In vitro Metabolism of Two Heterocyclic Amines, 2-Amino-9*H*-pyrido[2,3-*b*]indole (AαC) and 2-Amino-3-methyl-9*H*pyrido[2,3-*b*]indole (MeAαC) in Human and Rat Hepatic Microsomes

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Abstract: 2-Amino-9*H*-pyrido[2,3-*b*]indole (AαC) and 2-amino-3-methyl-9*H*-pyrido[2,3-*b*]indole (MeAαC) are two mutagenic and carcinogenic heterocyclic amines formed during ordinary cooking. In this study, we have investigated the *in vitro* metabolism of tritium-labelled AαC and MeAαC in hepatic microsomes from human pools, rats induced with polychlorinated biphenyl (PCB) (Aroclor 1254) and control rats. The microsomes were incubated with AαC and MeAαC and the detoxified and activated metabolites of AαC and MeAαC were separated and characterised by HPLC-MS. AαC is metabolised to two major and three minor detoxified metabolites, while MeAαC is metabolised to three major and one minor detoxified metabolites. Some AαC and MeAαC are activated by oxidation to the reactive metabolites N^2 -OH-AαC and N^2 -OH-MeAαC, respectively. These reactive N^2 -OH-metabolites react partially in the incubation system with formation of protein adducts, dimers and the parent compound by reduction of the N^2 -OH-metabolites. The distribution between the detoxified and activated metabolites in the different types of hepatic microsomes showed same pattern for both AαC and MeAαC. In PCB-induced rat microsomes, the major part of the metabolites are detoxified, only a little amount is activated. In control rat microsomes there is a fifty-fifty distribution between detoxified, only a little amount is activated show that, in human hepatic microsomes compared to rat hepatic microsomes, a major part of AαC and MeAαC are metabolically activated to the reactive N^2 -OH-MeAαC.

2-Amino-9*H*-pyrido[2,3-*b*]indole (A α C) and its methyl homologue, 2-amino-3-methyl-9H-pyrido[2,3-b]indole (Me-AaC), are two food-borne mutagenic and carcinogenic heterocyclic amines. A α C and MeA α C are often referred to as α -carbolines (fig. 1). A α C and MeA α C are formed as pyrolysis products of tryptophan-rich compounds and are also found in cooked food such as meat, chicken and fish (Gross & Gruter 1992; Holder et al. 1997; Skog et al. 1998; Solyakov et al. 1999) and in cigarette smoke condensates (Yoshida & Matsumoto 1980; Matsumoto et al. 1981; Manabe et al. 1990; Wakabayashi et al. 1995). MeAaC is also found in wine (Richling et al. 1997). AaC and MeAaC are mutagenic in bacterial test systems (Nagao et al. 1983; Holme et al. 1989; Wild et al. 1991). Dietary administration of A α C and MeA α C to mice and rats induced liver tumours (Ohgaki et al. 1984; Hasegawa 1992). AaC and MeAaC have, like other heterocyclic amines, two metabolic pathways, detoxification or activation. The first step in the metabolism of the heterocyclic amines is a phase I hydroxylation catalysed by cytochrome P450 enzymes. Detoxified

compounds are often ring-hydroxylated followed by phase II conjugation. Activated compounds are hydroxylated in their characteristic exocyclic amino group, usually followed by O-esterification catalysed by e.g. acetyltransferase or sulfotransferase (Eisenbrand & Tang 1993). Especially enzymes from the CYP1A-family are involved in the phase I metabolism of A α C and MeA α C to their corresponding N^2 -OH-derivates (Niwa *et al.* 1982; Sugimura 1985). Activated heterocyclic amines are able to form adducts with macromolecules such as protein and DNA. It is shown by ³²P-post-labeling analysis that MeA α C and A α C form one major DNA adduct (N^2 -deoxyguanin-8-yl-(Me)A α C) in primary hepatocytes from rats (Pfau *et al.* 1996 & 1997).

There are only few reports of the metabolism of A α C and MeA α C compared with other heterocyclic amines. Recently some of the major metabolites of A α C in human and rodent hepatic microsomes were characterized by Raza *et al.* (1996) and King *et al.* (2000). Previously, the metabolism of MeA α C in hepatic microsomes from PCB-induced rat was studied (Frandsen *et al.* 1998), but not the metabolism of MeA α C in human microsomes.

The aim of this study was to investigate the *in vitro* metabolism of A α C and MeA α C in hepatic microsomes from rat and man. In the present study we have investigated the *in vitro* metabolism of A α C and MeA α C in hepatic micro-

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somes from polychlorinated biphenyl (PCB)-induced rats, control rats and two different human pools and compared the distribution between activation and detoxification of the metabolites. N^2 -OH-derivaties of both A α C and MeA α C were synthesized for comparison with metabolites of the two heterocyclic amines.

Materials and Methods

Chemicals. AaC, [3H]-AaC and MeAaC were obtained from Toronto Research Chemicals (Toronto, Canada). Tritiation of MeAaC is described previously (Frandsen et al. 1998). Pooled human liver microsomes (from 15 donors) were obtained from in vitro Technologies (Baltimore, MD, USA) and pooled human liver microsomes (from 11 donors) was obtained from Gentest (Woburn, MA, USA). Polychlorinated biphenyl (PCB: Aroclor 1254) was obtained from Monsanto Industrial Chemical Co. (St. Louis, MO, USA). Isocitricdehydrogenase (from pork heart), nicotinamide adeninedinucleotide-phosphate and 3-[N-morpholino] propanesulfonic acid hemi sodium salt (MOPS) were obtained from Sigma Chemical Co. (St. Louis, MO, USA). HPLC grade acetonitrile and formic acid (distillated before use) were obtained from Romil (Cambridge, UK). Chromabond columns (C18ec and 2OH) were obtained from Macherey-Nagel (Duren, Germany). Soluene-350 and Hionic-Flour were obtained from Packhard (Meriden, CT, USA). All other chemicals were of analytical purity and obtained from Riedel-de Haën (Seelze, Germany), Merck (Darmstadt, Germany), Fisher Scientific (Loughborough, UK) and Rathburn (Walkerburn, Scotland, UK).

Synthesis of 2-nitro-3-methyl-9H-pyrido[2,3-b]indole $(NO_{2} MeA\alpha C$). A previously described method (Frandsen *et al.* 1998) was modified in the following way: A sample of 3.4 mg MeAaC was dissolved in 1 ml acetic acid and heated to 90°. One hundred µl of hydrogen peroxide (30%) was added drop-wise under stirring. Heating and stirring were continued for 30 min. The reaction mixture was diluted with 15 ml water and applied in small portions onto an activated Chromabond C18ec column. The column was washed with 5 ml water and eluted with 2 ml methanol. The eluate was placed in a 50° water bath and evaporated to dryness under a stream of nitrogen. The residue was dissolved in 2 ml of ethyl acetate and added 6 ml of heptane. The dissolved part of the residue was applied onto a Chromabond 2OH column equilibrated with heptane. The eluate was collected and the column was eluted with 2 ml ethyl acetate/heptane (1:1). The combined eluate was evaporated as described above, redissolved in 1 ml dimethyl sulfoxide (DMSO) and stored at 4°. The product was diluted in 1% formic acid in 10% acetonitrile and analysed by high performance liquid chromatography-mass spectrometry (HPLC-MS). The yield of NO₂-MeAaC was 1.6 mg (41%).

Synthesis of 2-hydroxyamino-3-methyl-9H-pyrido[2,3-b]indole $(N^2-OH-MeA\alpha C)$. A previously described method (Agus *et al.* 2000) was modified in the following way: All solvents were purged with argon before use and all solutions were stored under argon. Two hundred µl water was added to 1 ml 0.2 M ascorbic acid in DMSO. The solution was stirred at room temperature for 5 min. Forty µl 0.3 M copper sulphate was added drop wise under stirring. After 5 min. with stirring, 0.5 ml of 0.94 mg/ml NO2-MeAaC in DMSO was added drop-wise (30 sec.) under stirring. After 45 sec. the reaction was stopped by addition of 2 ml 0.1 M EDTA followed by 8 ml ice-cold water under stirring. The reaction mixture was kept on ice until purification. The reaction mixture was under argon applied in small portions on an activated Chromabond C18ec column. The column was washed with 4 ml ice-cold water, 2 ml ice-cold 10% methanol and 2 ml icecold water. N2-OH-MeAaC was eluted with 1.2 ml ice-cold DMF and stored at -20° . The synthesis product was diluted in 1% formic acid in 10% acetonitrile and analysed by HPLC-MS. The yield of N^2 -OH-MeA α C was 192 µg (44%).

Synthesis of 2-nitro-9H-pyrido[2,3-b]indole (NO_2 -A α C). NO₂-A α C was synthesised by the same method as the synthesis of N^2 -MeA α C. 3.6 mg A α C was used and the yield of NO₂-A α C was 1.6 mg (38%).

Synthesis of 2-hydroxyamino-9H-pyrido[2,3-b]indole (N^2 -OH-A α C). N^2 -OH-A α C was synthesised by the same method as the synthesis of N^2 -OH-MeA α C. 0.4 mg NO₂-A α C was used and the yield of N^2 -OH-A α C was 110 µg (59%).

Synthesis of MeA α C- and A α C-dimers. N²-OH-MeA α C dissolved in dimethyl formamid (DMF) was diluted to 50 µg/ml with argon-purged water. To the solution was added 5 µl acetic anhydride under a stream of argon. The reaction mixture was kept under argon and stirred at room temperature for 3 hr. MeA α C treated in the same way was used as reference. The syntheses products were diluted in argon-purged 1% formic acid in 10% acetonitrile and analysed by HPLC-MS. The same procedure was used to create A α C-dimers.

Preparation of rat hepatic microsomes. Adult male Wistar rats (age 7–8 weeks, weight ~ 200 g) were delivered from Møllegaard Breeding Center (Lille Skensved, Denmark). Microsomes from PCB-induced rats and control rats were prepared as previously described (Frandsen *et al.* 1994). Four rats were used to prepare a pool of PCB-induced hepatic rat microsomes. PCB (Aroclor 1254, 500 mg/kg, dissolved in corn oil) was injected intraperitoneally 5 days before sacrifice. Two rats were used to prepare a pool of control hepatic rat microsomes.

In vitro metabolism. The microsomal incubations were performed as previously described (Frandsen *et al.* 1998). Five μ g test substance (MeA α C, [³H]-MeA α C, A α C and [³H]-A α C dissolved in DMF) per ml incubation mixture was added after preincubation for 5 min. The reactions were terminated after 30 min. for the MeA α C incubations and after 45 min. for the A α C incubations by addition of one volume of ice-cold argon-purged ethanol. After centrifugation the supernatants were isolated and analysed by HPLC-MS.

Analytical. High performance liquid chromatography analyses were performed on a Agilent Technologies model 1100 liquid chromatograph equipped with a photodiode array detector (Agilent Technologies, Wallbronn,Germany). The products were separated on a Zorbax SB-C3, 5 μ m, 150×3 mm column from Agilent Technologies. The flow rate was 0.4 ml/min. and the oven temperature was 40°. Solvent were A: 1% formic acid and B: acetonitrile. Solvent programming was: 0–2 min., 2% B; 10 min., 25% B; 20 min., 80% B; 22 min., 2% B.

Positive ion electrospray mass spectra were obtained with an Agilent Technologies MSD 1100 mass spectrometer equipped with an electro-spray interface (Agilent Technologies, Wallbronn, Germany). The following interphase settings were used: nebulizer pressure 60 psi; drying gas(nitrogen) 10 l/min., 350°; capillary voltage 4000 V; fragmentor voltage 70 V.

When the incubations were conducted with tritiated materials the supernatants were analysed by HPLC and 1 min. fractions were collected (the same HPLC-conditions were used to analyse both tritiated and not-tritiated materials). Four ml Hionic-Flour were added to the collected fractions followed by liquid scintillation counting. The precipitates from the incubations with tritiated materials were washed twice with acetone and dissolved in Soluene-350. One hundred μ l of the solutions were added 4 ml of Hionic-Flour and analysed by liquid scintillation counting. Liquid scintillation counting was performed on a Tri Carb 3100TR using a Hion-

ic-Flour scintillation cocktail and with external standardization (Packhard, Meriden, CT, USA).

All incubations were repeated three times with similar results.

Results

Metabolism of MeA α C and A α C. Several metabolites of MeA α C and A α C were detected in microsomes from PCBinduced rats, control rats and humans after incubation with MeA α C and A α C. Fig. 2 shows the HPLC profiles of MeA α C and A α C and their metabolites from the microsomal incubations. Two different pools of human microsomes were used, but there were no particular difference between the metabolism of MeA α C and A α C in the two human hepatic microsomal pools.

In PCB-induced hepatic rat microsomes MeAaC is metabolised to three major metabolites (labelled 1-3) and one minor metabolite (labelled with arrow) eluting before the parent compound, MeA α C (fig. 2A). The mass spectra of all the early eluting metabolites showed molecular ions $[M+H]^+$ at m/z 214, indicating that they are hydroxylated metabolites. An earlier identification of the three major metabolites by electro spray mass spectrometry and ¹H-NMR has shown, that metabolite 1, 2 and 3 can be characterized as 6-OH-MeAaC, 3-CH2OH-AaC and 7-OH-MeAaC, respectively (Frandsen et al. 1998). UV spectra of the minor metabolite were nearly identical with the UV spectra of 6-OH-MeAaC and 7-OH-MeAaC (data not shown), therefore it is proposed that the minor metabolite could be another ring-hydroxylated metabolite. The tree early eluting major metabolites are all characterized as detoxified compounds (Frandsen et al. 1998). Small amounts of two other metabolites (labelled 4 and 5) are eluting after MeA α C. The mass spectra of the late eluting metabolites showed molecular ions $[M+H]^+$ at m/z 393, both with daughter ions $[M+H]^+$ at m/z 197. This high molecular weight indicates that dimers of a reactive metabolite are formed. The presence of a reactive metabolite was not detected during HPLC analysis, but its presence is indicated by binding of 8% of the radioactivity to the protein pellet.



MeAαC (Mw 197)

Fig. 1. Structure and molecular weights of 2-amino-9*H*-pyrido[2,3-b]indole (A α C) and 2-amino-3-methyl-9*H*-pyrido[2,3-b]indole (MeA α C).

Similar metabolite patterns of MeA α C are found in incubation with control rat and human microsomes (fig. 2B and 2C). However, the amounts of the late eluating metabolites 4 and 5 in control rat and human microsomes are considerable larger than the amount of metabolites 4 and 5 in PCB-induced rat microsomes.

Fig. 2D, E and F shows the metabolism of $A\alpha C$ in hepatic microsomes from PCB-induced rats, control rats and man. Also here a similar metabolite pattern in the three different types of microsomes is obtained. In PCB-induced rat and control rat microsomes AaC are metabolised to three major metabolites (labelled 1-3) and two minor metabolites (labelled with arrows) eluting before the parent compound, A α C. In human hepatic microsomes it is primarily metabolite 1 and 3 that are dominating, but also metabolite 2 is noticeable. The mass spectra of all the early eluting metabolites showed molecular ions $[M+H]^+$ at m/z 200, indicating that they are hydroxylated metabolites. Raza et al. (1996) have characterized the major metabolites of $A\alpha C$ in human microsome incubation as 3-OH-AaC and 6-OH-A α C. UV spectra of metabolite 1 and 3 were identical with the published UV spectra of 6-OH-A α C and 3-OH-A α C, respectively (data not shown). In the three chromatograms (fig. 2D, E and F) two other metabolites (labelled 4 and 5) are eluting after A α C. The mass spectra of the late eluting metabolites showed molecular ions $[M+H]^+$ at m/z 365, both with daughter ions $[M+H]^+$ at m/z 183, indicating that dimers of a reactive metabolites is formed. The last metabolite (labelled 6), eluting right before the parent compound, A α C, was found in the human microsomal incubations (fig. 2F). A small amount of metabolite 6 was also detectable in the preparation with PCB-induced rat microsomes by analysis of the MS data using extracted ion chromatogram (data not shown). Metabolite 6 has a molecular ion $[M+H]^+$ at m/z 200 with a daughter ion $[M+H]^+$ at m/zz 183. This metabolite was much more unstable, when stored in air at room temperature, than the other metabolites (labelled 1–5), which could indicate that this metabolite was the reactive N^2 -OH-A α C.

Synthesis of N-OH-MeA α C and N-OH-A α C. In order to evaluate the possible presence of unstable N²-hydroxylated metabolites, N²-OH-MeA α C and N²-OH-A α C were synthesised by two-step procedures. MeA α C and A α C were oxidized to NO₂-derivates with H₂O₂ in acetic acid. In an attempt to increase the yield of NO₂-MeA α C, we have tried to use different reaction conditions. However, oxidation of MeA α C with dimethyldioxirane, a method developed to synthesize NO₂-A α C (King *et al.* 2000), or oxidation with H₂O₂ of MeA α C diluted in triflour acetic acid, trichlor acetic acid, formic acid, diluted sulphuric acid and diluted phosphoric acid did not result in higher yields.

In the second step the NO₂-compounds were reduced to N^2 -OH-MeA α C and N^2 -OH-A α C using copper sulphate in ascorbic acid. These methods were modified from a method developed to synthesize N^2 -hydroxy-2-amino-3-methylimid-azo[4,5-f]quinoline (Agus *et al.* 2000). HPLC-MS analysis



Fig. 2. HPLC-chromatograms monitored at 360 nm showing the metabolism of MeA α C- and A α C in hepatic microsomes (micr.) from PCBinduced rats, control rats and man. Chromatographic conditions are described in Materials and Methods. The chromatograms show MeA α C and its metabolites in hepatic microsomes from PCB-induced rats (A), control rats (B) and man (C), and A α C and its metabolites in hepatic microsomes from PCB-induced rats (D), control rats (E) and man (F). Peaks labelled 1–3 and arrows without labels are detoxified metabolites, while peaks labelled 4–6 indicate activation of the parent compound.

of the synthetic N^2 -OH-A α C compound showed retention time, UV spectrum and molecular mass identical to the proposed N^2 -OH-A α C metabolite from the microsomal incubation of A α C, showing that some of the A α C was activated to the reactive N^2 -OH-compound. The synthetic N^2 -OH-MeA α C has a molecular ion $[M+H]^+$ at m/z 214 with a daughter ion $[M+H]^+$ at m/z 197 and elute in the HPLC-system at the retentiontime 14.7 min. The presence of a N^2 -OH-MeA α C metabolite was not detected in chromatogram A–C (fig. 2).



Fig. 3. HPLC-chromatogram monitored at 360 nm showing the synthetic A α C-dimers formed from N-OH-A α C. Chromatographic conditions are described in Materials and Methods.

Addition of acetic anhydride to solutions of N^2 -OH-MeA α C and N^2 -OH-A α C resulted in formation of three products, each. Fig. 3 shows the HPLC profile of N^2 -OH-A α C treated with acetic anhydride. A α C is the major product obtained together with two proposed dimers having identical retention times, UV spectra and mass spectra as the dimers found in the microsomal incubation mixtures. N^2 -OH-MeA α C treated with acetic anhydride gave similar results (data not shown). Due to the lack of reactivity of

the parent compound, dimers can not be formed from A α C or MeA α C alone. This indicates that the dimers found in the microsomal incubation mixtures are formed from N^2 -OH-A α C and N^2 -OH-MeA α C, respectively. Further characterisation of the dimers was not attempted.

Metabolic distribution. Fig. 4 shows the percentage distribution of the metabolised part of MeA α C and A α C in the hepatic microsomes from PCB-induced rats, control rats and humans. The calculations are made from liquid scintillation counting data (not shown) on fractions collected from HPLC analysis and dissolved protein precipitates. In the microsomal incubation of $[^{3}H]$ -MeA α C and $[^{3}H]$ -A α C in PCB-induced rat microsomes about 8 and 6%, respectively, of the radioactivity were counted in the protein pellet, indicating activation of the parent compound. In the control rat microsomal incubation of [³H]-MeAαC and [³H]-AaC about 21 and 13%, respectively, of the radioactivity were counted in the protein pellet, and in the human microsomal incubation of $[^{3}H]$ -MeA α C and $[^{3}H]$ -A α C about 9 and 11%, respectively, of the radioactivity were counted in the protein pellet.

Table 1 show the distribution between detoxification and activation of the total amount of metabolised MeA α C and A α C in the three types of microsomes. In PCB-induced rat microsomes about 82 and 92% of the metabolised MeA α C and A α C were detoxified, respectively. In control rat micro-



Fig. 4. Distribution of MeA α C- and A α C-metabolites in hepatic microsomes (micr.) from PCB-induced rats, control rats and man shown in percent of the total amount of metabolised parent compound.

control rats and man. The data are calculated as percent of the total amount of metabolised parent compound.				
	Total amount of detoxification and activation (%)			
	PCB rat micr.	Control rat micr.	Human micr.	
MeAaC-detoxification	82.2±5.1	46.0±6.5	35.8±1.1	
AaC-detoxification	$91.8 {\pm} 0.7$	51.7 ± 3.1	41.7 ± 2.9	
MeAaC-activation	17.8 ± 5.1	54.0 ± 6.5	64.2 ± 1.1	
AaC-activation	8.1 ± 0.7	48.3 ± 3.1	58.3 ± 2.9	

 Table 1.

 Distribution between detoxification and activation of MeA α C- and A α C-metabolites in hepatic microsomes (micr.) from PCB-induced rats, control rats and man. The data are calculated as percent of the total amount of metabolised parent compound.

Values are presented as means±S.D., N=3.

somes about 54 and 48% of the metabolised MeA α C and A α C were activated, and in the human hepatic microsomal incubation 64 and 58% respectively of the metabolised MeA α C and A α C were activated.

Discussion

Using hepatic microsomes from PCB-induced rats, control rats and two different human pools, the *in vitro* metabolism of A α C and MeA α C was investigated. In the microsomal incubation of MeA α C four early-eluting MeA α C-metabo-

lites were found. Three of them are detoxified metabolites, earlier characterized as 6-OH-MeA α C, 3-CH₂OH-A α C and 7-OH-MeA α C (Frandsen *et al.* 1998). A minor metabolite, with the same mass spectrum and a similar UV-spectrum as 6-OH-MeA α C and 7-OH-MeA α C, is probably also a ring-hydroxylated detoxified metabolite of MeA α C.

In our study of A α C metabolism in rat hepatic microsomes we found three major detoxification products and small amounts of two minor metabolites. A previous study of A α C metabolism in hepatic PCB-induced rat microsomes has shown that A α C is metabolised to five metabolites,

CH₂OH



Fig. 5. Metabolic pathway of MeAaC (only the major detoxified metabolites are shown).

three non-mutagenic and two mutagenic metabolites. The two were supposed to be a N^2 -hydroxy-derivate and a nitroso-derivate of AaC (Niwa et al. 1982). In the human microsomal preparation we found two major detoxification products and one minor, which were identical to the three major products in the rat microsome preparations. In a study of AaC metabolism in human hepatic microsomes, Raza et al. (1996) found two major detoxified metabolites characterized as 3-OH-AaC and 6-OH-AaC and four minor metabolites characterized as N2-OH-AaC, 2-nitroso- $A\alpha C$ and corresponding azoxy- and nitro-derivates. There are good indications that the two major metabolites from the human microsome preparation are 6-OH-A α C and 3-OH-AaC, as characterized by Raza et al. (1996). In our microsomal incubations of AaC we did not find nitroso-, azozy- or nitro-derivates of A α C, but we found a much higher amount of N^2 -OH-A α C (16%) in the human microsomal incubation.

Another interesting finding was that in all microsomal incubations of both $A\alpha C$ and $MeA\alpha C$, a considerable amount of the tritium labelled $A\alpha C$ and $MeA\alpha C$ were found in the protein fractions (fig. 4), indicating that these parts of the compounds also had been activated and bound to proteins.

In both the microsomal preparations of A α C and MeAaC, two late-eluting metabolites with molecular masses $[M+H]^+$ at m/z 365 and 393, respectively, were found. The same two sets of late-eluting products as well as the parent compounds were obtained, when N^2 -OH-A α C and N^2 -OH-MeA α C were added acetic anhydride. This indicates that N^2 -OH-A α C and N^2 -OH-MeA α C were reacting to form two dimers with identical retention times, UV-spectra and masses as found in the HPLC-MS profiles of the microsomal metabolism of AaC and MeAaC. This suggests that the late-eluting AaC and MeAaC metabolites are secondary metabolites, created from the primary and very reactive N^2 -OH-derivates and the parent compounds. Fig. 5 shows a suggested metabolic pathway for MeA α C, which is oxidized to three major detoxified metabolites; 3-CH₂OH-AaC, 6-OH-MeAaC and 7-OH-MeAaC, and to the very reactive metabolite N^2 -OH-MeA α C. N^2 -OH-MeA α C can react in three different ways; reduction back to MeAaC, protein adduct formation, and formation of two MeAaCdimers with the masses of 392. Our results indicate that the metabolic pathway for AaC seems to be similar, with two major detoxification products, 3-OH-AaC and 6-OH-AaC, and a similar activation/reaction pattern.

It is our experience that N^2 -OH-A α C is much more stable than N^2 -OH-MeA α C. This could explain why we did not find the primary N^2 -OH-MeA α C in the microsomal incubations, but only the secondary metabolites, dimer 1, dimer 2 and the protein bound MeA α C-derivates.

The metabolism of A α C and MeA α C in the three different types of microsomes results in the same metabolites, however in different amounts. In PCB-induced rat microsomes, the major part of the metabolites is detoxified (92 and 82%, respectively), only a little amount is activated (8 and 18%, respectively). A previous study of MeA α C metabolism in PCB-induced hepatic rat microsomes has shown similar results; 83% detoxification and 13% activation (Frandsen et al. 1998). In the control rat microsomes there is a nearly fifty-fifty distribution between detoxification and activation, 52% of the metabolised part of A α C was detoxified and 48% was activated, while 46% MeAaC was detoxified and 54% was activated. The major part of the A α C and MeAaC metabolites from the human microsomal incubation were activated, 58 and 64%, respectively. As regards the distribution of the A α C-metabolites in human microsomes, our data are not comparable with a previous study, where Raza et al. (1996) found that only 15% of A α C was activated and 85% was detoxified in human hepatic microsomes. In this study, however, binding of the activated metabolite to protein was not taken into consideration. In vitro studies of another heterocyclic amine, 2-amino-1-methyl-6phenylimidazo[4,5-b]pyridine (PhIP) has shown species variation in metabolic distribution similar to our results on A α C and MeA α C. The ratio of *N*-hydroxylation to the non genotoxic 4'-hydroxylated derivate of PhIP was 97:1, 3.3:1 and 1.7:1 for humans, rats and mice, respectively (Lin et al. 1995).

Conclusion. In this study we have investigated the *in vitro* metabolism of the α -carbolines, A α C and MeA α C in human and rat hepatic microsomes. We have synthesised N^2 -OH-derivates and dimers of both A α C and MeA α C for comparison with the activated metabolites found in the microsomal incubations. We have revised the methods for the synthesis of the N^2 -OH-derivates, and our HPLC-MS method is specially developed to conserve the activated metabolites of the α -carbolines.

Our data show that A α C and MeA α C have similar metabolic patterns. The results also show a remarkable difference in the metabolic pattern of the α -carbolines in human hepatic microsomes, in control rat microsomes and in PCBinduced rat microsomes respectively. In human hepatic microsomes, a major part of the α -carbolines are metabolically activated, in hepatic microsomes from control rats there is a fifty-fifty distribution between activation and detoxification and in PCB-induced hepatic microsomes the α carbolines are mainly detoxified.

In the light of these results we have proposed a new *in vitro* metabolic pathway for both A α C and MeA α C. Finally it is concluded that, due to the higher degree of activation in human microsomes, human exposure to A α C and MeA α C may result in a higher cancer risk than estimations based on long-term cancer experiment in rodents.

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