

**In my opinion, the study was well conducted, as well the manuscript written. The study is interesting providing new era in duck. I have some considerations:**

In the materials and methods section, describe how to design organized mating plans (), I mean, what was the standard of the number of this number of birds (Muscovy breed or sire line and Pekin breed for dam line) or hybrid mule duck ? Was the effective size of the population considered?

How many parental lines were genotyped by high-density arrays (600K array)? Was a special statistical test considered for the number of selected people (power statistical test)?

In the materials and method section, at the beginning of how to select 192 markers, the number of remaining markers from 600 K is presented. How did this number of SNP remain? What was the meaning or purpose of the respected authors in evaluating the power of 96 SNPs?

My suggestion is to evaluate the SNPs identified on specific chromosomes by checking for QTLs Database in these regions. The interesting thing to note in Figure 1 is the distribution of completely different allele frequencies in the two breeds, which needs to be discussed.

Figure 2 shows the distribution of selected SNPs on different chromosomes. Respected authors have mentioned macrochromosomes 1 to 8, but in the figure, the number of markers on chromosome 16 and 20 is also high, which needs to be discussed.

It is still very unclear to me how to select 96 SNPs? Please provide the Reference or References or even previous similar studies used. If possible, compare two genotyping technologies (Axiom and KASPar).

In the materials section, the method of collecting eggs and hatching has been done, but there is no mention of this in the results and discussion? Please, add the result, as well as analyze the Association between these traits and the selected SNPs.

In the table 1, the Minor allelic frequency and call rate is different in two breeds, so that in breed 1 it is twice as much as breed 2. Please explain the reason for it according to the pedigree and the breeding program and the duration of the breeding herds? Also discuss the low minimum allelic frequency in two breeds?

My suggestion is to calculate the amount of linkage disequilibrium chromosome by chromosome. The number of SNPs after quality control should be presented and discussed in a table, chromosome by chromosome.