Amino Acid Methods: Present and Future...

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## The Status Quo

 Questionnaire shows everybody using HPLC or ion-exchange amino acid analysers for routine quantitative services

Some use tlc /HVE to pre-screen urine and /or plasma samples

### Why would we want to change?

- Long run times for AA analyser, significant maintenance to keep running, temperamental
- Significant sample preparation times for HPLC, co-eluting peaks
- Analysers /staff running at capacity (or beyond)
  Need for rapid results in urgent cases

Some current solutions to the capacity problem...

- Pre-screening samples using tlc and HVE to reduce number of samples that need to be quantitated
- Using HPLC as a semi-quantitative screen (report as NSA or proceed to quant)
- Run two amino acid analysers
- Use tandem or underivatised HPLC method for PKU monitoring
- Use of short programs to reduce analyser time when only certain amino acids are required e.g. MSUD monitoring

### Why look for other alternatives?

Screening by tlc has its own problems....

- significant staff time
- technically demanding
- Interpretation and identification of amino acids requires significant experience

• Have to have low threshold for quantitating samples to be confident of not missing something "significant" –and even then....

## Would you have spotted this?

Glycine = 110  $\mu$ mol/L (200-600) Serine = 30  $\mu$ mol/L (50-350)

CSF glycine =  $<1 \mu mol/L (0-10)$ CSF serine =  $5 \mu mol/L (35-80)$ 

### Why look for other alternatives?

 Cost of two instruments
 Run time is not just a capacity issue, also a need for quick turnaround times in certain circumstances

## The ideal analyser would be...

Fast (run time <30 mins)</li>
 Little or no sample preparation
 Separation and positive identification of all diagnostically relevant amino acids
 Robust equipment, easy to maintain
 Cheap

## What are the possible alternatives?



## GC-MS

ERNDIM returns indicate a small number of labs using GC-MS for amino acids, (? In house methods or commercial kits)

 Commercially available EZ:faast amino acid analysis kits for GC-MS
 -Sample derivatisation with propriety reagent and analysis within 15 mins

## Pros

# Fast Quick derivatisation Analyse 50 amino acids /dipeptides in an 8 min run time

## Cons

Would need a dedicated GC-MS (can't use same column as organic acids)
 Citrulline and Arginine are NOT two of the 50

## Tandem-MS

 Use well established in Neonatal Screening
 Increasingly being used as a solution to amino acid analysis in specific circumstances or specific problem analytes

-e.g. Rapid screen in acutely ill child, monitoring of treatment in decompensated MSUD, sulphocysteine

Small number of labs are using it for routine analysis

## Rapid Screen of the acutely ill child

- A number of diagnostically useful amino acids can be easily measured by underivatised MS/MS method
- Can be measured on the same injection as acylcarnitines
- In minutes sample preparation and 3 minute run can give a host of information and either provide a diagnosis or narrow it down considerably
- What can be measured is limited by the problem of isobaric / isomeric compounds

## Monitoring in Decompensated MSUD

- A probable diagnosis can be made from the simple MS/MS method
- Need a different method to measure leucine, isoleucine and allo-isoleucine separately to allow planning and monitoring of treatment
- A chromatographic step is required for separation of the isomers

### Possible chromatographic options...

- Macrocyclic glycopeptides eg Chirobiotic TAG (teicoplanin aglycone)
- Porous graphite column (Hypercarb)
- -columns easily attached between sample manager and tandem with an extra piece of tubing
- -adds a few minutes to the run time
- -allows rapid measurement of leucine and its isomers, ideal for monitoring treatment during crisis when frequent sampling is required

### **Routine Amino Acid Analysis**

- Small number of labs are using tandem methods for routine amino acid analysis
- e.g. Piraud et al, Lyon (SSIEM abstract 140-P 2005)
- -using ion-pairing reverse phase liquid chromatographic method with MS/MS as the detector
- -run time is ~25mins
- -in routine use for 18 months, several thousand samples
- -have diagnosed and monitored wide range of disorders without problems

UPLC (ultra performance liquid chromatography)

 Souped up version of HPLC
 Relies on even smaller particle size (made possible by new material) and a system designed to tolerate very high pressures to provide better resolution and increased speed

The promise of the van Deemter plot



## UPLC cont...

- ♦ Run time <20 mins</p>
- Better resolution than HPLC
- Requires derivatisation step but this is much shorter than the PITC method (<30 mins)</p>
- Cost of equipment similar to current amino acid analysers
- Appears to be capable of analysing all necessary amino acids
- Unfortunately amino acid analysis by UPLC is still very much in development

## UPLC Physiological Amino Acids UV Detection @ 250 nm



# One stage further: UPLC-MS/MS

- Using MS/MS as the detector would allow positive identification of peaks
  - -Best of both worlds, UPLC separates isobaric compounds, MSMS "separates" coeluting peaks
- No derivatisation of samples required
- Rapid, high through-put system suitable for diagnosis, monitoring and urgent analysis with minimal sample preparation
- Same system could be used for other assays –would open up possibilities for the larger, specialist labs

#### The Future....

- New technologies could alter the way we operate allowing more flexibility
- Higher through-put systems could put an end to pre-screening samples by tlc etc
- In the next few years newer technologies will become more and more of a realistic alternative –which way labs decide to go will ultimately depend on staff expertise, costs, existing facilities and equipment, workloads and clinical needs