Improving the prediction of Amino Acid Digestible in the Intestine through Meta-analysis

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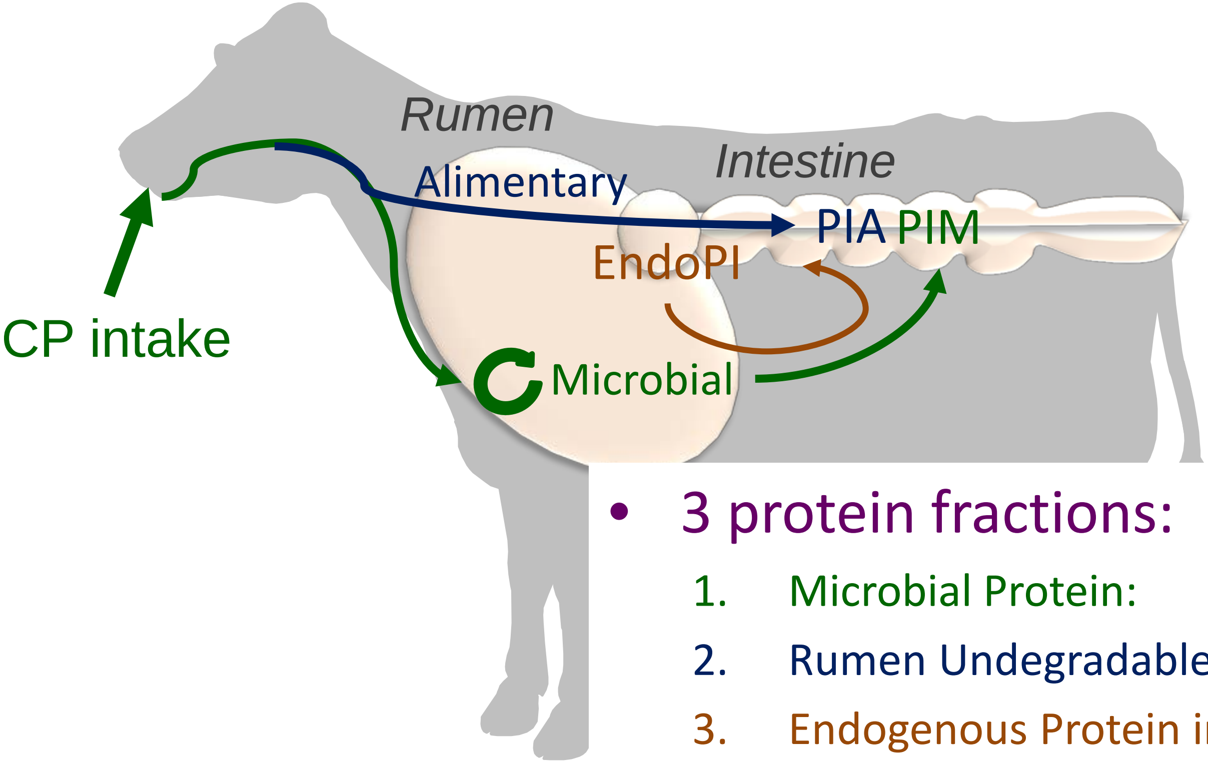
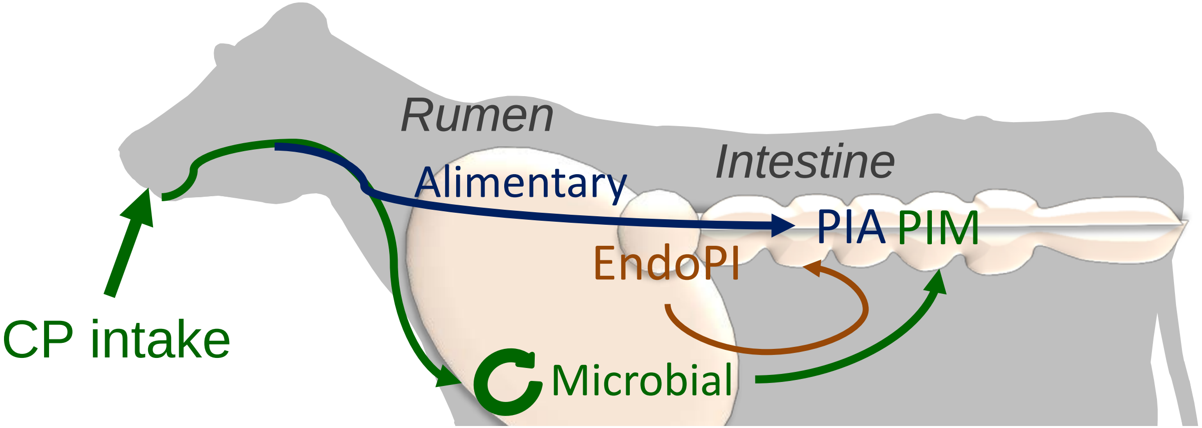
Amino Acid absorbed in the Intestine



- 3 protein fractions:

	INRA
1. Microbial Protein:	PIM
2. Rumen Undegradable Protein (RUP):	PIA
3. Endogenous Protein in the duodenum:	EndoPI

First INRA model for Amino Acid supply (Rulquin et al., 1998)



- [AA] in the duodenum (% of 16 AA)
- 16 AA: Lys, Met, His, Leu, Ile, Val, Phe, Thr, Arg,
  Ala, Asp, Glu, Gly, Pro, Ser, Tyr

- A theoretical model: a factorial approach

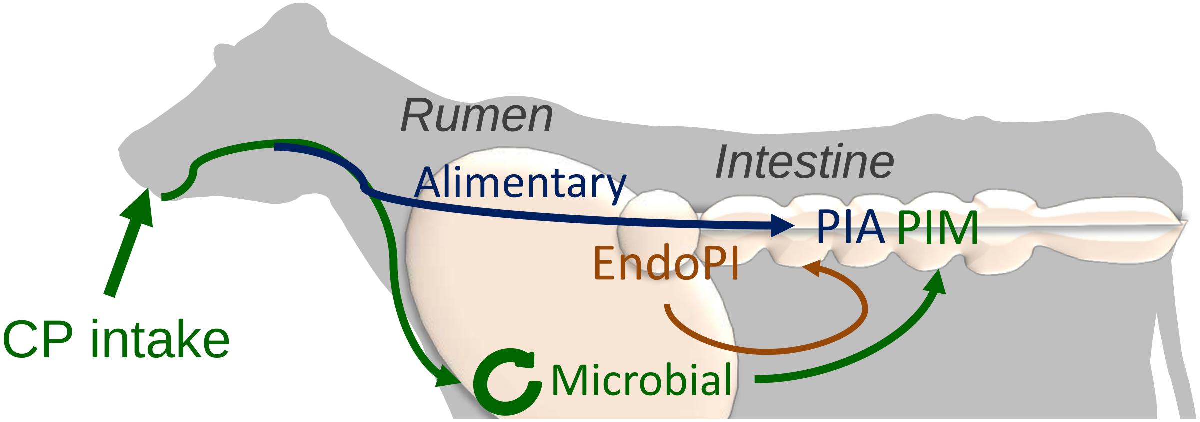
$$th\_AA_n\text{flow} = \sum_{f=1}^{F}(PIM \times [AA_n]_{Mic.} + PIA \times [AA_n]_f + EndoPI \times [AA_n]_{endo}) \times DMI_f \quad \text{(g/d)}$$

Liquid associated bacteria
Meta-analysis *(Rulquin, 2001)*
80 % of AA in Microbial CP

[AA] of the feed f

One profile Orskov (1986)
50% of AA in EndoCP

First INRA model for Amino Acid supply (Rulquin et al., 1998)



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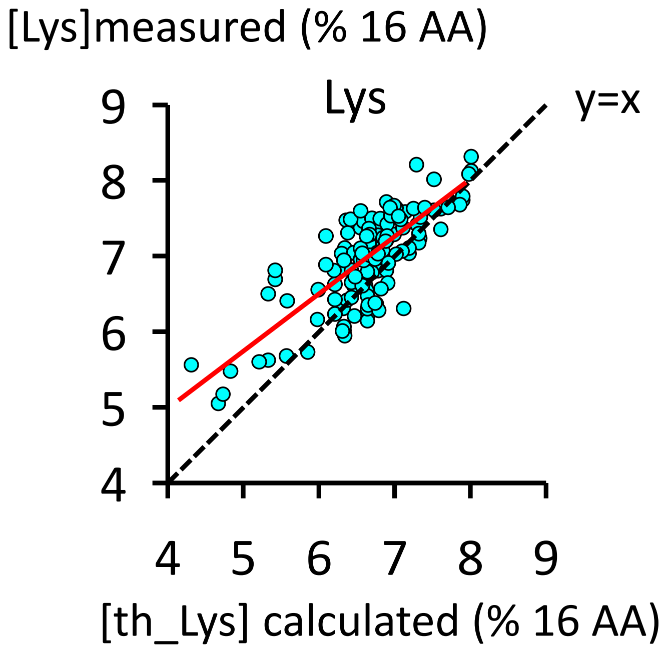
$$[th\_AA_n] = \frac{th\_AA_n flow}{\sum_{n=1}^{16} th\_AA_n flow} \qquad \text{(\% 16 AA)}$$

Comparison of theoretical calculation to measured [AA]

- Meta-analysis (Rulquin et al., 1998)



- Linear model:

$[AA_n]$measured = Team + a + b x$[th_AA_n]$ + ε

- Correction factors introduced:

$[AA_n]$predict. = a + b x [th_AAn]

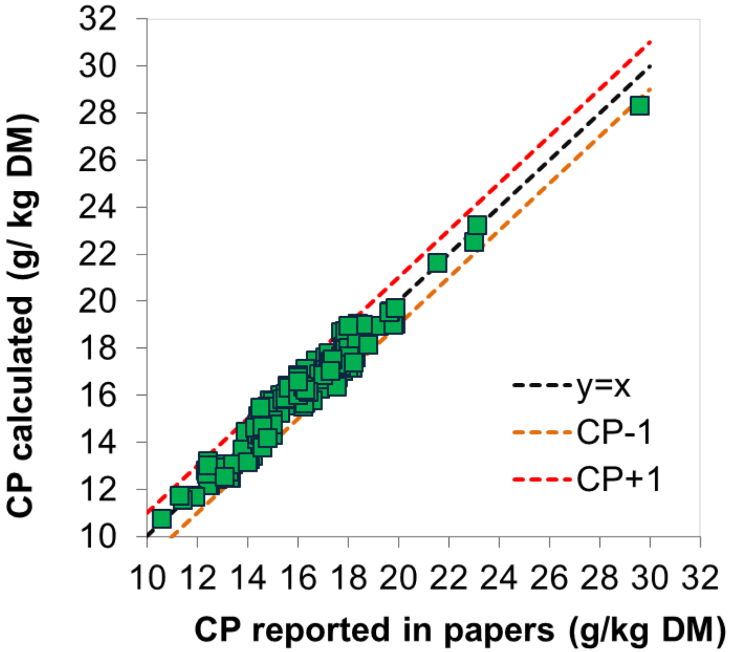
Questions

- INRA Systali:
  - The calculation of the 3 intestinal protein fractions were changed
  - Database of Rulquin (1998) : 30 papers from 1977 to 1992

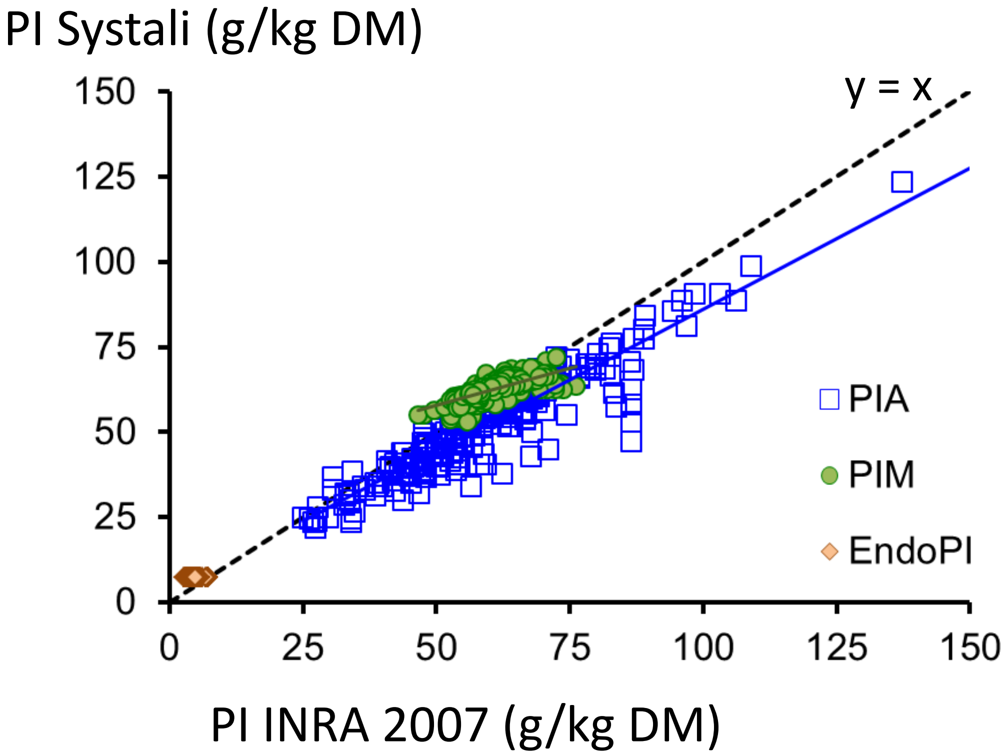
- With the 3 new intestinal protein fractions in INRA Systali and a new database
  1. Are correction factors still necessary?
  2. Did new correction factors improved the predictions of [AA] compared to past ones?

New database

- Papers from 1977 to 2013 on cattle
- Feed values calculated using INRA Systali feed tables & equations
  - Chemical composition (CP, NDF, starch)
- 64 papers, 243 diets
  - 156 diets for dairy cows
  - 57 diets common with Rulquin (133)
- New statistical model:
  $[AA_n]_{meas.} = Expe. + a + b\,x[th\_AAn] + \varepsilon$



Results: changes in intestinal proteins observed for diets

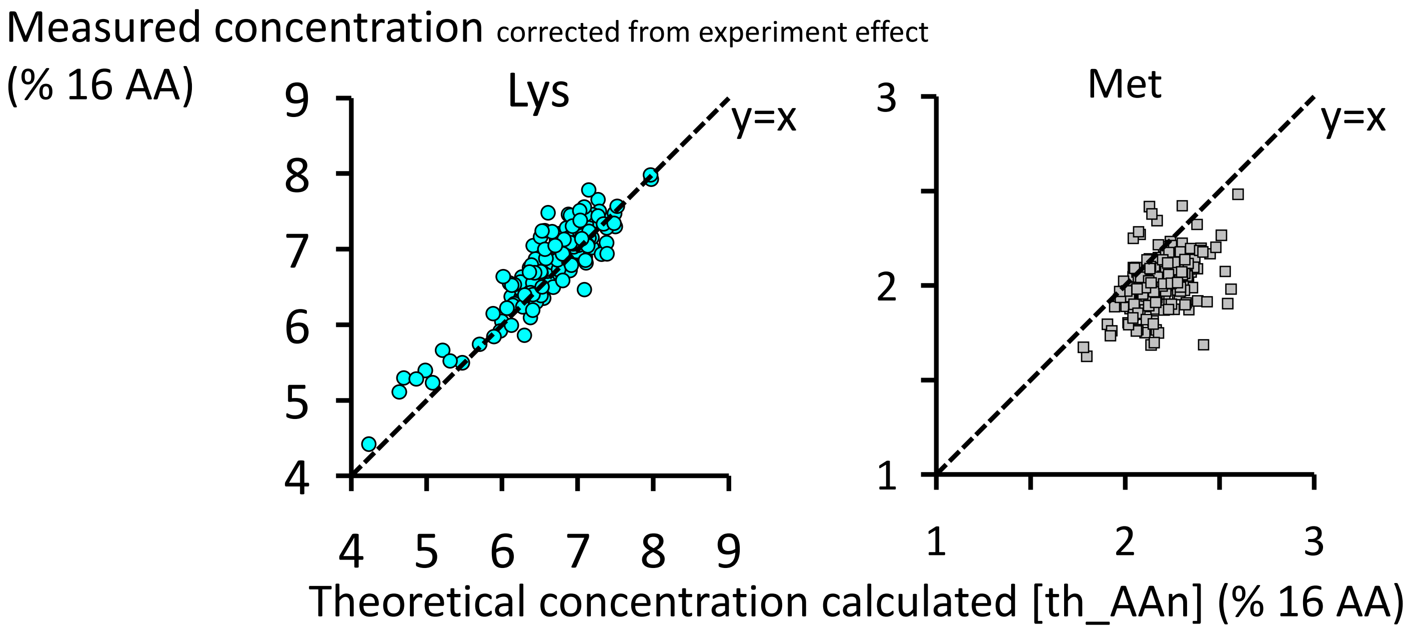


PIM:
- FOM
- Microbial protein efficiency of synthesis

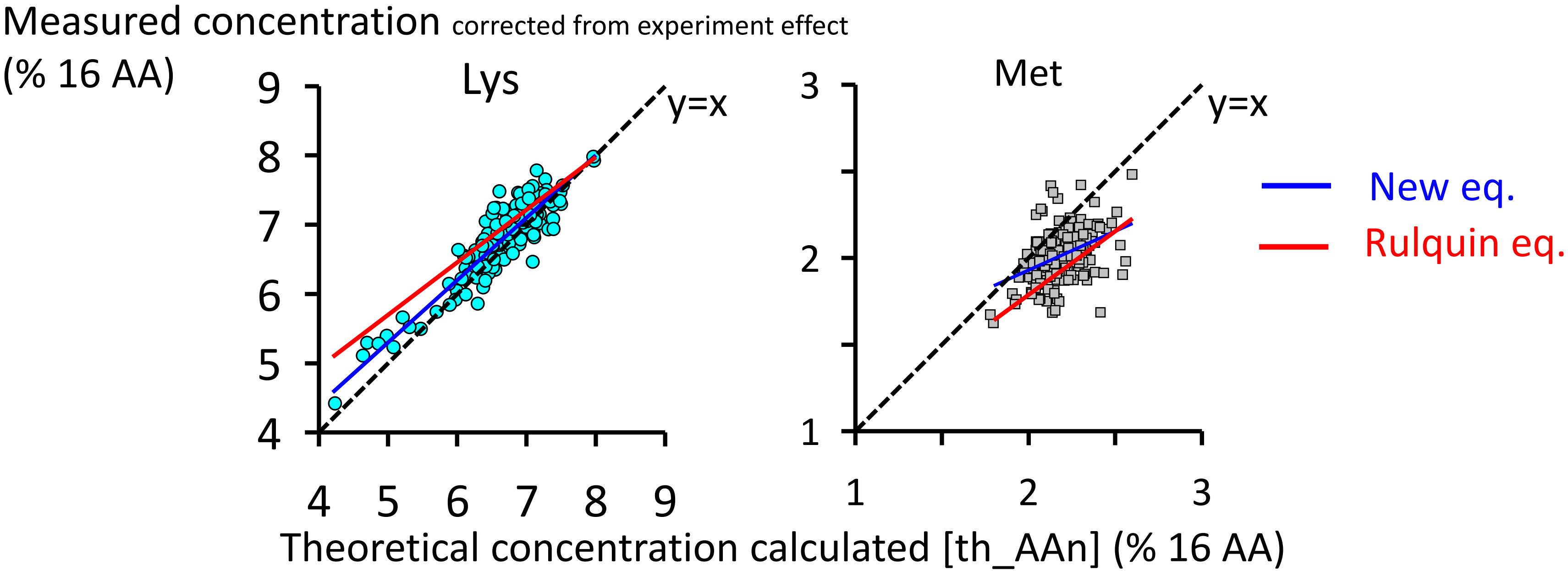
PIA: Transit rate

EndoPI: 7.1 g/kg of DMI

Results: correction factors are still necessary

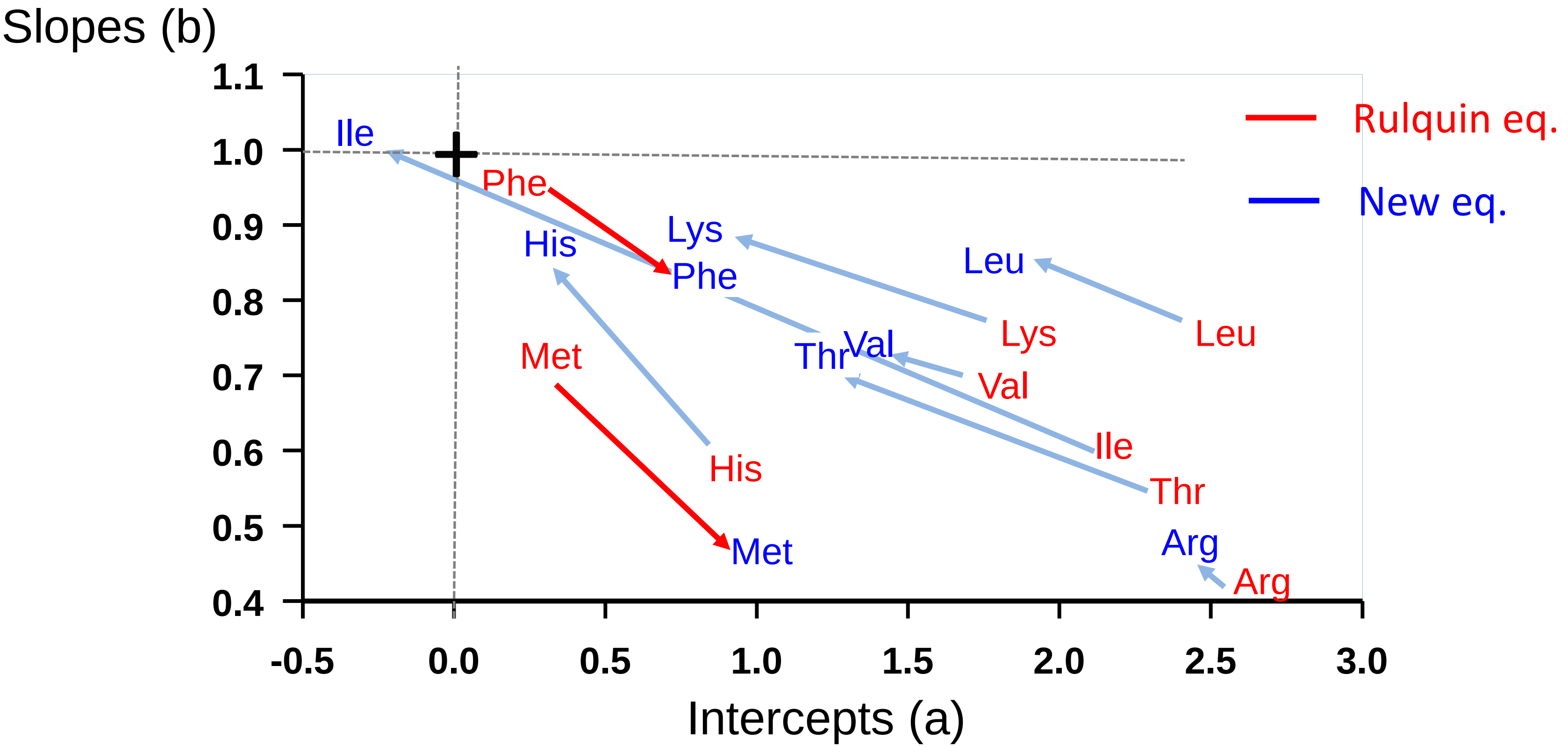


Results: new correction factors better fit the data

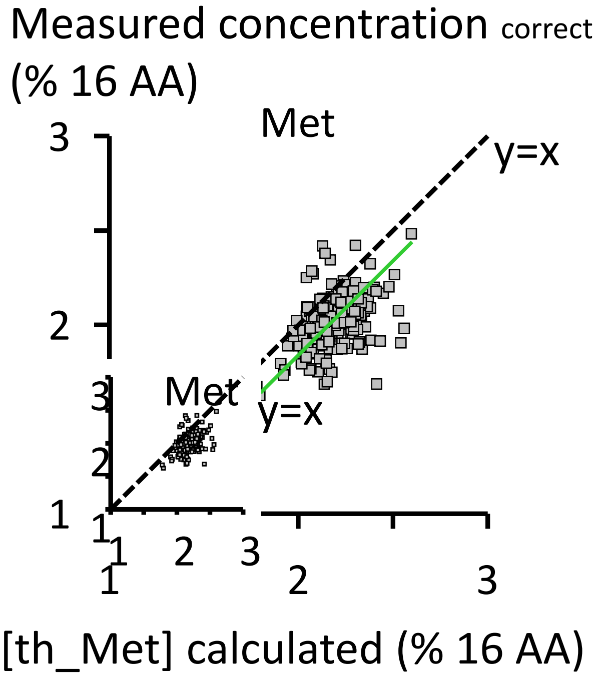


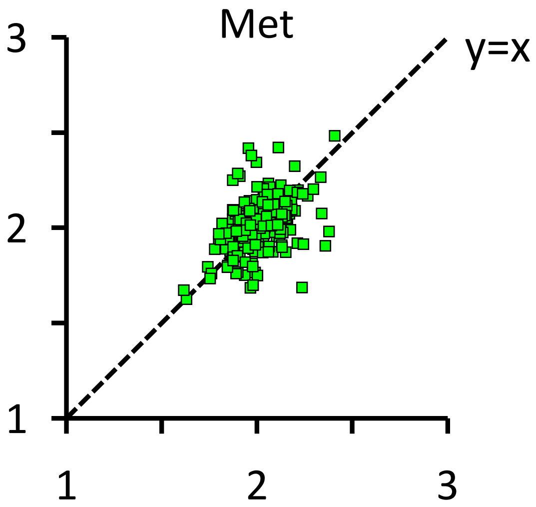
RMSE	0.24 *vs.* 0.39	0.14 *vs.* 0.34
Adj.R^2	0.92 *vs.* 0.61	0.91 *vs.* 0.41

Less important correction factors are necessary for EAA



Final correction factors applied to predict Met supply in Systali





[Met]predict. = -0.16 + 1 x [Th_Met]

— Final equation for Systali

Conclusions

- With the new database and the new intestinal protein fractions calculated using the new INRA Systali:
    1. Correction factors are still necessary
       However less important corrections are required
    2. New correction factors fit better the data than past ones for almost all the 16 AA

- Perspectives
    - Even if biases are less important, biases still exist
    - Research necessary to better fit Phe supply

Thanks to: Systali collaborators

INRA Feed Unit Systems for Ruminants

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Clémence Panzuti M2 Stat

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Thank you for your attention !