Objective

Use genomics to identify genes / genomic regions associated with resistance / susceptibility to PRRS virus infection

Led by

Joan Lunney – USDA – ARS Beltsville
Bob Rowland – Kansas State University
Jim Reecy – Iowa State University
Jack Dekkers – Iowa State University

Strong Industry Participation

PHGC Breeding Companies

Fast Genetics, Genesus, Choice Genetics
PIC/Genus, TOPIGS, PigGen

Canada

60K SNP chip
Illumina

2007
Groups of ~200 commercial crossbred pigs infected with PRRS virus isolate NVSL97-7985 between 18 and 28 d of age.
Host Response Phenotypes

Body weight

Log(viremia)

$h^2 = 0.29$

$h^2 = 0.41$

$r_p = -0.25$

$r_g = -0.47$
<table>
<thead>
<tr>
<th>Trial</th>
<th>Parents</th>
<th>Parental Breeds</th>
<th># piglets</th>
<th>Sex</th>
</tr>
</thead>
<tbody>
<tr>
<td>PHGC 1-3</td>
<td>Sires</td>
<td>LW</td>
<td>562</td>
<td>All Barrows</td>
</tr>
<tr>
<td></td>
<td>Dams</td>
<td>LR</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PHGC 4</td>
<td>Sires</td>
<td>Duroc</td>
<td>195</td>
<td>Barrows + gilts</td>
</tr>
<tr>
<td></td>
<td>Dams</td>
<td>LW/LR comp</td>
<td></td>
<td></td>
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<tr>
<td>PHGC 5</td>
<td>Sires</td>
<td>Duroc</td>
<td>199</td>
<td>Barrows + gilts</td>
</tr>
<tr>
<td></td>
<td>Dams</td>
<td>LR/LW comp</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PHGC 6</td>
<td>Sires</td>
<td>LR</td>
<td>198</td>
<td>All Barrows</td>
</tr>
<tr>
<td></td>
<td>Dams</td>
<td>LR</td>
<td></td>
<td></td>
</tr>
<tr>
<td>PHGC 7</td>
<td>Sires</td>
<td>Pietran</td>
<td>197</td>
<td>Barrows + gilts</td>
</tr>
<tr>
<td></td>
<td>Dams</td>
<td>LW/LR comp</td>
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<td></td>
</tr>
<tr>
<td>PHGC 8</td>
<td>Sires</td>
<td>Duroc</td>
<td>200</td>
<td>Barrows + gilts</td>
</tr>
<tr>
<td></td>
<td>Dams</td>
<td>Y/LR</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Viral Load

- Chr 4
  - 1 Mb region explains 15% of genetic variance
  - Includes important candidate genes
    - GBP1
    - GBP2
    - GBP5
    - GTF2B
    - PKN2

Weight Gain

- Chr 4
  - 11% of genetic variance
Effects of WUR10000125 on Viral Load

Trials 1-8

WUR genotype

Virus Load (area under the curve)

Boddicker et al. 2012, 2014a,b

MAF = 0.17
Effects of WUR10000125 on Weight Gain

Trials 1-8

WUR genotype

- AA
- AB
- BB

- Trial 1-3
  - PHGC
    - Sires: LW
    - Dams: LR

- Trial 4-8

Weight Gain (kg)

- All: n=983
- 1-3: n=345
- n=43

Boddicker et al. 2012, 2014a,b
SSC 4 region effects over time

PHGC1-8

Viremia (Log10 Templates/ml, qPCR)

Days Post Infection

Boddicker et al. 2012, 2014a,b
SSC 4 region effects over time
PHGC1-8

Boddicker et al. 2012, 2014a,b
**Generation 1 & 2 PRRS trials**

<table>
<thead>
<tr>
<th>Trial Number</th>
<th>n</th>
<th>Breed</th>
<th>PRRSv Isolate</th>
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</thead>
<tbody>
<tr>
<td>1-3</td>
<td>530</td>
<td>LW x LR</td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>195</td>
<td>Duroc x LW/LR</td>
<td>NVSL</td>
</tr>
<tr>
<td>5</td>
<td>184</td>
<td>Duroc x LR/LW</td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>123</td>
<td>LR x LR</td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>194</td>
<td>Pietran x LW/LR</td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>188</td>
<td>Duroc x LW/LR</td>
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</tr>
<tr>
<td>15</td>
<td>184</td>
<td>LR x LW</td>
<td>KS06</td>
</tr>
<tr>
<td>10</td>
<td>176</td>
<td>LR x LW</td>
<td></td>
</tr>
<tr>
<td>11</td>
<td>176</td>
<td>LW x LR</td>
<td></td>
</tr>
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<td>12</td>
<td>174</td>
<td>LR x LW</td>
<td></td>
</tr>
<tr>
<td>14</td>
<td>180</td>
<td>Duroc x LR/LW</td>
<td></td>
</tr>
</tbody>
</table>

Total 2304 challenged pigs with deep phenotypes
A major QTL for host response to PRRS on SSC 4

Boddicker et al. 2012, 2014a,b; Hess et al. 2015
A major QTL for host response to PRRS on SSC 4

Hess et al. 2015 \( r_g(VL) = 0.86 \pm 0.19 \)

\[ \text{Log}_{10}(\text{Viremia}) \]

Days Post Infection

Days Post Infection
A major QTL for host response to PRRS on SSC 4

Hess et al. 2015 $r_g(VL) = 0.86 \pm 0.19$ $r_g(WG) = 0.86 \pm 0.27$

**Diagram:**
- **Viremia NVSL AA**
- **Viremia NVSL AB**
- **Weight NVSL AA**
- **Weight NVSL AB**
- **Viremia KS06 AA**
- **Viremia KS06 AB**
- **Weight KS06 AA**
- **Weight KS06 AB**
Genomic regions do not overlap between PRRSV isolates
But pathways do

Identification of other host response QTL

Waide et al.

Viral Load

KS06

WUR = 7

NVSL

WUR = 21

$\text{rg}(\text{NVSL, KS06}) = 0.86 (+0.19)$
Identification of other host response QTL

$WUR = 16$

$rg(NVSL, KS06) = 0.86 \pm 0.27$

Weight Gain

KS06

NVSL

Single SNP across Chromosomes
Genomic Prediction
Prediction using high-density SNPs

Training population

Phenotypes

SNP Genotypes

Estimate SNP effects

Selection candidates

SNP Genotypes

Genomic Prediction

Meuwissen et al. 2001
Can we use Genomic Prediction across isolates?

NVSL Trials

KS06 Trials

r/h

Whole Genome  Genome - WUR  WUR only

0.0 0.1 0.2 0.3 0.4 0.5

NVSL

KS06

19
Conclusions

- Piglet response to experimental PRRSv challenge has a sizeable genetic component.

- Chromosome 4 contains a major gene for host response to PRRSv in growing piglets.

- Genetic selection for improved host response to PRRS is possible and can be an important component in the fight against PRRS
1. Experimental infection of nursery pigs with a specific PRRSV strain

2. Experimental infection of nursery pigs with another PRRSV strain

3. Experimental co-infection of nursery pigs: PRRS + PCV2 (incl. PRRS vaccination)

4. Field trials
Thanks to all Partners

Scientific Collaborators

**Iowa State University**
Nick Boddicker  Andrew Hess
Emily Waide  Chris Eisley
Jenelle Dunkelberger
James Koltes  Eric Fritz-Waters
Martine Schroyen  Nick Serao
Jim Reecy  Chris Tuggle
Susan Carpenter

**Kansas State University**
Bob Rowland  PRRS group
Ben Trible  Megan Niederwerder
Maureen Kerrigan  Becky Eaves  et al

**USDA-ARS**
Joan Lunney group
Igseo Choi  Sam Abrams

**University of Alberta**
Graham Plastow group

**Univ. Saskatchewan**
John Harding group

**Roslin Institute**
Steve Bishop
Andrea Doeschl-Wilson
Zeenath Islam  Graham Lough

**Univ. Minnesota**
Monserat Torremorrell

Funding

Industry Partners

Application of Genomics to Improve Swine Health and Welfare