



Plant & Animal Genomes XVIII Conference

January 9-13, 2010
Town & Country Convention Center
San Diego, CA

W619 : Swine Genome Sequencing

Insights From Whole Genome Sequence Alignment Of The Domestic (*Sus scrofa* And Javan Warty (*Sus verrucosus*) Pigs

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One of the most important questions within evolutionary genomics to be answered is what changes in the genome result in sexual incompatibility and how does the genome change in response to the changing environment of the different species. The pig (*Sus scrofa*) is the best known member of a group of closely related species all belonging to the Suidae family. The Suidae family consists of over 12 different species that have survived to date and these species have evolved over a relative short time span of 1-10 million years. This makes the Suidae family particularly useful for addressing questions related to speciation, which have become feasible at the nucleotide level by recent developments in next generation sequencing technology and the availability of a high quality annotated sequence of the porcine (*Sus scrofa*) genome. We therefore, have initiated sequencing the first of these other Suidae; the Javan Warty pig (*Sus verrucosus*). We have sequenced the genome of the Javan warty pig at an estimated 9x depth using Illumina GA sequencing using two different libraries with insert sizes of 150-200 bp and 350-600 bp as well as a mate pair library of mate pairs 2-5 Kb apart in the genome of this pig. Paired end reads of 70 bp in length were generated from all three libraries. Results about the comparison of the genomes of *Sus scrofa* and *Sus verrucosus* will be presented at the meeting.

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