

A rapid method for the isolation and analysis of destruxins from *Metarhizium anisopliae* culture broth

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INTRODUCTION

Destruxins (dtxs) are a substance class mainly produced by the entomopathogenic fungus *Metarhizium anisopliae* (Pedras et al. 2002). Currently about 35 derivatives of these cyclic hexadepsipeptides are known. They belong to different sub-series, differing in the nature of the D- α -hydroxyacid HA (dtx A-F), and the amino acids 2 (subscript 1), 3 (subscript 2), and 4 (desmethyl series).

Destruxins are highly potent insecticides and it has been proven unequivocally that their presence is correlated with fungal virulence (Kershaw et al. 1999). They are, like most fungal decapeptides, forming ion channels across membranes (Hinaje et al. 2002). Their ability to inhibit the bone-resorbing activities of osteoclasts has been shown recently (Nakagawa et al. 2003).

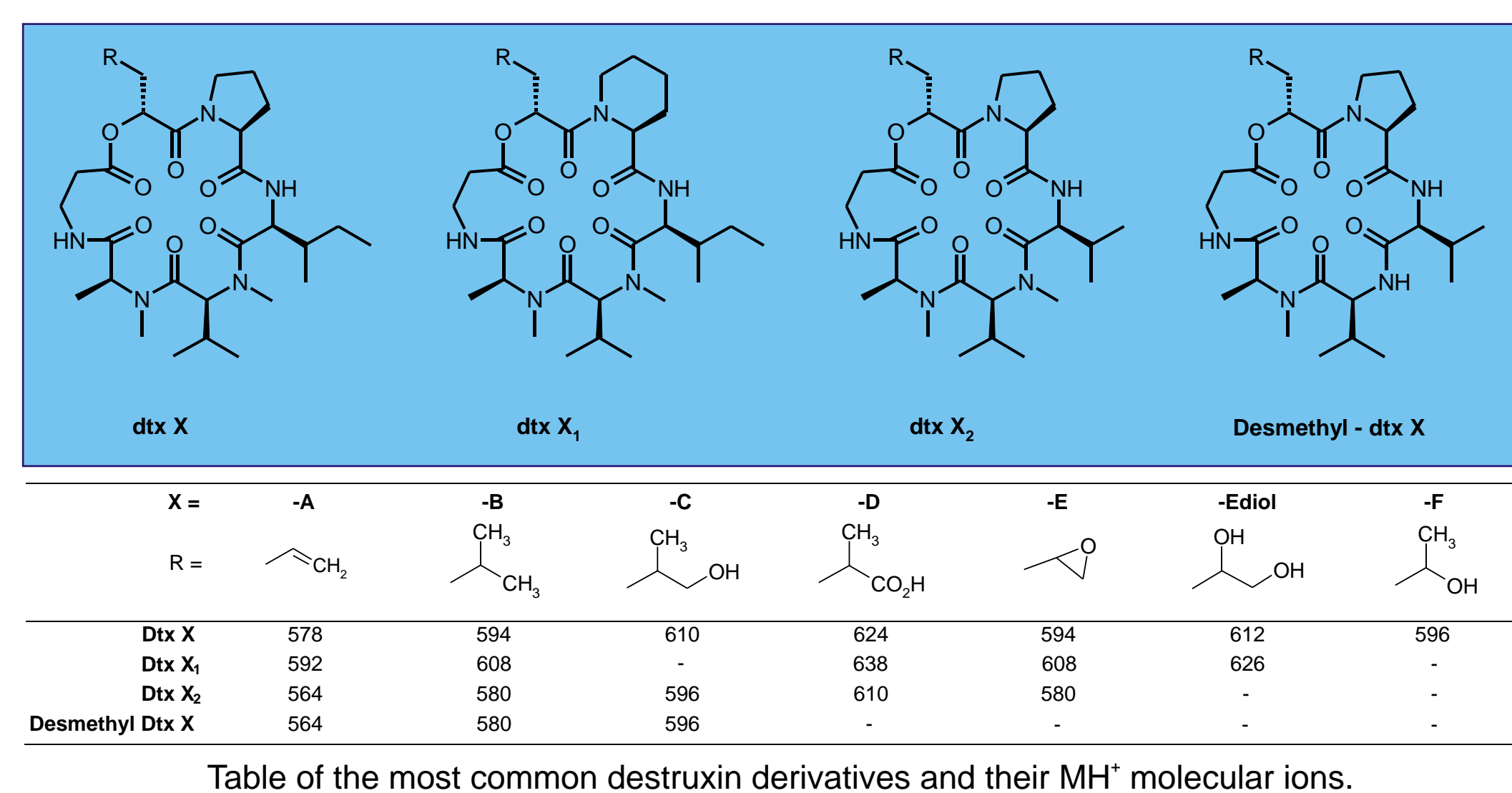


Photographs by H. Strasser, M. Kirchmair (ELM), and M. Traugott (top left)

RESULTS

- A new sensitive (LODs <0.5 ppm), robust (reprod. <2.5% RSD), and fast (t_r dtxB = 9 min) method for the detection and quantification of destruxins has been developed.
- The sample preparation was simplified, an ultrafiltration step replaces more time consuming procedures.
- Identification of a broad variety of destruxin derivatives was achieved by MS/MS experiments using a HPLC-ESI-iontrap coupling.
- The developed method was successfully applied to the quantification of destruxins from fungal culture broth.
- The *in situ* instability of one of the most bioactive derivatives, destruxin E, was monitored. A half-life time of 64 hours was determined.

STRUCTURES and MASSES



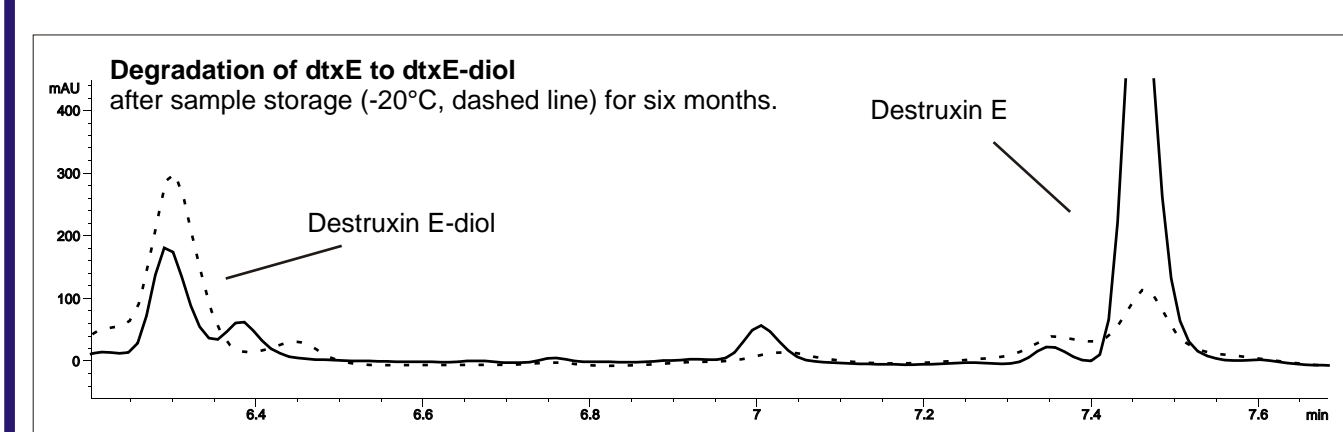
METHOD APPLICATION TO CULTURE BROTH

CULTIVATION CONDITIONS AND SAMPLE PREPARATION

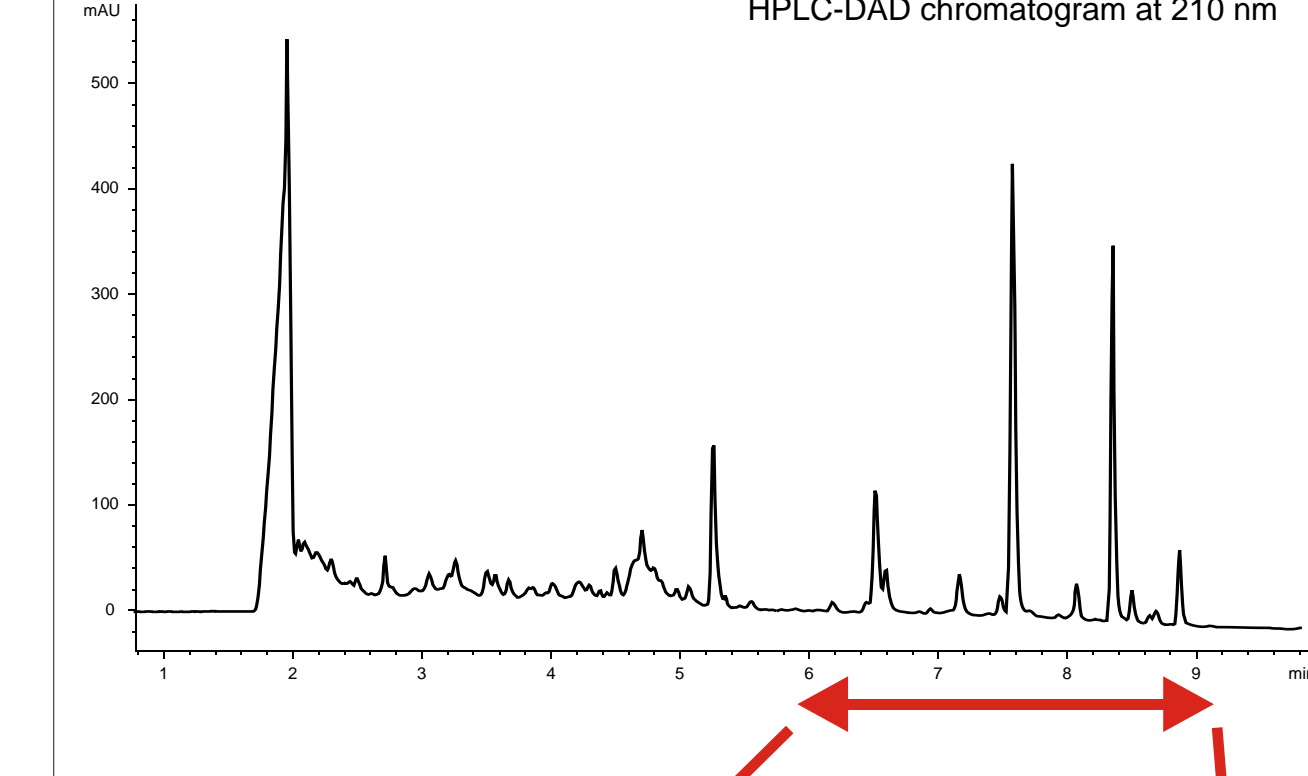
Metarhizium anisopliae strain BIPESCO5 (KVL275) cultures were grown on S2G medium petri dishes until sporulation. Spores were sampled with a 0.1% Tween-80 solution with a germination activity of $98.6 \pm 2.5\%$. 100 mL Erlenmeyer flasks (four parallels, 20 ml S2G medium) were incubated with $7.6 \pm 0.4 \times 10^7$ spores per culture and incubated on a rotary shaker (200 rpm) at 25 °C and 80 % relative humidity. Samples were drawn in daily intervals. Culture medium (culture supernatant) and mycelium were separated by filtration over a 0.22 μ m cellulose acetate filter. The biomass content was determined and the pH of the supernatant was measured. The culture filtrates were stored at -20°C until further workup. Two mL of stored culture filtrates were finally purified by centrifugation over a 10kDa membrane (Vivaspin2, CTA membrane, Sartorius, Göttingen, Germany) and used for HPLC analysis without further dilution. The recovery rate of the filtration step was found to be $93.4 \pm 2.0\%$ for dtxA at 3ppm. All HPLC solutions were stored at -20°C.

DESTRUXIN E DEGRADATION

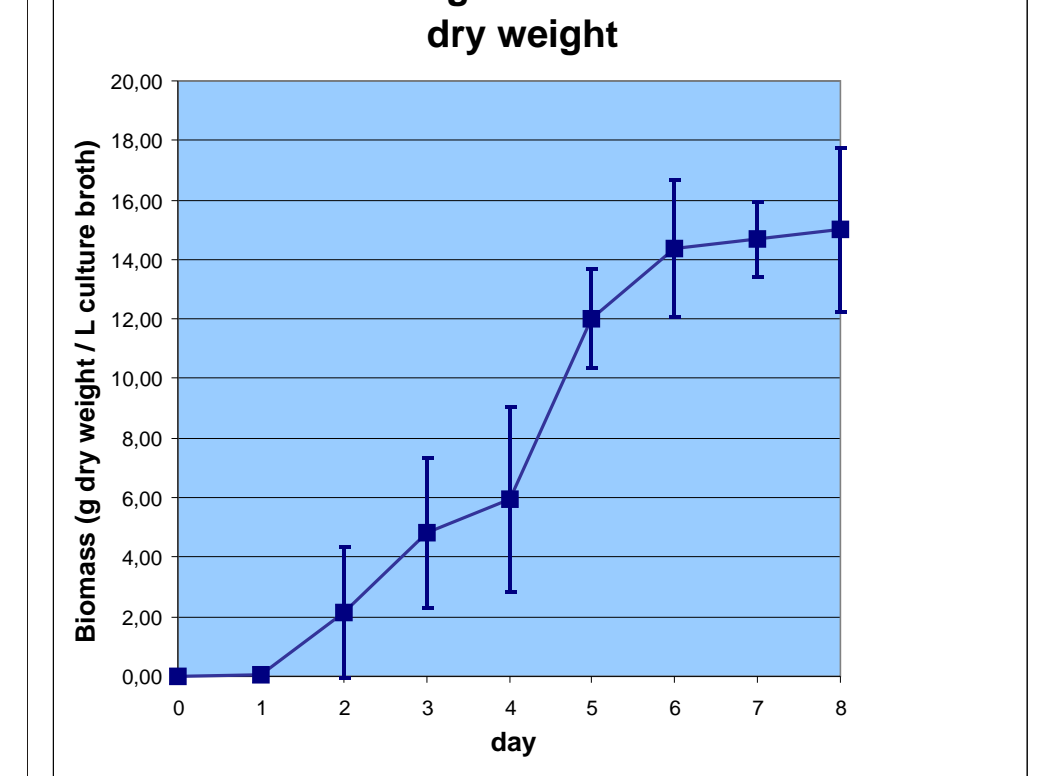
The epoxide derivative destruxin E degrades readily to destruxin E-diol in the culture filtrate. At room temperature a half-life time of 64 ± 2 hours was determined. Even under storage conditions (-20°C) the degradation of this derivative is remarkable.



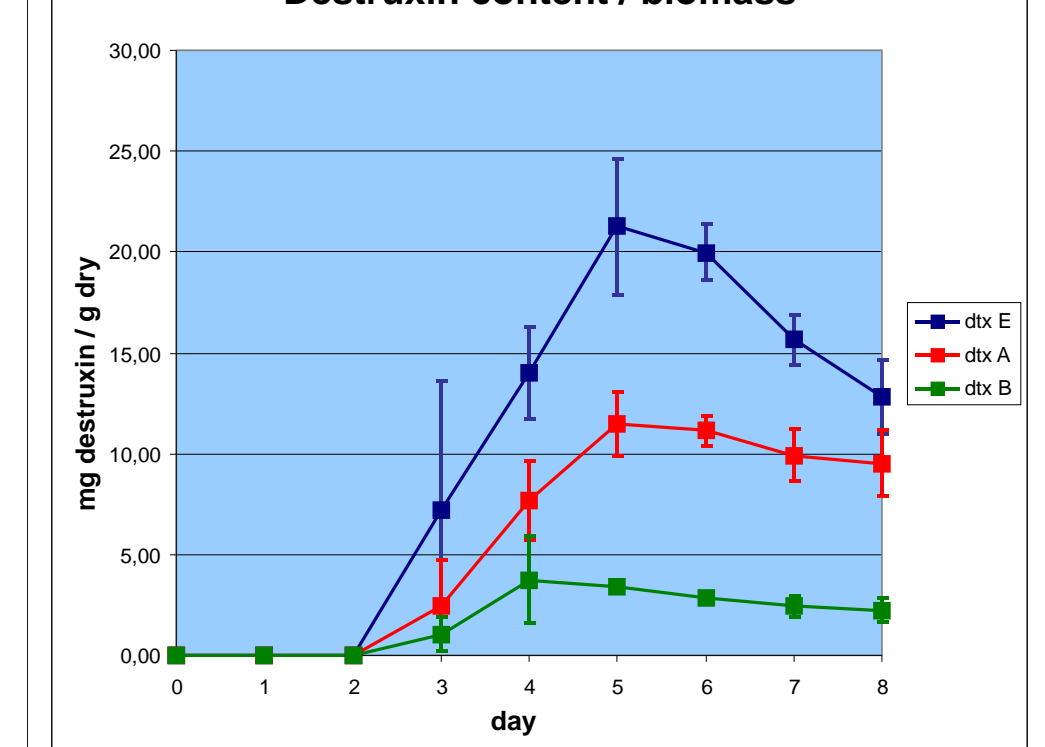
Metarhizium anisopliae culture broth HPLC-DAD chromatogram at 210 nm



Fungal biomass dry weight



Destruxin content / biomass



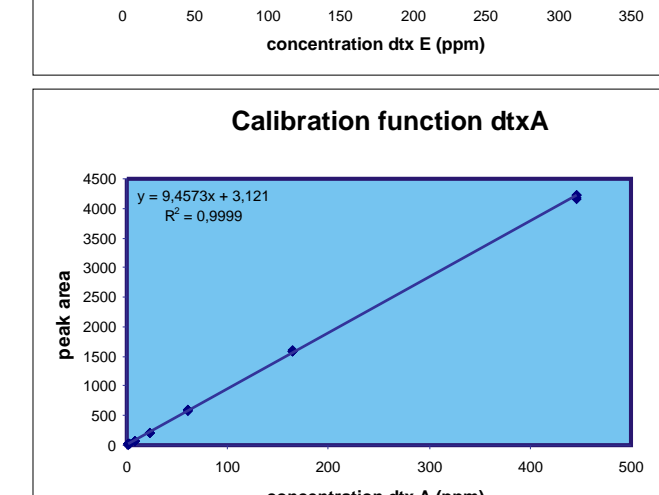
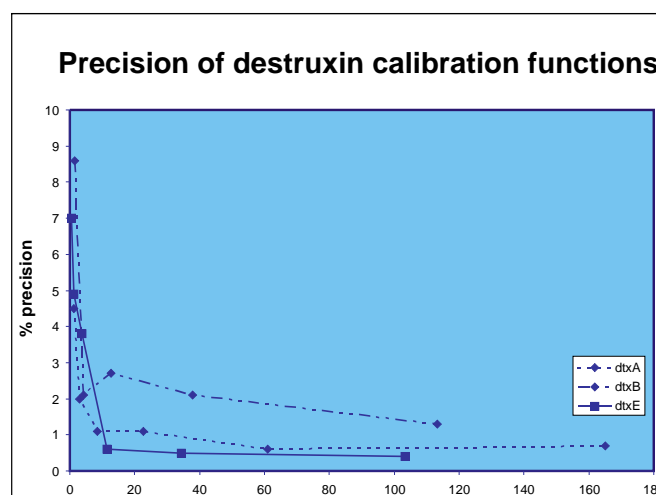
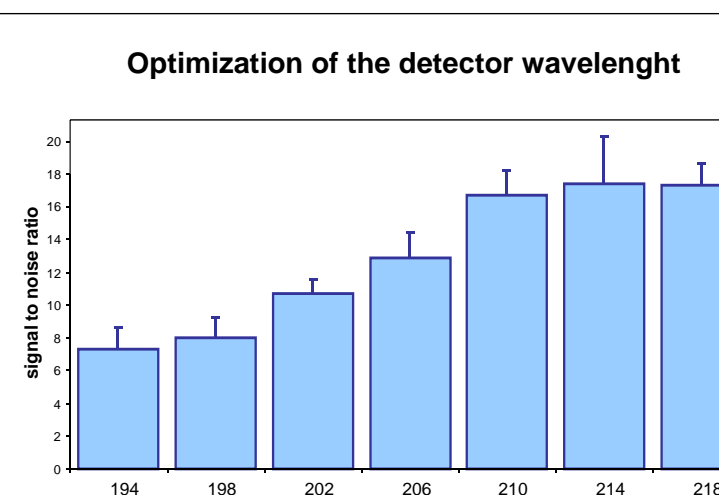
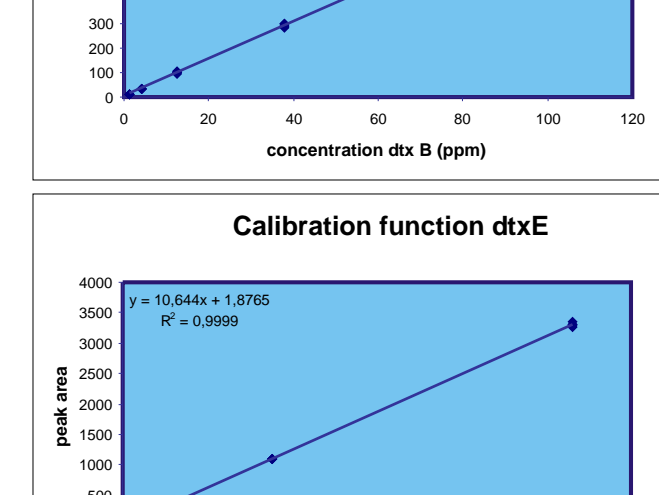
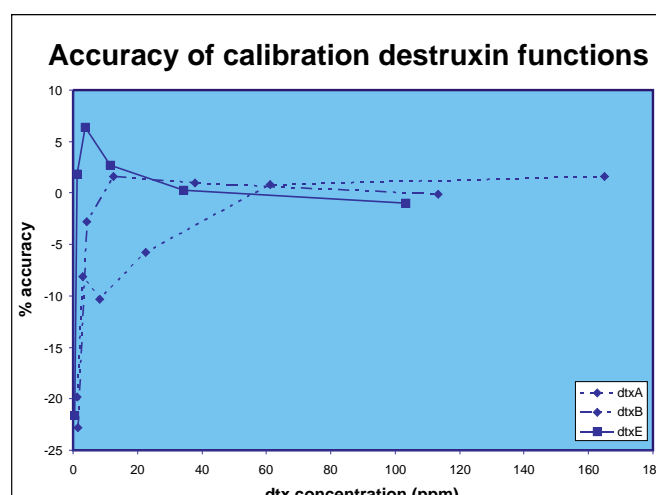
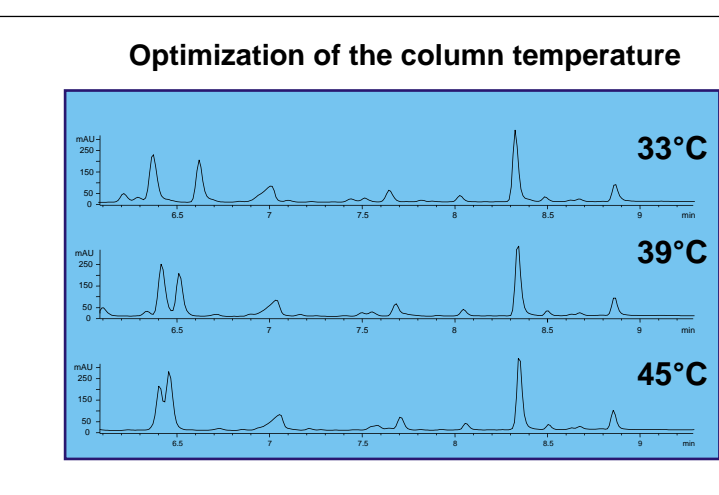
HPLC-DAD METHOD DEVELOPMENT AND VALIDATION

VALIDATION DATA

	dtxA	dtxB	dtxE
LOD (ppm):	0.19	0.41	0.10
LOQ (ppm):	0.65	1.38	0.34
Repeatability			
intraday (% RSD):	<0.4	<2.3	<3.2
interday (% RSD):	<0.6	<2.4	n.d.

HPLC-DAD METHOD

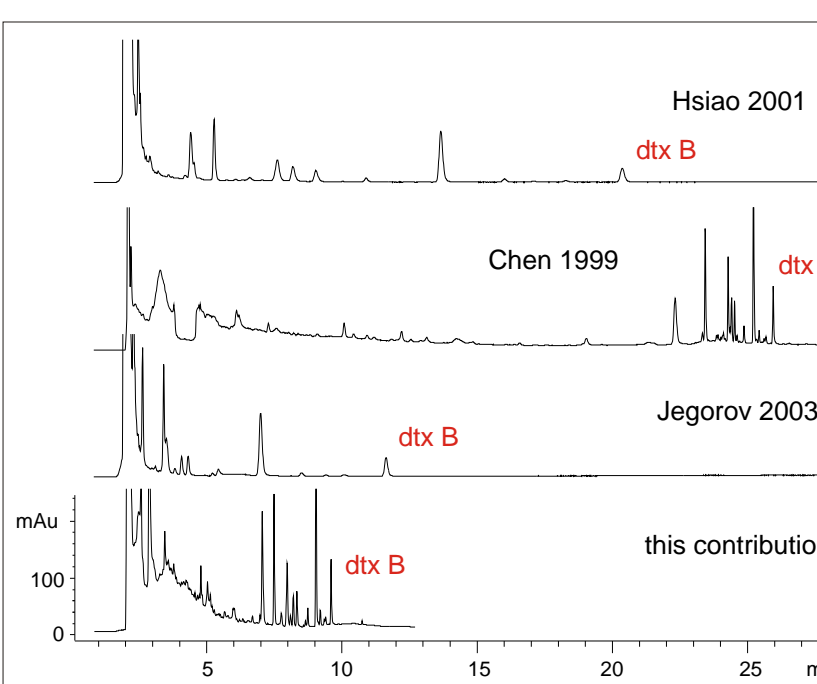
Instrumentation: Agilent HP1090 liquid chromatograph.
Stationary phase: Zorbax SB-C18 (4.6 mm x 150 mm), particle size 3.5 μ m.
Mobile phase: H₂O(A)-ACN(B) at 1 ml/min at 23°C. Elution profile: t = 0 min 5% B, t = 6 min 50% B, t = 8 min 98% B, t = 12 min 98% B, 8 min post time.
Detection: UV-DAD 210 nm. Injection volume: 10 μ l.
AcOH (pH = 2) lowers the resolution. Temperature has no influence. 90.7 \pm 20.4 % dtxA recovery at LOD. 92.1 \pm 6.6 % dtxA recovery at 46 ppm.



COMPARISON WITH OTHER METHODS

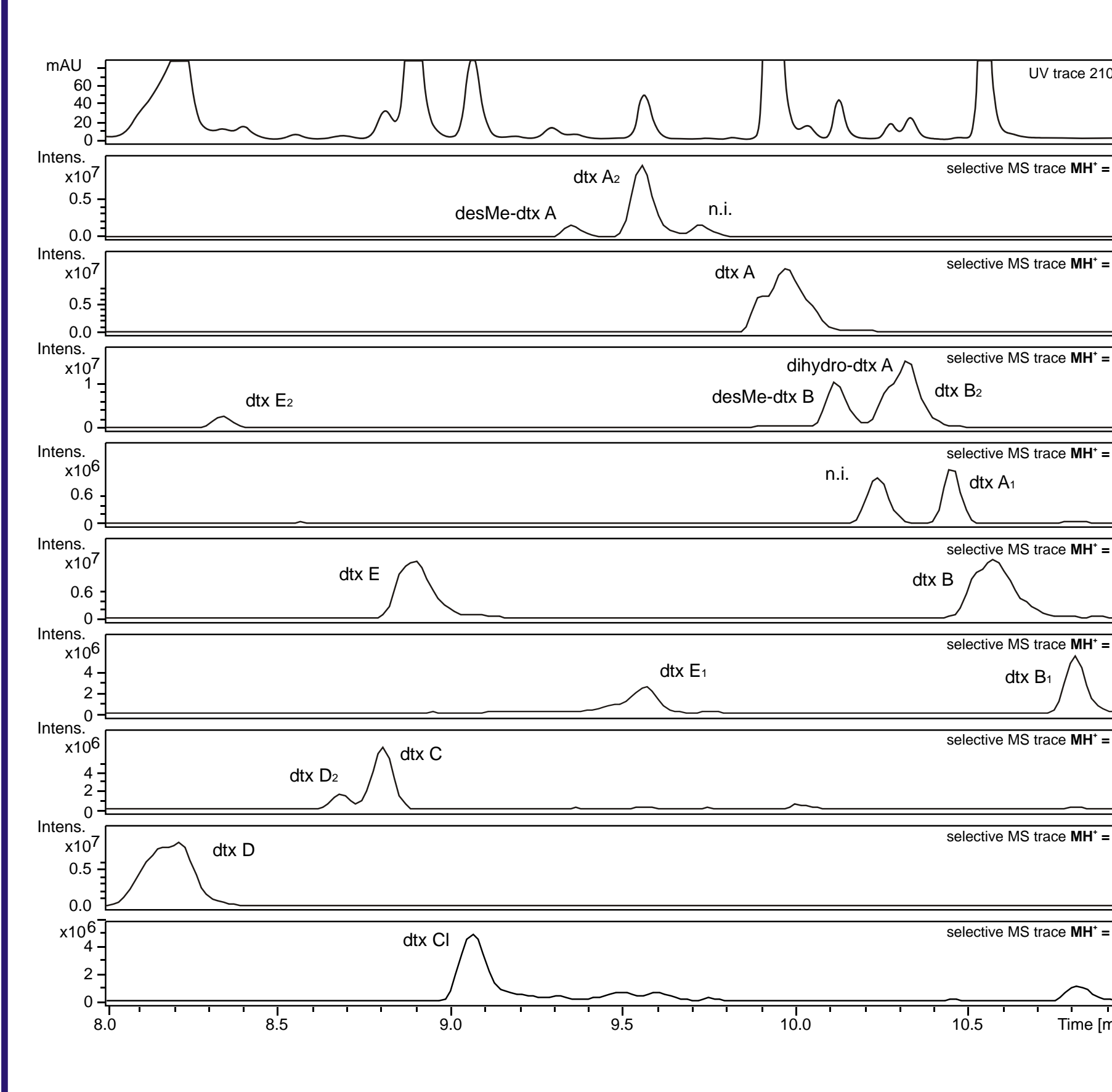
	extraction	HPLC method	t_r dtx B	LOD
this contribution	none	gradient / C-18	9 min	<0.5 ppm
Jegorov 2003	liquid / liquid	gradient / C-18	24 min	-
Hsiao 2001	liquid / liquid	gradient / C-18	24 min	>50 ppm
Kershaw 1999	SPE	isocratic / C-18	10 min	-
Chen 1999	not given	gradient / C-18	18 min	>50 ppm
Jegorov 1998	liquid / liquid	isocratic / C-18	-	-
Loutelier 1996	liquid / liquid	isocratic / C-18	37 min	>3 ppm

All literature methods use time consuming sample preparation procedures, mostly dichloromethane extractions. In most cases, retention times for dtxB are at least twice the retention time achieved by the presented method. All methods utilized RP-C18 stationary phases and ACN/H₂O mixtures as mobile phase. For method comparison literature methods were adapted to the stationary phase used in this contribution.



DERIVATIVE IDENTIFICATION WITH HPLC-MS/MS

IDENTIFIED DESTRUXINS



HPLC-DAD/MS METHOD

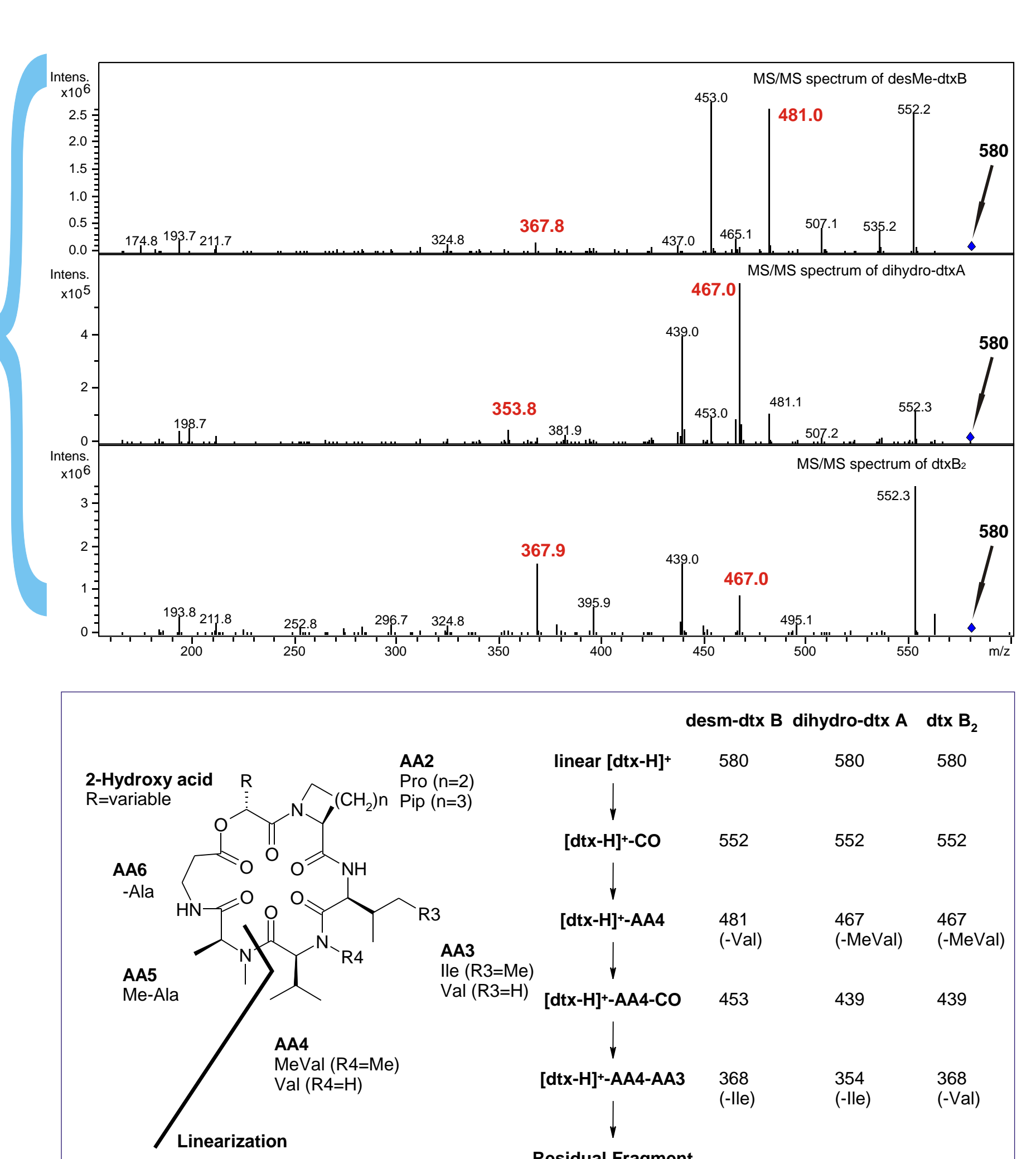
Instrumentation:
Agilent HP1100 liquid chromatograph.
Bruker Esquire3000TM ion trap MS.
Chromatography identical HPLC-DAD.
Retention time shift = 1.6 min.
Mass spectrometry parameters:
Ion source: ESI, positive mode
Spray voltage: 4500 V
Nebulizer gas: N₂, 40 psi
Dry gas: N₂, 10 l/min 350°C
Scan range: 100-1000 m/z

RETENTION RULES

Series	dtx ₂	dtx	dtx ₁
E	8.3	8.6	9.6
A	9.5	9.9	10.4
B	10.3	10.5	10.8

The relative retention within a destruxin series (e.g. A, B, E) depends on the nature of AA 2 and 3.

DECONVOLUTION OF ISOBARIC GROUPS



Primary ionization occurs typically between AA5 and AA4. The linearized amino acid chain is degraded by a series of fragmentation reactions (Jegorov 2003 and 1998). The loss of AA4 and AA3 is detectable in a single MS/MS experiment starting with the protonated linearized destruxin derivative. Differences in the amino acid sequence allow the assignment of isobaric derivatives with similar retention behaviour.

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ACKNOWLEDGEMENT

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