Reviewer Report

Title: Introgression of Eastern Chinese and Southern Chinese haplotypes contributes to the improvement of fertility and immunity in European modern pigs

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Reviewer name: Marina Sanchez

Reviewer Comments to Author:

Chen et al. in their manuscript "Population genomic data reveal origin and phenotypic effect of Chinese haplotypes introgressed into European modern pigs" performed a thorough analysis explaining the introgression history of Chinese pigs from two distinc locations - Southern (SCN) and East (ECN) China - into an European breed, French Large White (FLW)
The authors unravel introgression signatures from ECN and SCN and link them to immunity and reproductive traits respectively. They expand in two examples, the GOLM1-NAAR35 haplotype and the KATNAL1. Finally, they shed light in to the AHR intogressed haplotype introgressed form ECN pigs into Large-White pigs however showing that the AHR haplotype derived from ancient pig species.
I consider this a very well written article of clear relevance to the field. I have the following minor comments:
Minor comments:
The authors mention Bosse et al. Nature Communications 2014 analysis as the pipeline used in their manuscript. In Bosse the authors use and independent method to verify gene flow between pig populations, namely D-statistics. Do the authors think that D-statistics in here would provide more robustness to their analysis
Page 6 Line 120: ECN pigs represented by Jinhua pigs and SCN pigs represented by Luchuan pigs appeared as the two ancestral lineages of Chinese pigs when K=3 (fig. 1d).
Please consider adding … Jinghua pigs (JH) …
Page 6 Line 129: We detected 5107 and 5024 50-Kb regions with signatures of potential introgression from SCN or ENC pigs into FLW pigs.
To help follow-up studies it would be convenient to report an excel table with the set of detected regions with potential signatures of introgression, and not only the seven with "strong singatures of introgression" (supplementary Table 2).
Page 30 Line 704: Fig1. Population relationship and structure. (a) Neighbour-joining (NJ) tree based on an identity-by-state matrix among individuals. (b) Principal component analysis (PCA) of Chinese and European pigs.
The figure shows in panel (a) the PCA analysis and in panel (b) the NJ tree.
Supplementary Figure 3. The colored dashed in the phylogenetic tree represent different genetic groups.
Some clarification or legend on that would be much appreciated, SCN, ECN, NCN…
Page 7 Line 36. SCN pigs and ECN pigs were enriched in the immune-related signalling and fertility pathways, respectively (fig. 2e).

ECN genes are related to "positive regulation of dephosphorilation", is that related to fertility?
Page 15 Line 335. Better clarification on FLW pigs versus OUT animals were only 1.51 and 1.41, respectively (supplementary fig S13.
Supplementary Figure 12 is not mentioned in the text.

Methods

Are the methods appropriate to the aims of the study, are they well described, and are necessary controls included? Choose an item.

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Are the conclusions adequately supported by the data shown? Choose an item.

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