

## Optimization of introgression breeding programs with MoBPS

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Performing introgression of one or more beneficial QTL that are only present in a wild type or gene bank material into an elite breeding population is a complex optimization problem. On the one hand, a high genetic share of the elite line is to be maintained to regain its productivity level and economic competitiveness. On the other hand, fast introgression can cause inbreeding depression with resulting lower long-term gain and potentially causing health and animal welfare issues. Depending on the species and its reproduction biology, the amount of resources and resulting number of animals in the program, optimal mating strategies can be different. We focused our analysis on introgression schemes in chicken but also considered other species. Introgression schemes were evaluated based on the speed of introgression, short and long-term performance on simulated traits and inbreeding levels. In terms of the design of the introgression scheme, we considered different mating strategies (e.g. optimum genetic contribution selection) and assessed potential benefits of genotyping. This is not only relevant for genomic selection but also to track the share of the genome originating from the elite line. Additionally, one might consider putting an emphasis on regions physically close to the beneficial QTLs, as recovering the elite line genotype in those regions is most challenging. Finding a closed solution to such a complex allocation problem with uncertain mating strategy is virtually impossible. Instead, we propose the usage of the Modular Breeding Program Simulator (MoBPS). The software is an R-package openly available at <https://github.com/tpook92/MoBPS> which supports the simulation of complex and large scale breeding programs with focus on livestock and crop populations. User-input can be inserted in a web-based application including a tool to visualize the mating scheme between different breeding groups.