NAP-NS1, NAP-NS1-β-Ala, **1**, **2**, ^{nat}Cu-1, ^{nat}Cu-2) showed higher affinities with respect to the cyclic peptide conjugates (**Fig. 3**). Indeed, NAP-NS2-β-Ala, **3**, ^{nat}Cu-3 exhibit a considerably decrease of the receptor affinity, with K_i values of 12 nM, 81 nM and 138 nM,

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respectively. In all cases, the NOTA coupling and the metalation with ^{nat}Cu lead to a reduction of the receptor affinity; this was particularly evident for NAP-NS2-β-Ala peptide. Among the linear peptides, the NOTA derivate (**2**) and the Cu-compound (^{nat}Cu-**2**) revealed a slight reduction of the affinity with respect to NAP-NS1-β-Ala, with K_i values of 1.2 nM and 3.5 nM.

Fig. 3 Representative competition curves of the three native peptides; **1**, **2**, **3** and ^{nat}Cu-**1**, ^{nat}Cu-**2**, ^{nat}Cu-**3**, and NDP-MSH versus [¹²⁵I]I-NDP-MSH binding, **a**) on B16F10: ▲ NAP-NS1, △ NAP-NS1-β-Ala, ● NAP-NS2-β-Ala, ○ NDP-MSH; **b**) on B16F10: ▲ **1**, △ **2**, ● **3**, ○ ^{nat}Cu-**1**, ◇ ^{nat}Cu-**2**, * ^{nat}Cu-**3**; **c**) on MeWo cells: ▲ NAP-NS1-β-Ala, △ **2**, ● ^{nat}Cu-**2**, ○ NDP-MSH. Each data point arises from 3 samples. Each curve is representative for 4 assays

For investigation in MeWo human melanoma cells the linear peptides NAP-NS1-β-Ala, **2** and ^{nat}Cu-**2** were applied and data compared with those of the standard peptide NDP-MSH (K_i value of 0.73 ± 0.08 nM, **Fig. 3c**). NAP-NS1-β-Ala, **2** and ^{nat}Cu-**2** compounds showed a high receptor affinity. Notably, in MeWo cells, the affinity of both NDP-MSH and the new investigated compounds was somewhat lower than that in murine B16F10 cells (**Table 1**).

Kinetic assays To determine kinetic binding characteristics [⁶⁴Cu]Cu-**2** was selected for association and dissociation assays on B16F10 cells. **Fig. 4** illustrates a fast association and dissociation time course of [⁶⁴Cu]Cu-**2** with association and dissociation times of about 20 min. After 60 min about 90% of maximal [⁶⁴Cu]Cu-**2** binding was achieved. After association, the dissociation of [⁶⁴Cu]Cu-**2** binding was initiated by addition of NDP-MSH. Nonspecific binding was about 20%. The association and dissociation half-life was 19.4 min and 12.6 min, with an association constant (K_{on}) of 0.0358 nM⁻¹min⁻¹ and a dissociation constant (K_{off}) of 0.0552 min⁻¹, respectively. According to the equation K_d = K_{off}/K_{on}, a resulting K_d of 1.54 nM for [⁶⁴Cu]Cu-**2** in B16F10 cells was determined. The calculated K_d value of [⁶⁴Cu]Cu-**2** to B16F10 cells matched well the K_d value from the saturation assays (K_d 1.74 nM).

Fig. 4 Association and dissociation of [⁶⁴Cu]Cu-**2** binding in homogenized B16F10 cells. After association of 2 h, dissociation was induced by addition of NDP-MSH (final concentration: 6.1 μM) (arrow) and followed up another 2 h. The curve represents one of three independent experiments. Data are mean of triplicates ± SD

Saturation binding assay **Fig. 5** shows typical saturation graphs, obtained incubating [⁶⁴Cu]Cu-**1**, [⁶⁴Cu]Cu-**2** and [⁶⁴Cu]Cu-**3** in homogenates of B16F10, and [⁶⁴Cu]Cu-**2** in MeWo and TXM13 cells. Results were compared to those obtained with the standard [¹²⁵I]I-NDP-MSH peptide.

Fig. 5 Representative graphs of the saturation assays **a)** of [⁶⁴Cu]Cu-1 (left), [⁶⁴Cu]Cu-2 (middle), [⁶⁴Cu]Cu-3 (right) on B16F10 cells, **b)** of [⁶⁴Cu]Cu-2 on MeWo (left) and TXM13 (right) cells, and **c)** of [¹²⁵I]I-NDP-MSH on B16F10 (left), MeWo (middle) and TXM13 (right) cells. ▲ total binding, △ nonspecific binding, ● specific binding. Each curve is representative for three independent experiments

For each compound, the K_d and B_{max} values are presented in **Table 2**. In murine B16F10 cells, the novel ⁶⁴Cu-labeled NAPamides showed high receptor affinity with K_d values in the nanomolar range. For [⁶⁴Cu]Cu-2, data collected in human melanoma MeWo and TXM13 cells, show B_{max} values lower than those obtained in the murine melanoma cell line. In all the cell lines, the affinity of [¹²⁵I]I-NDP-MSH was somewhat higher.

On B16F10 homogenate, the nonspecific binding of the compounds, determined at K_d concentrations, was <10% for [⁶⁴Cu]-1, [⁶⁴Cu]-2 and [¹²⁵I]I-NDP-MSH and in the range of 30-45% for [⁶⁴Cu]-3. Meanwhile, on MeWo and TXM13 cells, the nonspecific for [⁶⁴Cu]-2 and [¹²⁵I]I-NDP-MSH was in the range 30-45% (**Fig. 5**). Furthermore, assays with [⁶⁴Cu]-1, [⁶⁴Cu]-2 and [⁶⁴Cu]-3, as well as [¹²⁵I]I-NDP-MSH using the MC1 receptor-negative cell line HEK-293 revealed no specific binding.

Table 2 Binding parameter of [⁶⁴Cu]Cu-1, [⁶⁴Cu]Cu-2 and [⁶⁴Cu]Cu-3 on homogenate of B16F10, MeWo and TXM13 cells (mean ± SEM of three assays)

Cell line	B16F10		MeWo			TXM13	
	K_d (nM)	B_{max} (fmol/mg)	K_d (nM)	B_{max} (fmol/mg)	K_d (nM)	B_{max} (fmol/mg)	
[⁶⁴ Cu]-1	0.6 ± 0.2	83 ± 10					
[⁶⁴ Cu]-2	1.7 ± 0.2	47 ± 4	2.6 ± 0.4	17 ± 2	1.8 ± 0.7	32 ± 2	
[⁶⁴ Cu]-3	2.1 ± 0.2	21 ± 2					
[¹²⁵ I]I-NDP-MSH	0.2 ± 0.01	37 ± 9	0.2 ± 0.03	1.4 ± 0.1	0.3 ± 0.1	8.0 ± 1.6	

Biodistribution and in vivo stability

Biodistribution and metabolism studies of [⁶⁴Cu]Cu-2 were performed using male Wistar rats, in order to have a first insight into its potential relevance as a radiotracer for in vivo imaging of melanoma. The biodistribution data of [⁶⁴Cu]Cu-2 are presented in **Table 3**. The data were obtained at 5 min and 60 min p.i, after intravenous bolus injection of the radiotracer. 5 min after injection high uptake values were obtained for kidney and intestine, moderately high for lung, blood and hair / skin (see also **Fig. 6**). The other organs show rather low uptake. 60 min after injection, the uptake in the organs decreased,

except for the uptake in the intestine. However, the addition of the uptake from kidney and urine is definitely higher compared to uptake of liver and intestine, already 5 min p.i, but more than twice at high 60 min p.i. showing clearly the excretion pathway via the kidney (**Fig. 6c**).

Table 3 Biodistribution data after injection of 0.3 ± 0.03 MBq of $[^{64}\text{Cu}]\text{Cu-2}$ (500 μL) in desflurane anesthetized Wistar rats, 5 min and 60 min p.i., respectively. Data are expressed as standard uptake value (SUV = ratio of measured radioactivity per tissue weight to injected radioactivity per rat body weigh) after i.v. injection of 0.3 ± 0.03 MBq $[^{64}\text{Cu}]\text{Cu-2}$ (500 μL), presented as mean of 8 rats from each group \pm SD

Organ	5 min p.i.	60 min p.i.
Brain	0.06 ± 0.01	0.01 ± 0.00
Pancreas	0.62 ± 0.20	0.16 ± 0.06
Spleen	0.54 ± 0.22	0.13 ± 0.04
Adrenals	0.83 ± 0.17	0.22 ± 0.08
Kidneys	6.50 ± 1.37	2.13 ± 0.43
Heart	0.78 ± 0.10	0.13 ± 0.02
Lung	1.19 ± 0.13	0.22 ± 0.03
Thymus	0.57 ± 0.14	0.12 ± 0.04
Thyroid*	0.07 ± 0.01	0.01 ± 0.00
Liver	0.74 ± 0.15	0.18 ± 0.02
Femur	0.59 ± 0.07	0.13 ± 0.05
Intestine*	3.74 ± 0.75	7.42 ± 1.35
Stomach*	0.83 ± 0.17	0.51 ± 0.35
Blood	1.46 ± 0.14	0.24 ± 0.05
Hair/ Skin	1.39 ± 0.16	0.28 ± 0.03
Muscle	0.57 ± 0.18	0.14 ± 0.11
Testes	0.39 ± 0.07	0.14 ± 0.04

*for this organs %ID/g tissue was determined.

Fig. 6 Biodistribution after injection of 0.3 ± 0.03 MBq of $[^{64}\text{Cu}]\text{Cu-2}$ (500 μL) in desflurane anesthetized Wistar rats, **a**) 5 min p.i., **b**) 60 min p.i. Data are expressed in mean SUV \pm SD (n = 8); **c**) accumulation of $[^{64}\text{Cu}]\text{Cu-2}$ in liver and intestine together as well as in kidney and urine together, at 5 min and 60 min p.i., respectively

Metabolic analysis showed that 2 h p.i. two main metabolites are present in kidney, to a smaller extent already in urine, and to an even smaller part also in liver and blood. The main radioactive peaks appeared to be unchanged $[^{64}\text{Cu}]\text{Cu-2}$ (**Fig. 7**).

Fig. 7 HPLC profiles of $[^{64}\text{Cu}]\text{Cu-2}$ meatabolites in blood, urine, kidney and liver samples, at 2h p.i. of 15 MBq $[^{64}\text{Cu}]\text{Cu-2}$ (500 μL , 5% ethanol) compared to pure $[^{64}\text{Cu}]\text{Cu-2}$ injection solution

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3 Metabolic analysis of blood plasma yielded a decrease of original [⁶⁴Cu]Cu-2 of about 15% 20 min
4 after injection. 85% of [⁶⁴Cu]Cu-2 was determined also at 60 and 120 min after injection like a plateau
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11 **Fig. 8** Representative rat plasma activity curve of [⁶⁴Cu]Cu-2 up to 120 min p.i. (15 MBq in 500 μL,
12 5% ethanol)

13 14 15 **Discussion**

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17 NOTA was easily coupled with peptides via the isothiocyanate group. The resulting thiourea moiety
18 displays high stability in buffer and serum (Lang et al. 2011; Shao et al. 2014; Kim et al.2015). NOTA
19 peptide conjugates are steadily labeled with ⁶⁴Cu at pH 6.2. Both linear and cyclic peptides were found
20 to be stable in buffer and serum and displayed hydrophilic character. Inserting the linker between
21 NOTA and the peptide no change of stability in buffer or serum as well as no influence on lipophilicity
22 of the radiolabeled peptides was observed. Two isomers were detected for the linear ⁶⁴Cu labeled
23 NOTA peptides, because of the different conformation of the acid groups from NOTA when
24 coordinating to ⁶⁴Cu (Schlesinger et al. 2011). Considering the rapid isomeric conversion (within 10
25 min), after routine labeling, for biologic applications no separation was performed. The isomeric ratio
26 was found to be constant between 1:7 and 1:11.

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38 Competition studies were performed using the standard peptide [¹²⁵I]NDP-MSH. Based on K_d and on
39 the concentration of the standard, K_i values were calculated to obtain concentration-independent values
40 comparable with values from other studies. Results of affinity assays with α-MSH derivatives from
41 other research groups were mainly presented as IC₅₀. This of course gives a tendency about high or low
42 affinity, however, it is not directly comparable with values from different studies.

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48 The murine B16F10 was used as gold standard for a MC1R expressing cell line to compare data with
49 other studies. However, this study primarily aims at characterization of binding in MC1R expressing
50 human melanoma cells, MeWo and TXM13, in order to identify an appropriate mouse xenograft model
51 for further studies. There are five MCR subtypes, MC1 to MC5). It has been asserted that only the
52 MC1R subtype occurs in melanocytes and is about 10 to 20 times higher expressed in melanoma tissue
53 and cultured melanoma cells (Siegrist and Eberle 1995; Loir et al. 1999) than in healthy skin tissue.

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Low MC1R expression has been found also in the adrenal glands, hepatocytes, and cortical neurons of the cerebellum (Salazar-Onfray et al. 2002). However, even if the standard [¹²⁵I]NDP-MSH peptide derived from α -MSH shows no selectivity when comparing binding affinity to MC1, MC3, MC4 and MC5 receptors (Schiöth et al. 1996; Kopanchik et al. 2005), it is a worthwhile pharmaceutical lead for development of appropriate MC1R peptides due to the overexpression of this receptor in melanomas. The MC2R subtype possesses less than 50% amino acid homology with the other MCRs and does not bind α -MSH peptides (Schiöth et al. 1996).

In all cell lines, the measured K_d values of [¹²⁵I]NDP-MSH are in reasonably agreement with K_d values reported in the literature (Siegrist et al. 1988, 1989, 1996; Eberle et al. 1991; Lunec et al. 1992; Chluba-de Tapia et al. 1996; Schiöth et al. 1998; Ringholm et al. 2004). There was a tendency for [¹²⁵I]NDP-MSH to exhibit slightly lower affinity in human melanoma cells MeWo and TXM13 compared to murine B16F10 cells. Compared to the three NAPamides investigated, unlabeled NDP-MSH had the highest affinity not only in the murine cell line, as found formerly (Chen et al. 2000), but also in the human cells.

Interestingly, after NOTA-conjugation to no linker linear peptide, the affinity was not changed as well as after metalation with ^{nat}Cu or ⁶⁴Cu. NAPamids, that have been investigated before, also showed high affinity but after conjugation with DOTA some loss was recorded (Froidevaux et al. 2004, 2005). However, in the present study, a slight decrement of affinity was observed after conjugating the ϵ Ahx- β -Ala-linker to the linear peptide, and clear affinity loss was measured after conjugation of the cyclic peptide and even more after ^{nat}Cu insertion. A slight affinity decrease has also been observed when ^{nat}Cu was inserted to the DOTA-NAPamide (Cheng et al. 2007) confirming this tendency of affinity decrease after ^{nat}Cu inclusion into the NOTA-NAPamides. However, among the tested compounds, ^{nat}Cu-1 (no linker) did not show affinity change suggesting that the ϵ Ahx- β -Ala linker influenced the binding capability of the peptide. In the study from Froidevaux et al. (2004) two DOTA-NAPamides derivatives were compared whereby the NAPamide with DOTA on the Lys¹¹ showed higher affinity than the β -Ala³ coupled DOTA-NAPamide. The ϵ -Ahx- β -Ala³ coupled NOTA-NAPamide without the terminal Lys¹¹ (2) was similar affine as the DOTA-Lys¹¹ coupled one (Cheng et al. 2007; Bapst et al. 2007).

Considering the cyclized peptides, rhenium-cyclized α -MSH derivatives had affinities in the subnanomolar (Cheng et al. 2004) and low nanomolar range (Giblin et al. 1998; Cheng et al. 2002;

Miao et al. 2003) whereas assays with NAP-NS2 and its conjugates yielded in K_i values > 10 nM.

Similar to the NAP-NS2 conjugates DOTA-GMSH (Lim et al. 2012), a cyclic HYNIC α -MSH (Garcia et al. 2014), and β -Ala-Nle-cyclic α -MSH derivatives (Guo et al. 2010; Morais et al. 2013) are based on melanotan II nevertheless exhibited MC1R affinities higher than NAP-NS2. There are many possibilities to investigate exchange, adding or removing of amino acids within an α -MSH peptide as well as couple different linkers that result in steric, polarity or charge effects and thus influencing the binding to the MC1R. Since the NAP-NS1 and NAP-NS2 coupled with ϵ -Ahx- β -Ala linker were established as basic MSH derivatives in this study and the linear NAP-NS1 conjugate displayed higher affinity on murine melanoma cells, the ^{64}Cu -labeled linear ϵ -Ahx- β -Ala-NOTA-NAP-NS1 (**2**) was applied in further assays such as binding kinetics and saturation on human melanoma cells.

Association and dissociation of [^{64}Cu]Cu-**2** binding in B16F10 cells was rather fast, at least the association course appeared similar as the [^{125}I]NDP-MSH binding association in MC1R expressing cells whereby its dissociation course was not complete (only 40%) [**Error! Bookmark not defined.**]. The time course of [^{125}I]NDP-MSH was described to be slightly slower (Siegrist et al. 1988; Tatro et al. 1990).

The high affinity of [^{125}I]NDP-MSH at MC1Rs was observed in several studies (Tatro et al. 1990; Schiöth et al. 1998; Kopanchuk et al. 2005), however, affinities in the low nanomolar range obtained with the ^{64}Cu -labeled NAPamides investigated are sufficient with regard to imaging. The B_{max} values of the labeled peptides investigated were not consistent. Thus, the linker in [^{64}Cu]-**2** might have a steric influence, in the same manner as in the cyclic variant [^{64}Cu]-**3**.

The human metastatic cell line MeWo have been shown to express MC1Rs clearly (Funasaka et al. 1999) and was applied as orthotopic tumor mouse model (Petrangolini et al. 2003). For TXM13 cells a rather high amount of MC1Rs was determined compared to other human melanoma cell lines (Siegrist et al. 1989; Miao et al. 2003), however in B16F10 even about 20.000 binding sites per cell were found (Cheng et al. 2007). The affinity of [^{125}I]I-NDP-MSH was in the same order of magnitude in B16F10 and the human cells comparable with former data, where also a low specific binding part was determined in human melanoma cells (Siegrist et al. 1989). The K_d values of [^{64}Cu]-**2** were in the same range for murine and for human cells.

Data of biodistribution confirmed that the major excretion pathway of [^{64}Cu]-**2** is the kidney as it was determined from many studies before (Froidevaux et al. 2004; Chen et al. 2001; Cheng et al. 2002;

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Miao et al.2002; Bapst et al. 2009). In the present study, fortunately a radioactivity reduction of two-third was observed in the kidney after 60 min p.i. Uptake in the kidney has to be concerned seriously since it is a dose-limiting organ for investigations with radiotracers because nephrotoxicity is not to be underestimated especially regarding to targeted radiotherapy. After filtration by the glomerulus and reabsorption by the tubular cells low-molecular proteins and peptides will be delivered to renal lysosomes and metabolized after hydrolyzation (Maak et al. 1979). Thus, final radioactive metabolites do not leave the lysosomes quickly (Behr et al. 1998). It has been shown, that the nonspecific kidney accumulation after injection of radiolabeled MSH derivatives can be reduced significantly by coinjection of L-lysine (Froidevaux et al. 2004; Chen et al. 2000; Flook et al. 2013). Furthermore, negatively charged MSH peptides contribute as well to a decreased kidney retention (Behr et al. 1998). Probably, tubular reabsorption is facilitated by ionic interactions between positively charged peptides and negatively charged surfaces of proximal tubular cells, implying that renal uptake gets higher with positively charged peptides (Froidevaux et al. 2005). Thus, [⁶⁴Cu]-**2** of present study has a charge of -1 for chelate unit, presenting moderate low kidney uptake. For comparison we obtained for the kidney 5.9 ± 1.0 and 2.0 ± 0.3 % ID/g when determined 5 min and 60 min, respectively, after injection of [⁶⁴Cu]-**2**. This was much lower as found for a [⁶⁴Cu]Cu-DOTA-NAPamide (Cheng et al. 2007) where the chelator was conjugated on the N-terminal; moreover, [⁶⁴Cu]-**2** includes the β -alanine linker that might have an influence especially also for the liver uptake that was higher as well in the study of Chen et al. (2007). However, the referred studies were performed in mice. Presumably, depending on the position of the chelator and/or coupling of a linker NAPamide derivatives show higher or lower kidney accumulation, but mainly low liver uptake (Froidevaux et al. 2004; Bapst et al. 2009; Froidevaux et al. 2002). Labeling with ¹⁸F also showed rather moderate kidney accumulation, but unfortunately low tumor uptake (Cheng et al. 2007a). The cyclic variations of MSH conjugates in general present a higher kidney accumulation than the linear NAPamides (Behr et al. 1998; Chen et al. 2000; Cheng et al. 2004a; Guo et al. 2009, 2009a; Eberle et al. 2010). However, a ⁶⁴Cu labeled cyclic NOTA conjugate showed lower moderate kidney uptake and improved tumor accumulation compared to the same cyclic peptide conjugated with DOTA (Guo and Miao 2012). The NOTA-NAPamide with DOTA at Lys¹¹ position was assumed to degrade to a main metabolite H-Lys([¹¹¹In]DOTA)-NH₂ found in mice urine (Flook et al. 2013).

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Based on the receptor non-selective α -MSH analog NDP-MSH (Kopanchuk et al. 2005) and also the

1 investigated derivatives have not been presented as MC1R selective peptides. However, even MC1Rs
2 were found to be overexpressed in melanoma, the peptides pass the excretion pathway through the
3 kidney that was found to express low levels of MC1R, MC3R, MC4R and MC5R, in human, mouse or
4 rat kidney (Ni et al. 2006; Si et al. 2013; Lindskog et al. 2014). Several studies showed that the uptake
5 of the radiolabeled MSH derivatives could be blocked in the respective tumor after additional
6 application of a non-labeled MSH analog. At the same time the studies present mainly no significant
7 change of the uptake data for kidney after treatment with 'cold' MSH analogs (Gercia et al. 2014;
8 Cheng et al. 2007a; Guo et al. 2012). In the study of Froidevaux et al. (Froidevaux et al. 2004) the
9 kidney uptake decreased by about 25%, but increased kidney uptake was measured in the study of
10 Cheng et al. (2007). Thus, it is suggested that at least the decrease of uptake in the tumor is MC1R
11 related. Whereas in kidney the MCR expression is too low. However a more MC1R selective α -MSH
12 peptide could be useful in the future.
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26 **Conclusions**

27 In this study, we investigated the pharmacological behavior of a linear α -MSH peptide with and
28 without linker and chelator and a cyclic α -MSH peptide with linker and chelator. The cyclic peptide
29 exhibited a bit higher hydrophilicity than the linear peptides, while binding affinity to MC1R of the
30 cyclic peptide and modifications was lower than that of the linear peptides. Coupling the linker to the
31 peptide had negligible influence on in vitro pharmacological behavior. [^{64}Cu]Cu-1, [^{64}Cu]Cu-2 and
32 [^{64}Cu]Cu-3 were stable in buffer and serum. [^{64}Cu]Cu-2 revealed rapid cellular association and
33 dissociation in murine cells. Linear peptide derivatives showed high binding affinities on murine
34 B16F10 cells as well as on human MeWo and TXM13 cells. Fewer binding sites were observed on
35 human MeWo cells. Rat biodistribution of [^{64}Cu]Cu-2 confirmed a reasonable renal excretion pathway.
36 Two main metabolites were found in the kidney 2h after application. In the plasma about 85% of
37 originally compound was still determined 1h and 2h after injection. Definitely, [^{64}Cu]Cu-2 should be
38 used for further pharmacokinetic studies on tumor bearing mice with regard to a future application in
39 human to diagnose melanoma.
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56 **Compliance with ethical standards**

57 *Ethical approval* The animal experiments were performed in accordance to the guidelines of the
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German Regulations of Animal Welfare. The protocol was approved by the local Ethical Committee for
Animal Experiments (reference number 24-9168.21-4/2004-1).

Conflict of interest The authors declare that they have no conflict of interest.

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