The ECO-FCE project is funded by the European Union Seventh Framework Programme (FP7 2007-2013) under grant agreement No. 311794.
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The focus of ECO FCE was to:

Advance understanding and knowledge to

♦ Improve the feed use efficiency and reduce the ecological impact of pigs and chickens
The potential impact of ECO FCE

Based on a 5% improvement in FE, on 10% of the pigs and chickens in the countries involved in the project

- Feed costs ↓ €13.7M/yr
- N excretion ↓ 2300 tonne/yr
- P excretion ↓ 400 tonne/year
ECO FCE addressed these through:

- Use of current knowledge
- Investigating new feeding strategies
- Advancing the understanding of common factors attributable to high and low feed efficiency potential
- Identification of genetic regions coding for improved feed efficiency
- Development of new statistical models to select for improved feed efficiency
Outcomes from search of current knowledge

♦ A vast array of knowledge exists **BUT**

♦ The quality of this information is highly variable **AND**

♦ The consistency of information across publications is low

♦ This makes:
  ♦ The full utilisation of this knowledge impossible to achieve and
  ♦ Meta analysis on a large scale very difficult
ECO FCE proposes the adoption of:

♦ A system to improve the consistency of M&M information in peer review papers, (Arrive guidelines (NC3R’s))

♦ An automated upload of M&M and Results information

♦ ECO FCE has developed the knowledge, through trial and error, to advance such concepts.
Outcomes from feeding systems

♦ Nutritional conditioning of broilers has potential to improve early life performance of birds and reduce P excretion

♦ *In Ovo* symbiotic in chickens and inoculation early in the pigs life can have life long effects on gut microbiota

♦ Precision feeding of pigs in commercial penning can improve feed efficiency, especially of males
Outcomes from feeding systems

♦ The efficacy of enzymes differs greatly depending on feed ingredient

♦ In vitro tests for enzyme efficacy show promise in their ability to assess the relative impact of enzymes on different raw materials.

♦ Enzymes/ingredient combinations:
  ♦ Galactosidase in soya bean meal based diets showed promised
  ♦ Xylanase/β Glucanase in wheat DDGS/RSM based diets – no effects
  ♦ Protease in wheat DDGS/RSM based diets – no effects
### Pigs - high vs low feed efficiency

<table>
<thead>
<tr>
<th></th>
<th>Difference between High and Low RFI?</th>
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<tbody>
<tr>
<td>Microbiota richness and diversity</td>
<td>N</td>
</tr>
<tr>
<td>Composition of low relative abundance taxa</td>
<td>Y (But inconsistent across site)</td>
</tr>
<tr>
<td>Feeding Behaviour</td>
<td>Y</td>
</tr>
<tr>
<td>Mucosal Permeability (Jejunum)</td>
<td>Y</td>
</tr>
<tr>
<td>Activation of the Jejunum immune response</td>
<td>Y</td>
</tr>
<tr>
<td>Differentially expressed genes (DEGs)</td>
<td>Liver - 803, Duodenum – 62, Jejunum – 86, Hypothalamus - 78</td>
</tr>
</tbody>
</table>

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# Chickens - high vs low feed efficiency

<table>
<thead>
<tr>
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<th>Different between High and Low RFI?</th>
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<tbody>
<tr>
<td>Bacterial OTU’s</td>
<td>Y (but inconsistent between sites)</td>
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<tr>
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<td>Y</td>
</tr>
<tr>
<td>Activation of the Jejunum immune response</td>
<td>Y</td>
</tr>
<tr>
<td>Differentially expressed genes</td>
<td>Duodenum – 172, Jejunum – 120 Ileum – 81</td>
</tr>
</tbody>
</table>

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Genetic regions for FE

♦ Entropy analyses and multi-marker strategies ID’ed major genomic regions for FE on chicken chromosomes 1 and Z.

♦ For Pigs - Entropy analyses suggested the most informative SNP’S for FE related traits were mainly located on chromosomes: 1, 4, 5, 7, 9, 12, 14 and 17 (Potential candidate genes: Water homeostasis, glycolysis, mitochondria assembly and beta-oxidation)

♦ ECO FCE, with industry partners, developed an industry directed panel of SNP markers to breed faster for improved feed efficiency amongst breeding stock.
Genetic Models

♦ Modelling confirmed that improved feed efficiency was better achieved through selection for RFI than for FCR

♦ Manipulation of the Genomic Feature Model (GFBLUP), using information from the project, resulted in it having a better predictive ability than the standard GBLUP
Some key areas of Future potential

♦ Automation of current knowledge

♦ More clarity is required on enzyme/ingredient combinations which have impact

♦ Harnessing the impact of early life gut microbiota

♦ Genotype x Environment

♦ Integrating Multi layers of ‘Omics’ into breeding models
Discussion...