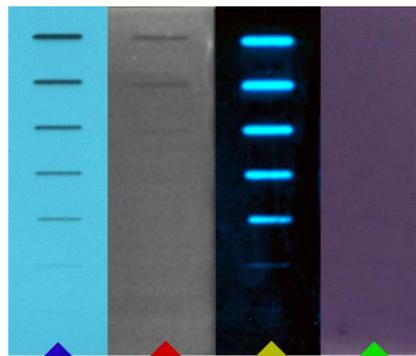


## Highlights

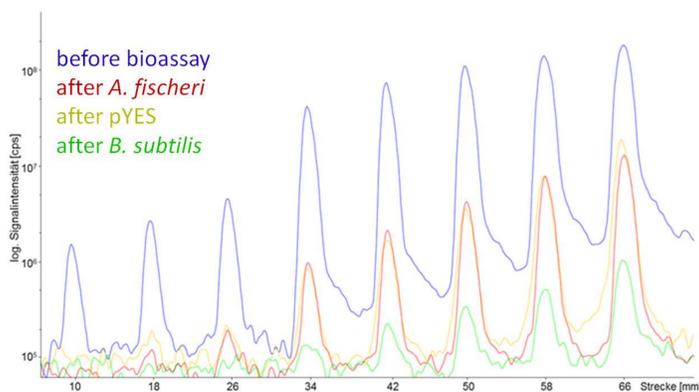
- 1<sup>st</sup> step: Direct bioautography (DB) to screen for bioactive compounds in complex samples
- 2<sup>nd</sup> step: Matrix discriminating desorption-based mass spectrometry (HPTLC-DB-DART-MS)
- Characterization or quantification in one MS scan along a track or substance window
- Time-saving approach to evaluate bioactive characteristics and mass spectrometric information



Increasing matrix complexity

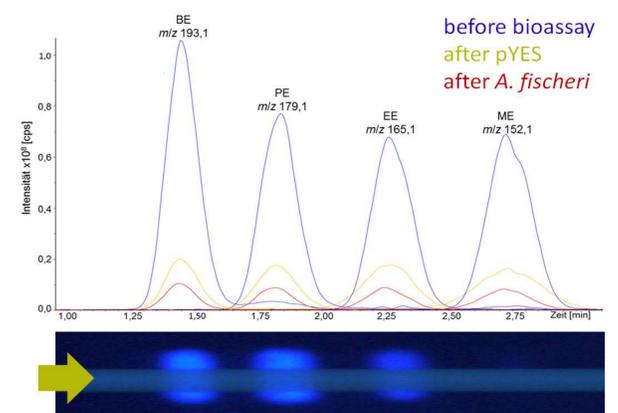
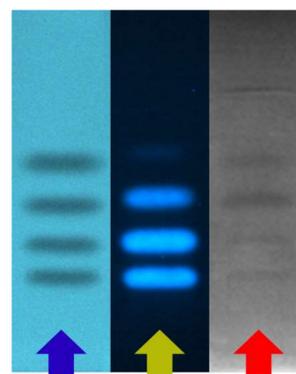
## Influence of different bioassay media on scanning DART-MS?

- ✓ Applied paraben standards (3-960 ng/band) quantitatively recorded via modified DART-MS [1, 2]
- ✓ Bioassay-dependent MS signal for *Aliivibrio fischeri* [3], planar yeast estrogen screen (pYES) [4] and *Bacillus subtilis* [5]: decreased with increasing matrix complexity!

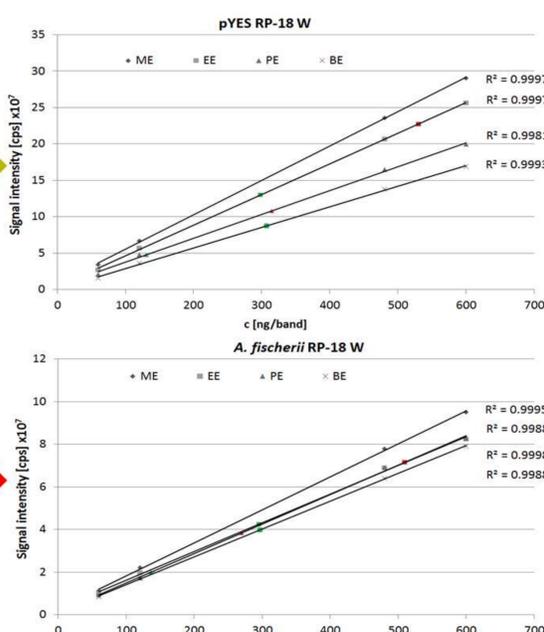
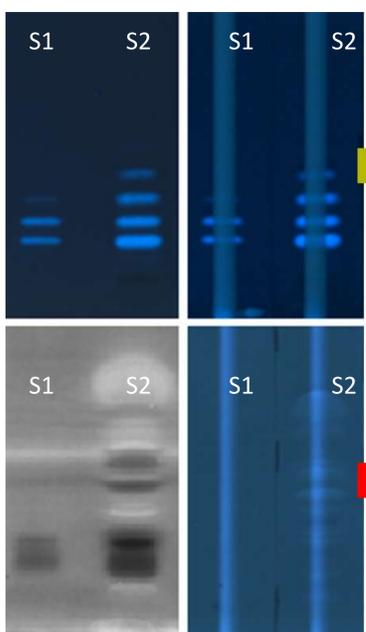


## MS signal decay after DB ?

- ✓ Separated paraben standards (each 600 ng/band) followed by DB with pYES and *A. fischeri*
- ✓ MS detection of the parabens via EIC chromatograms still sufficient for quantification!



	Signal decay [%]	
	<i>A. fischeri</i>	pYES
ME	88	65
EE	89	67
PE	90	76
BE	91	81



## Why DART-MS scanning after DB?

- ✓ Results for bioactivity and MS of the same zone
- ✓ Reliable quantitation with a mean %RSD of 4.6% on normal and reversed phase layers
- ✓ Discriminating DART-MS: reduced contamination of the MS system and reduced ion suppression by the bioassay medium compared to ESI-MS
- ✓ Quantification by MS is not dependent on separation performance or zone shape after DB



		Amount in sample [mg/100g]							
		Sample 1				Sample 2			
		ME	EE	PE	BE	ME	EE	PE	BE
without	NP	103	56	30	165	75	37	65	
BioAssay	RP	97	59	34	147	69	30	67	
<i>A. fischeri</i>	NP	96	51	27	173	69	24	53	
	RP	101	51	27	157	59	27	59	
pYES	RP	111	53	31	170	60	26	62	