Problematizing selection mapping from an animal science perspective

Handout to a talk given at ASAS 2022

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Introduction

Genomes cited as examples of the development of farm animal genomics: chicken (Hillier et al. 2004), pig (Groenen et al. 2012), cattle (Elsik, Tellam, and Worley 2009). SNP chips cited: cattle (Matukumalli et al. 2009), pig (Ramos et al. 2009), chicken (Groenen et al. 2011).

Rubin et al. (2010) performed a large scale, at the time, selection mapping study of domestic chickens. For a follow-up, see Qanbari et al. (2019).

There are many other examples of selection mapping in domestic animals; some have identified known loci for mono- or oligogenic traits and large-effect loci for complex traits, e.g. Rubin et al. (2012) in pigs and Druet et al. (2013), Qanbari et al. (2014) and Freitas et al. (2021) in cattle.

We published two population genetic studies on the feral chickens of Kauai, looking at population structure (Gering et al. 2015) and selection mapping (Johnsson et al. 2016). More is coming as Dom Wright, Eben Gering and their groups have continued working on feralisation.

The neural crest cell hypothesis for domestication entails that universal domestication traits are due to changes in the migration and proliferation of neural crest cells (Wilkins, Wrangham, and Fitch 2014). Some selection mapping studies (e.g Pendleton et al. (2018) in dogs and Wang et al. (2018) in the farm fox selection experiment) have identified genes and pathways that they interpret as support for the neural crest cell hypothesis. See Johnsson, Henriksen, and Wright (2021) for a criticism along the lines of this talk.

Population genetic limitations

Selection mapping works best for recent selection

A simulation study shows how a linkage disequilibrium-based selection signatures are mostly erased within $0.1\ N_e$ generations (Przeworski 2002). The result that a neutral new mutation has an expected fixation time of $4N_e$ is due to Kimura and Ohta (1969).

Girdland Flink et al. (2014) and Loog et al. (2017) found that the *TSHR* sweep (from Rubin et al. (2010)) happened around 500-1000 years ago, too recently to be selection during early domestication.

Works best for simple architectures

Jain & Stephan analyzed a population polygenic model of adaptation after an environmental shift (Jain and Stephan 2017a, 2017b), illustrating how adaptation can proceed either by small or large shifts in allele frequency, depending on the effect and mutation rates.

Depends on genome features

Johri et al. (2022) discuss how features of the genome like mutation, recombination and historical natural selection, as well as population history, affects the ability to detect selection and ought to be modelled if we want to be certain that it is selection we detect.

An example is Hartfield et al. (2021), who modelled population history in the Holstein breed, checking the ability of their chosen method (singleton density scores) to detect polygenic adaptation (and found it lacking).

Practical concerns

Researcher degrees of freedom

Examples of some of the selection mapping methods cited: H_{12} (Garud et al. 2015), *EHH* (Sabeti et al. 2002), *iHS* (Voight et al. 2006), *hapFLK* (Fariello et al. 2013), singleton density score (Field et al. 2016).

Annotation term enrichment

Wijesooriya et al. (2022) recently discussed researcher degrees of freedom in annotation term enrichment.

Pavlidis et al. (2012) simulated neutral variants on the *Drosophila* genome, took the tails of the distribution and found enriched annotation terms that one could spin hypothetical stories around.

Finding the function of individual sweeps

Because the selected allele will likely be fixed or close to fixed, one needs some intercrossing or comparative strategies to perform genetic analysis (Johnsson 2018). Examples of investigating the function of sweepp haplotypes in crosses of chickens: *BCO2* (Fallahshahroudi et al. 2019), *TSHR* (Fallahshahroudi et al. 2021), *ADRA2C* (Elfwing et al. 2014).

Discussion

The Charlesworth quote is from Charlesworth (2019).

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