A connection between the binding properties of imprinted and non-imprinted polymers: a change of perspective in molecular imprinting

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EXPERIMENTAL SECTION

Materials. Bisphenol A (BPA), chloramphenicol (CAP), cortisol (COR), diclofenac (DIC), ibuprofen (IBU), metribuzin (MET), naproxen (NAP), pyrimethanil (PYR), theophylline (THO), 2,2-dimethoxy-2-phenylacetophenone (DMPA), all the functional monomers (acrylamide, AM; 2-hydroxyethyl methacrylate, HEMA; methacrylic acid, MAA; 4-vinylpyridine, 4VP), cross-linkers (divinylbenzene, DVB; ethylene dimethacrylate, EDMA; glycerol dimethacrylate, GDMA; pentaerithrytole tetraacrylate, PETA; pentaerithrytole triacrylate, PETRA; trimethylolpropane trimethacrylate, TRIM) were from Sigma–Aldrich–Fluka (Milan, Italy). Acetic acid and all the organic solvents were from VWR International (Milan, Italy). When necessary, polymerization inhibitors in monomers were removed by cleanup on activated alumina columns. Ligands stock solutions were prepared by dissolving 20.0 mg of substance in 4.00 ml of acetonitrile and stored in the dark at -20 °C. All the solvents were of HPLC quality, other chemicals were of analytical grade. For the libraries screening, MultiScreen Resist Filtration System, vacuum manifold and MultiScreen 12×8 wells filter microplates with hydrophilic PTFE membrane were purchased from Millipore (Billerica, USA). The SPE vacuum manifold was from Macherey-Nagel (Duren, Germany), whereas the SPE empty polypropylene columns were from Alltech (Milan, Italy). The HPLC apparatus was an Accela High Speed LC consisting of a 1250 quaternary solvent delivery pump, a thermostated autosampler provided with 25 μ l injection system, a diode array UV-Vis detector and a data acquisition system Xcalibur 2.0 from ThermoScientific (Milan, Italy).

Polymeric combinatorial libraries. The polymeric combinatorial libraries were prepared starting from 96 different polymer combinations reported in the supporting informations (table S2). In 3 ml thick wall borosilicate glass vials, prepolymerization solutions with a molar ratio template:functional monomer:cross-linker 1:3:27 were prepared by dissolving 0.05 mmoles of template in the porogenic solvent. When the non-imprinted polymers were prepared, the template was substituted by 11 µl of porogenic solvent. Then, 0.15 mmoles of functional monomer, 1.35 mmoles of cross-linker and 100 µl of a solution of DMPA (1% of the vinyl groups present in the prepolymerization mixture) were added to a proper amount of dry porogenic solvent. The vials were sonicated in an ultrasonic bath for 10 minutes, sealed, and the mixtures were photopolymerized at 4 °C overnight using a 200 W medium-pressure mercury lamp. The bulk polymers obtained were broken with a steel spatula, ground in a mechanical mortar and mechanically wet-sieved to 15-38 µm. The template molecule was extracted from the imprinted combinatorial library by packing the polymers in polypropylene SPE columns and exhaustively washing with acetic acid-methanol 1:9 (v/v) till no template was detectable by the HPLC analysis of the eluate. No efforts were made to measure the amount of template molecule recovered. The same treatment was made in a single washing step for the non-imprinted polymers. The washed polymers were dried under vacuum at 70 °C for 2 h, transferred to glass vials and stored at room temperature. Finally, amounts of about 10 mg of imprinted or non-imprinted polymers were exactly weighed in the wells of an 8x12 filtration microplate in accordance with the scheme reported in the supporting information (table S1). Then the microplates were sealed and stored at room temperature. Later, any binding assay microplates were washed sequentially with 5 x 300 μ l of acetic acid-methanol 1:9 (v/v) and 5 x 300 μ l of acetonitrile and dried under a gentle stream for 2 h.

Ligand binding measurements. To measure the ligand binding through a single-point binding assay, 200 µl of 50 µg/ml ligand solutions in acetonitrile were added to the microplate wells, while binding isotherms for naproxen and ibuprofen were measured by adding 200 µl of 5, 10, 15, 25, 50, 75 and 100 µg/ml ligand solutions in acetonitrile to the microplate wells. Then, the microplate was incubated overnight at 4 °C in a TLC chamber saturated with acetonitrile. The ligand solution was filtered, manually transferred into 100-µl HPLC autosampler vials and the free fraction of the ligand was measured by HPLC (*vide infra*). To evaluate the reproducibility of the binding assay, each partition was repeated three times and the amount of free ligand was evaluated as the average of the single values measured. Statistic tests on the ligand binding were performed by using the statistic module of SigmaPlot 11.0 (Systat Software Inc., Richmond, CA, USA), while the calculation of the binding isotherms was performed by using TableCurve 2D 5.0 (Systat Software Inc., Richmond, CA, USA). Non-linear least square fitting was applied to the averaged experimental data by using the Langmuir isotherm model:

$$B = \frac{B_{\max} K_{eq} F}{1 + K_{eq} F} \tag{1}$$

where B is the amount of ligand bound to the polymer, F is the amount of ligand not bound to the polymer, Keq is the apparent affinity constant and Bmax is the binding site density. To assure robust results, Pearson VII limit minimization was chosen as the minimization method. To avoid being trapped in local minima which give incorrect results, the fitting was carried out several times using different initial guess values for the isotherm parameters. The calculated parameters of the isotherm model (p) were not considered significant and the fitting was rejected when the associated standard error (s) did not satisfy the p > 2s constraint.

HPLC analysis. Reverse phase HPLC analysis was used for quantification of the free ligand. Chromatographic separation was performed on a Hypersil Gold reverse-phase C18 (50×2.1 mm) from Thermo Scientific (Milan, Italy). The mobile phase consisted of acidified (0.5% v/v acetic acid) methanol–water 50+50 (v/v) for theophylline (λ =272 nm), 56+44 (v/v) for ibuprofen (λ =221 nm), 60+40 (v/v) for cortisol (λ =254 nm), 65+35 (v/v) for metribuzin (λ =296 nm) and 70+30 for bisphenol A (λ =278 nm), chloramphenicol (λ =276 nm), diclofenac (λ =277 nm), naproxen (λ =233 nm) and pyrimethanil (λ =270 nm). The mobile phase flow-rate was set to 0.50 ml/min. Reference standard solutions for ligands of concentration 0.1, 0.25, 0.5, 1, 2.5, 5 and 10 µg/ml were analyzed three times consecutively and peak areas were plotted against concentration. A calibration curve was drawn using weighted linear regression (weight = 1/conc.). The amount of ligand bound to the polymer was calculated by subtracting the concentration of free ligand from the known initial concentration.

Chart S1: template structures



bisphenol A, BPA logP 3.32, pK 9.78



diclofenac, DIC logP 4.98



naproxen, NAP logP 3.18, pK 4.19



chloramphenicol, CAP logP 1.15



ibuprofen, IBU logP 3.21, pK 4.80



pyrimethanil, PYR logP 2.84, pK 10.04



cortisol, COR logP 1.79



metribuzin, MET logP 1.70, pK 11.54



theophylline, THO logP -0.02, pK 7.82

Table S1: functional monomers, cross-linker and porogenic solvents used to prepare polymeric libraries. AM: acrylamide, HEMA: 2hydroxyethylmethacrylate, MAA: methacrylic acid, 4VP: 4-vinylpyridine, DVB: divinylbenzene, EDMA: ethylene dimethacrylate, GDMA: glycerol dimethacrylate, PETA: pentaerithrytole tetraacrylate, PETRA: pentaerithrytole triacrylate, TRIM: trimethylolpropane trimethacrylate, MeCN: acetonitrile, CHCl₃: chloroform, THF: tetrahydrofurane, TOL: toluene.

		EDMA	DVB	GDMA	TRIM	PETA	PETRA	EDMA	DVB	GDMA	TRIM	PETA	PETRA		
	-	01	02	03	04	05	06	07	08	09	10	11	12	_	
MAA	A	MAA 12.7 μl EDMA 255 μl TOL 268 μl	MAA 12.7 μl DVB 192 μl TOL 205 μl	MAA 12.7 μl GDMA 275 μl TOL 288 μl	MAA 12.7 μl TRIM 431 μl TOL 445 μl	MAA 12.7 μl PETA 341 μl TOL 354 μl	MAA 12.7 μl PETRA 436 μl TOL 449 μl	MAA 12.7 μl EDMA 255 μl CHCl ₃ 268 μl	MAA 12.7 μl DVB 192 μl CHCl ₃ 205 μl	MAA 12.7 μl GDMA 275 μl CHCl ₃ 288 μl	MAA 12.7 μl TRIM 431 μl CHCl ₃ 445 μl	MAA 12.7 μl PETA 341 μl CHCl ₃ 354 μl	MAA 12.7 μl PETRA 436 μl CHCl ₃ 449 μl	A	MAA
AM	В	AM 10.6 mg EDMA 255 μl TOL 266 μl	AM 10.6 mg DVB 192 μl TOL 203 μl	AM 10.6 mg GDMA 275 μl TOL 286 μl	AM 10.6 mg TRIM 431 μl TOL 442 μl	AM 10.6 mg PETA 341 μl TOL 341 μl	AM 10.6 mg PETRA 436 μl TOL 447 μl	AM 10.6 mg EDMA 255 μl CHCl ₃ 266 μl	AM 10.6 mg DVB 192 μl CHCl ₃ 203 μl	AM 10.6 mg GDMA 275 μl CHCl ₃ 286 μl	AM 10.6 mg TRIM 431 μl CHCl ₃ 442 μl	AM 10.6 mg PETA 341 μl CHCl ₃ 341 μl	AM 10.6 mg PETRA 436 μl CHCl ₃ 4476 μl	В	AM
4VP	C	4VP 16.2 μl EDMA 255 μl TOL 272 μl	4VP 16.2 μl DVB 192 μl TOL 198 μl	4VP 16.2 μl GDMA 275 μl TOL 291 μl	4VP 16.2 μl TRIM 431 μl TOL 447 μl	4VP 16.2 μl PETA 341 μl TOL 357 μl	4VP 16.2 μl PETRA 436 μl TOL 452 μl	4VP 16.2 μl EDMA 255 μl CHCl ₃ 272 μl	4VP 16.2 μl DVB 192 μl CHCl ₃ 198 μl	4VP 16.2 μl) GDMA 275 μl CHCl ₃ 291 μl	4VP 16.2 μl TRIM 431 μl CHCl ₃ 447 μl	4VP 16.2 μl PETA 341 μl CHCl ₃ 357 μl	4VP 16.2 μl PETRA 436 μl CHCl ₃ 452 μl	С	4VP
HEMA	D	НЕМА 18.2 µl EDMA 255 µl TOL 273 µl	HEMA 18.2 μl DVB 192 μl TOL 210 μl	HEMA 18.2 μl GDMA 275 μl TOL 293 μl	HEMA 18.2 μl TRIM 431 μl TOL 449 μl	HEMA 18.2 μl PETA 341 μl TOL 359 μl	HEMA 18.2 μl PETRA 436 μl TOL 454 μl	НЕМА 18.2 µl EDMA 255 µl CHCl ₃ 273 µl	HEMA 18.2 μl DVB 192 μl CHCl ₃ 210 μl	НЕМА 18.2 µl GDMA 275 µl CHCl ₃ 293 µl	HEMA 18.2 μl TRIM 431 μl CHCl ₃ 449 μl	НЕМА 18.2 μl РЕТА 341 μl CHCl ₃ 359 μl	НЕМА 18.2 µl РЕТКА 436 µl СНСІ ₃ 454 µl	D	HEMA

chloroform

S4

HEMA	Н	272 μl HEMA 18.2 μl EDMA 255 μl	198 µl НЕМА 18.2 µl DVB 192 µl	291 μl HEMA 18.2 μl GDMA 275 μl	447 μl HEMA 18.2 μl TRIM 431 μl	357 μl HEMA 18.2 μl PETA 341 μl	452 μl HEMA 18.2 μl PETRA 436 μl	272 μl HEMA 18.2 μl EDMA 255 μl	198 µl НЕМА 18.2 µl DVB 192 µl	291 μl HEMA 18.2 μl GDMA 275 μl	447 μl HEMA 18.2 μl TRIM 431 μl	357 μl HEMA 18.2 μl PETA 341 μl	452 μl HEMA 18.2 μl PETRA 436 μl	Н	HEMA
4VP	G	4VP 16.2 μl EDMA 255 μl TOL 272 μl	4VP 16.2 μl DVB 192 μl TOL 198 μl	4VP 16.2 μl GDMA 275 μl TOL 291 μl	4VP 16.2 μl TRIM 431 μl TOL 447 μl	4VP 16.2 μl PETA 341 μl TOL 357 μl	4VP 16.2 μl PETRA 436 μl TOL 452 μl	4VP 16.2 μl EDMA 255 μl CHCl ₃ 272 μl	4VP 16.2 μl DVB 192 μl CHCl ₃ 198 μl	4VP 16.2 μl) GDMA 275 μl CHCl ₃ 291 μl	4VP 16.2 μl TRIM 431 μl CHCl ₃ 447 μl	4VP 16.2 μl PETA 341 μl CHCl ₃ 357 μl	4VP 16.2 μl PETRA 436 μl CHCl ₃ 452 μl	G	4VP
AM	F	AM 10.6 mg EDMA 255 μl TOL 266 μl	AM 10.6 mg DVB 192 μl TOL 203 μl	AM 10.6 mg GDMA 275 μl TOL 286 μl	AM 10.6 mg TRIM 431 μl TOL 442 μl	AM 10.6 mg PETA 341 μl TOL 341 μl	AM 10.6 mg PETRA 436 μl TOL 447 μl	AM 10.6 mg EDMA 255 μl CHCl ₃ 266 μl	AM 10.6 mg DVB 192 μl CHCl ₃ 203 μl	AM 10.6 mg GDMA 275 μl CHCl ₃ 286 μl	AM 10.6 mg TRIM 431 μl CHCl ₃ 442 μl	AM 10.6 mg PETA 341 μl CHCl ₃ 341 μl	AM 10.6 mg PETRA 436 μl CHCl ₃ 4476 μl	F	AM
MAA	Е	MAA 12.7 μl EDMA 255 μl TOL 268 μl	MAA 12.7 μl DVB 192 μl TOL 205 μl	MAA 12.7 μl GDMA 275 μl TOL 288 μl	MAA 12.7 μl TRIM 431 μl TOL 445 μl	MAA 12.7 μl PETA 341 μl TOL 354 μl	MAA 12.7 μl PETRA 436 μl TOL 449 μl	MAA 12.7 μl EDMA 255 μl CHCl ₃ 268 μl	MAA 12.7 μl DVB 192 μl CHCl ₃ 205 μl	MAA 12.7 μl GDMA 275 μl CHCl ₃ 288 μl	MAA 12.7 μl TRIM 431 μl CHCl ₃ 445 μl	MAA 12.7 μl PETA 341 μl CHCl ₃ 354 μl	MAA 12.7 μl PETRA 436 μl CHCl ₃ 449 μl	E	MAA

tetrahydrofuran

acetonitrile

S5

Note S1: Box plots graphically depict the numerical data considered in this work (bound-to-free values, apparent affinity constants and binding site densities) through their descriptive statistics: the smallest observed, lower quartile (25th percentile of data), median (50th percentile of data), upper quartile (75th percentile of data) and largest observed or calculated data. It shows differences between data populations without making any assumptions of the underlying statistical distribution. Thus, it is suitable to represent both parametric and non-parametric statistical distributions. In the figures, the upper and lower solid boundaries of the boxes indicate the 25th and 75th percentiles, the lines within the boxes mark the medians (50th percentiles), whiskers above and below the boxes indicate the 90th and 10th percentiles, circles above and below whiskers experimental or calculated values external to the 10-90th percentile range, potentially identifying outlyer data. Spacings between the different parts of the box are related to the degree of dispersion and skewness in the data structures.