Analysis of Genes Affecting Ascites Susceptibility in Broilers

Douglas Rhoads
Collaborators: Nicholas Anthony, Gisela Erf, Robert Wideman, Heidi Kleuss
Credits

• Graduate Students: Sriram Krishnamoorthy, Sharath Munnaluri, Khaloud AlZahrani, Brenda Flack, Nyoman Fitri
• Adnan Al-Rubaye: qPCR analysis of candidate genes (P0607)
• Shatovisha Dey: AGTR1 and UTS2D SNPs (P0608)
• Sohita Ojha: Sperm mobility and PGC cultures. (P0599)
• Undergraduates: N. Brooke Peeples, MariAlison Murry, Lynde DeLung, Joshua Blaylock
• Funding: NIH NHLBI R15, Arkansas Biosciences Institute, NIFA-AFRI
Contents

• Review of Background
• Proposed Work for 2011
• What we got done
Ascites

• Water belly
  – Rapid growth under poor conditions
    • Hypoxia, dust, rapid early body growth
  – Losses about $10M/yr
  – Control with ventilation and feed restriction
  – Physiology and histology similar to human PAH

• Anthony: Genetically selected breeder lines for >14 generations using sib selection and hypobaric chamber

<table>
<thead>
<tr>
<th>Line</th>
<th>Simulated Altitude</th>
<th>Percent Survival</th>
</tr>
</thead>
<tbody>
<tr>
<td>RES</td>
<td>12,000 ft</td>
<td>93%</td>
</tr>
<tr>
<td>REL</td>
<td>12,000 ft</td>
<td>40%</td>
</tr>
<tr>
<td>SUS</td>
<td>8,000 ft</td>
<td>2%</td>
</tr>
</tbody>
</table>
GWAS Project

• NRSP8/NC1007 USDA project
• Identified 8 chromosomal regions
• Used VNTRs to further analyze these regions
  – 5 confirmed in one or more populations
• Identified candidate genes in 3 regions based on PAH in humans or mice
  – Gga 9:13-14 Mbp
    • AGTR1
    • UTS2D
  – Gga 9: 16 Mbp
    • HTR2B
  – Gga 2:2 Mbp
    • ACE
Plans for 2011

- New phenotyped population of SUS
  - Genotype for VNTRs
- New GWAS for REL samples
- Complete ACE resequence
- SNPloplotyping for HTR2B and AGTR1
  - SUS and REL
HTR2B

- 3 exons; Exon 3 is only coding exon
  - SNP early in Exon 3
  - SNP frequencies markedly different in 3 commercial lines

NC1170 Rhoads 2012
AGTR1

- Identified two alleles based on 16 SNPs distinct from JF (tm2 is WL)
- No significance in REL or 3 commercial lines
  - Different from data from VNTRs

![AGTR1 SNPlotypes](chart1.png)

- n=278

![AGTR1 REL](chart2.png)

- n=200

![PHS009&010 Line Y](chart3.png)

- P=0.0002
UTS2D

• 5 exons; sequenced intron 3
  – 12 SNPs defining 5 alleles (4 non-JF/WL and 3 others in our lines)
  – SNPlotyping underway
  – Female association in REL

<table>
<thead>
<tr>
<th>Line</th>
<th>DNA</th>
<th>4086</th>
<th>4146</th>
<th>4155</th>
<th>4192</th>
<th>4198</th>
<th>4269</th>
<th>4282</th>
<th>4300</th>
<th>4316</th>
<th>4431</th>
<th>4495</th>
<th>4528</th>
<th>4539</th>
<th>4547</th>
</tr>
</thead>
<tbody>
<tr>
<td>JF</td>
<td>G</td>
<td>TAA</td>
<td>C</td>
<td>A</td>
<td>G</td>
<td>C</td>
<td>G</td>
<td>T</td>
<td>G</td>
<td>C</td>
<td>C</td>
<td>T</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>WL</td>
<td>G</td>
<td>GAG</td>
<td>A</td>
<td>C</td>
<td>G</td>
<td>A</td>
<td>T</td>
<td>C</td>
<td>A</td>
<td>G</td>
<td>C</td>
<td>A</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>281</td>
<td>KAR</td>
<td>a</td>
<td>C</td>
<td>G</td>
<td>A</td>
<td>R</td>
<td>Y</td>
<td>T</td>
<td>G</td>
<td>G</td>
<td>C</td>
<td>T</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RES</td>
<td>8301</td>
<td>KAR</td>
<td>a</td>
<td>Y</td>
<td>G</td>
<td>A</td>
<td>A</td>
<td>Y</td>
<td>Y</td>
<td>R</td>
<td>G</td>
<td>Y</td>
<td>M</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RES</td>
<td>8415A</td>
<td>TAA</td>
<td>T</td>
<td>G</td>
<td>T</td>
<td>G</td>
<td>A</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>A</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RES</td>
<td>8465A</td>
<td>TAA</td>
<td>T</td>
<td>G</td>
<td>T</td>
<td>G</td>
<td>A</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>A</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RES</td>
<td>8496</td>
<td>KAR</td>
<td>a</td>
<td>Y</td>
<td>G</td>
<td>R</td>
<td>A</td>
<td>Y</td>
<td>Y</td>
<td>R</td>
<td>R</td>
<td>C</td>
<td>M</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RES</td>
<td>8550</td>
<td>KAR</td>
<td>a</td>
<td>C</td>
<td>G</td>
<td>R</td>
<td>A</td>
<td>Y</td>
<td>T</td>
<td>G</td>
<td>R</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RES</td>
<td>8553</td>
<td>KAR</td>
<td>a</td>
<td>C</td>
<td>G</td>
<td>R</td>
<td>A</td>
<td>Y</td>
<td>T</td>
<td>G</td>
<td>A</td>
<td>Y</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>609</td>
<td>TAA</td>
<td>T</td>
<td>G</td>
<td>G</td>
<td>A</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>A</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>739</td>
<td>TAA</td>
<td>T</td>
<td>G</td>
<td>R</td>
<td>R</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>R</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>760</td>
<td>TAA</td>
<td>T</td>
<td>G</td>
<td>G</td>
<td>A</td>
<td>G</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>G</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>785</td>
<td>KAR</td>
<td>a</td>
<td>C</td>
<td>G</td>
<td>A</td>
<td>R</td>
<td>Y</td>
<td>Y</td>
<td>G</td>
<td>X</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>789</td>
<td>KAR</td>
<td>a</td>
<td>Y</td>
<td>G</td>
<td>R</td>
<td>A</td>
<td>Y</td>
<td>T</td>
<td>G</td>
<td>R</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>852</td>
<td>TAA</td>
<td>T</td>
<td>G</td>
<td>G</td>
<td>A</td>
<td>G</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>G</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>907</td>
<td>KAR</td>
<td>a</td>
<td>Y</td>
<td>G</td>
<td>R</td>
<td>A</td>
<td>Y</td>
<td>T</td>
<td>G</td>
<td>A</td>
<td>Y</td>
<td>C</td>
<td></td>
<td></td>
</tr>
<tr>
<td>SUS</td>
<td>1090</td>
<td>TAA</td>
<td>T</td>
<td>G</td>
<td>R</td>
<td>R</td>
<td>C</td>
<td>T</td>
<td>G</td>
<td>R</td>
<td>C</td>
<td>C</td>
<td>C</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

UTS2D REL

P=0.006
Current Understanding

- Some of our loci are relevant in commercial lines
- Major loci are not shared in all lines
  - Need to do higher density screen
- Some loci affecting ascites in broilers are shared with PAH in mammals
Work planned for 2012

• Determine expression levels of candidate genes in affected tissues
  – Lung, kidney, heart
• Expanded sequence of promoter regions for candidate genes
• Further SNP analysis in experimental and commercial lines
• New GWAS in REL