




Peer Community In Animal Science

Providing innovative genetic solutions to the future challenges of the poultry industry: extraction of a small-sized Single-nucleotide polymorphism (SNP) panel using factorial design for parentage assignment in a population consisting of pure and hybrid ducks

Seyed Abbas Rafat  based on peer reviews by **Arash Javanmard** and 2 anonymous reviewers

Chapuis, Hervé, Brard-Fudulea, Sophie, Hazard, Azélie, Vignal, Alain, Demars, Julie, Rouger, Romuald, Teissier, Marc, Gilbert, Hélène (2024) Cost-efficient assignment panel for ducks. Setup of a cost-efficient assignment panel for duck populations. HAL, ver. 2, peer-reviewed and recommended by Peer Community in Animal Science.

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One of the achievements of animal genetics is that it finds solutions along with the emergence of new needs of the animal husbandry community or the adoption of new laws. Muir and Cheng (2013) research serves as a classic example of using the innovations of animal genetics to meet new legal challenges, such as the restriction of beak cutting in laying hens. Muir and Cheng (2013) investigated the genetic diversity to deal with the cannibalism of intact chickens. In 2021, the European Citizens' Initiative urged the European Commission to legislate against the use of cages for farm animals in the livestock industry. Chapuis et al., (2024) presented a successful solution to the poultry industry about this (future) law by presenting a cost-efficient assignment SNP panel.

In animal breeding, access to pedigree information is necessary for genetic progress. Since the 1970s, the development of genomic science and molecular techniques has shown their ability in this field. Despite the substantial reduction of genotyping costs in the last 20 years, the practical use of genome-wide genotyping for thousands of SNPs remains challenging. Therefore, the search for a small, cost-effective SNP panel is ongoing, with objectives including genetic diversity (Viale et al., 2017), product traceability (Dominik et al., 2021), species and hybrid identification (Harmoinen et al., 2021) and pedigree construction in wild populations (Ekblom et al., 2021). Furthermore, especially in recent decades, small panels of markers have been proposed for parentage assignment in different animals. For example, Domínguez-Viveros et al., (2020) developed panels with 42 to 63 markers for different sheep breeds in Mexico. Similar panels for parentage assignment have been proposed for salmon (May et al., 2020), rainbow trout (Liu et al., 2016), French sheep (Tortereau et al., 2017), Spanish sheep (Calvo et al., 2021), and European bison (Wehrenberg et al., 2024), with marker numbers of 142, 95, 180, 173, and 96, respectively. Massault et al., (2021) showed by simulation that a panel with at least 50 markers is sufficient for progeny assignment in pearl oysters. These examples highlight that extracting a small panel of markers (usually less than 200) from the total genotyping introduced in different species, can open new horizons for applying genomic information in animal breeding.

Chapuis et al. (2024) addressed the challenge of finding an efficient set of markers that can be used in the hybridization of two species of the Pekin duck and the Muscovy duck. They used KASPar technology to setup a panel, with SNPs existing in both species and their hybrids. This panel has sufficient polymorphism to use in practice. Thus, it can be considered as a step forward compared to previous work done on microsatellites. A final list of SNPs was constructed from a reference set comprising 600 K genotyping of *Anas platyrhynchos*, *Cairina moschata* and mule duck.

In addition to developing of a cost-efficient assignment panel, the work of Chapuis et al. (2024) presented a factorial design to maintain genetic diversity while considering specificities of duck production. The use of factorial design in avian pedigreed populations is relatively novel, making this research particularly innovative. The study's approach to factorial design in populations with limited size may be generalized to similar poultry species. Furthermore, sufficient effective size of population is selected. So, the panel can be used in other populations outside the tested populations. A notable feature of this panel is the use of neutral SNPs, which ensures that markers will not be lost due to future selection pressures over time.

The paper of Chapuis et al. (2024) exemplifies the application of molecular genetics to address challenges in the poultry industry. The use of kinship matrix instead of relationship matrix, taking into account the unique characteristics of duck production, could be another novelty of the paper. According to the reviewers' comments, the results can be beneficial in the future, particularly with the introduction of the specific factorial design.

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Reviews

Evaluation round #1

DOI or URL of the preprint: <https://hal.inrae.fr/hal-04542880>

Version of the preprint: 1

Authors' reply, 30 August 2024

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Decision by [Seyed Abbas Rafat](#) , posted 29 May 2024, validated 29 May 2024

Cost-efficient assignment panel for ducks. Setup of a cost-efficient assignment panel for duck populations

Dear Hervé Capuis,

Thank you for submitting a manuscript to PCI Animal Science.

Manuscript entitled "Cost-efficient assignment panel for ducks. Setup of a cost-efficient assignment panel for duck populations." which you submitted to PCI Animal Science has been reviewed.

I would like inform you three reviewers acknowledged that your manuscript had valuable results.

The reviewers highlighted a number of issues with the manuscript that need to be addressed before the paper can be considered for recommendation by PCI Anim Sci.

I look forward to receiving your revision.

Best Regards,

Seyed abbas Rafat

Reviewed by anonymous reviewer 2, 29 May 2024

Dear editor

please see attach file,

best regards

[Download the review](#)

Reviewed by [Arash Javanmard](#), 27 May 2024

Dear Editorial Board for PCI Animal Sci,

I would like to express my sincere appreciation for the opportunity to review the preprint entitled "Cost-efficient assignment panel for ducks: Setup of a cost-efficient assignment panel for duck populations" with the potential for publication.

I regret the delay in my response, as I was deeply engrossed in my other commitments. Below:

I have outlined a comprehensive and detailed summary of my feedback and recommendations for the manuscript:

1. The research scenario is captivating, particularly in light of the challenges posed by commercial SNP chip panels for diverse breeds. I highly recommend that the authors emphasize the specific benefits of the panel for Pekin and Muscovy ducks and provide further insights into why these two breeds were specifically chosen for the study. Exploring the historical background and genetic relatedness of these breeds could add depth to the research.

2. The abstract is well-crafted and informative. However, I suggest providing more comprehensive details about 192 SNP in the initial process and elucidating the relationship between SNP 96, 134, and 128 SNP.

Additionally, including the population sizes of Muscovy and Pekin ducks in the abstract would augment its informativeness and provide a clearer context for the study.

3. Accurately reflecting the diversity is crucial, and it is essential to specify the representation of the panel across the chromosomes of Pekin and Muscovy ducks. Providing detailed information on the distribution of SNP along all chromosomes of poultry genomes will be essential to reflect the true face of diversity.

4. The introduction would benefit from expansion, providing more in-depth background information on Pekin and Muscovy ducks and delving into the motivations behind the research. Highlighting the historical and genetic significance of these duck breeds and the specific research problems they address would add substantial value to the introduction.

5. The "Materials and Methods" section is comprehensive and well-articulated. However, I recommend providing an accessible and detailed explanation of the KASpar technology for the benefit of the readers. Explaining the technology and its relevance to the study in an understandable manner will enhance the comprehension of the methods employed.

6. The discrepancy in minor allele frequency values in Table 1 prompts the question of whether the number of suggested SNPs in the panel could be reduced without compromising genotyping outcomes. The authors should provide a robust justification for this information, including a detailed discussion on the implications of altering the suggested SNP numbers and its potential impact on genotyping outcomes.

7. The results section is articulate and insightful. I found the discussion in this section to be enlightening and thought-provoking, and I appreciate the authors' thoroughness in presenting the results.

8. The conclusion should be more nuanced, offering a specific and concise summary of the outcomes. Providing a detailed and comprehensive summary of the outcomes, along with their implications and potential future directions, will enhance the conclusion section.

9. The references are meticulously cited and encompassing, and I appreciate the authors' attention to detail and the inclusion of a comprehensive range of updated references. In conclusion, with some minor revisions, I firmly believe that the manuscript is poised for publication.

I appreciate your attention to these detailed and comprehensive suggestions and hope that they contribute to the further enhancement of the manuscript.

With the Best Regards

Arash Javanmard

[Download the review](#)