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## Community annotation of immunity-related genes in the pig genome

Immune Response Annotation Group (IRAG)

Coordination: [Christopher K Tuggle](#)<sup>1,2</sup> and Claire Rogel-Gaillard<sup>3</sup>

Participants: Jane Loveland<sup>4</sup>, Hirohide Uenishi<sup>5</sup>, Harry Dawson<sup>6</sup>, Joan Lunney<sup>7</sup>, Yongming Sang<sup>8</sup>, Shuhong Zhao<sup>9</sup>, Elisabetta Giuffra<sup>3</sup>, Sara Botti<sup>10</sup>, James Reecy<sup>11</sup>, Jennifer Harrow<sup>4</sup>, Tom Freeman<sup>2</sup>, Alan L Archibald<sup>2</sup>, Michael Murtaugh<sup>12</sup>, David Hume<sup>2</sup>, Takeya Morozumi<sup>5</sup>, Hiroki Shinkai<sup>5</sup>, Bertrand Bed'hom<sup>3</sup>, Frank Blecha<sup>8</sup>, Guolong Zhang<sup>13</sup>, Katherine Mann<sup>7</sup>, [Jie Zhang](#)<sup>9</sup>, Celine Chen<sup>6</sup>, Zhi-Liang Hu<sup>11</sup>, Ryan Cheng<sup>1</sup>, Tinghua Huang<sup>1</sup>, Yasiara Rodriguez<sup>1</sup>, Anna Anselmo<sup>10</sup>, Bouabid Badaoui<sup>10</sup>, John Schwartz<sup>12</sup>, Ronan Kapetanovic<sup>2</sup>, Dario Beraldi<sup>2</sup>, and the Swine Genome Sequencing Consortium

<sup>1</sup>Department of Animal Science and Center for Integrated Animal Genomics, Iowa State University, Ames, IA, USA

<sup>2</sup>The Roslin Institute and Royal (Dick) School of Veterinary Studies, University of Edinburgh, Easter Bush, Midlothian, EH25 9RG UK

<sup>3</sup>INRA, UMR de Génétique Animale et Biologie Intégrative, Jouy-en-Josas, France

<sup>4</sup>Wellcome Trust Sanger Institute (WTSI), Hinxton, Cambridgeshire CB10 1HH, UK

<sup>5</sup>Animal Genome Research Program, NIAS/STAFF, Tsukuba, Ibaraki, Japan

<sup>6</sup>Diet, Genomics and Immunology Laboratory, Beltsville Human Nutrition Research Center, ARS, USDA, Beltsville, MD

<sup>7</sup>USDA, ARS, BARC, Animal Parasitic Diseases Laboratory, Beltsville, MD USA

<sup>8</sup>College of Veterinary Medicine, Kansas State University, Manhattan, KS USA

<sup>9</sup>Key Lab of Agricultural Animal Genetics, Breeding, and Reproduction of Ministry of Education, Huazhong Agricultural University, Wuhan 430070, PR China

<sup>10</sup>Parco Tecnologico Padano, Integrative Biology group, 26900 Lodi, Italy

<sup>11</sup>Department of Animal Science and NRSP-8 Bioinformatics Coordination project, Iowa State University, Ames, IA, USA

<sup>12</sup>Department of Veterinary and Biomedical Sciences, University of Minnesota, St. Paul, MN 55108, USA

<sup>13</sup>Department of Animal Science, Oklahoma State University, Stillwater, OK 74078, USA

Corresponding authors

Claire Rogel-Gaillard: [claire.rogel-gaillard@jouy.inra.fr](mailto:claire.rogel-gaillard@jouy.inra.fr)

Christopher K Tuggle: [cktuggle@iastate.edu](mailto:cktuggle@iastate.edu)

The pig is an excellent model for human immunology, yet the structure and function of the pig immunome is poorly characterized. Increased understanding of the pig immunome would benefit biomedicine as well as progress toward porcine disease resistance through genetics. The international Immune Response Annotation Group (IRAG) comprises scientists that work on swine immunity and resistance to disease. The main purpose of IRAG is to use computational curation to refine the currently available automated annotation of immunity-related genes through sequence-based comparison to such genes in other species. Global gene expression data are being used to identify both shared and species-specific immune responses. A list of over 1,000 genes was compiled using gene ontology annotation (GO:0002376; immune system process), a core set of genes involved in host-pathogen interplay (Jenner and Young, 2005), the online Porcine Immunology and Nutrition database, and gene sets under positive selection in humans (Barreiro and Quintana-Murci, 2010) and cattle (Bovine Genome Sequencing and Analysis Consortium, 2009). Sequence data and text searches using information from these genes were used to find candidate regions for annotation. Manual annotation for ~1,500 loci has been completed by group members using genome sequence assembly 9 (Sscrofa9) and WTSI Otterlace software, which provides alignments of genomic contigs with publicly available sequence data. These alignments are analyzed to confirm and extend exon-intron boundaries, propose new alternative splice products, and improve protein sequence predictions. Preliminary results have provided

evidence for 46 gene duplications and many new alternative splice variants. Forty-three immune genes were not found. All results will be checked against assembly 10. To confirm functional relevance to immunome characterization for the genes selected for annotation, a correlation-based network of 58 porcine Affymetrix-based expression datasets was created. This analysis confirmed IRAG gene immune function as their tissue expression patterns across 30+ tissues and cell types closely matched known immune-related genes. A refined analysis of transcriptomic data from experimental infections or immune stimulations provided evidence for involvement of the IRAG gene set in immune response. Our future challenge will be to identify the underlying biology specific to the pig species from this major annotation effort.