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**ABSTRACT**

This research was composed of 3 experiments: experiment I: estimation of QTL location and effects, experiment II: estimation of the power of test by simulation, and experiment III: estimation of genetic progress in model including QTL effect. The objectives of the first experiment were to 1) investigate the QTL affecting milk yield in crossbred Holstein by microsatellites as genetic markers from yield deviation and estimated breeding value, and 2) find suitable statistical method to estimate the QTL locations. The objective of the second experiment was to investigate the optimum population size for QTL analysis by simulation method. Finally, the objective of the last experiment was to investigate the genetic progress when using QTL markers in selection program by simulation method. In experiment I, 3 sires with total of 273 daughters of crossbred Holstein dairy cattle from Chok Chai Dairy Farm, Nakorn Rachasima province, were studied using daughter design. Ten microsatellite markers located throughout the chromosome 3 were used. Yield deviation calculated from first lactation (YDF), yield deviation calculated from all lactations (YDA), breeding value estimated from first lactation (EBVF), and breeding value estimated from all lactations (EBVA) were the data sets used for QTL analysis. Simple interval mapping (SIM) with least square (LS), composite interval mapping (CIM) with LS, and SIM with maximum likelihood (ML) were used to estimate the QTL location and its effect. Thresholds for statistical significance of QTL analysis were determined from interval mapping of 10,000 permutations. F ratio and likelihood ratio (LR) were used as the statistic test value for LS and ML analysis. The
results showed that there was the non significant association at P ≥ 0.05 between the trait and QTL-linked marker in every data set, however, base on the test statistic value profile, it had possibility that QTL located between 26 and 28 cM. These positions were between microsatellite MB101 and ILSTS096. There was the similar pattern of the statistic test value in the same type of data. However, the different pattern was found when using the different type of data (YD and EBV). The patterns of test statistic from SIM with LS, CIM with LS, and SIM with ML were slightly different. In the experiment II, when the number of sire and the number of daughter per sire were varied, the results revealed that with QTL effects as a proportion to SD of 0.5-1.5 and sample sized of 3 sires and 80 daughters per sire (which is the case in experiment I) had insufficient power of test. This result showed high possibility that the QTL maybe located between 20 and 40 cM, which was similar result when EBV data were used. In addition, when the magnitude of QTL effects was small, medium, and high, the suitable sample size should be 5 sires with 200, 80, and 50 daughters per sire, respectively. In the last experiment, the magnitude of QTL effects and QTL frequencies were varied from small to high, the results found that when small QTL effect was found in the population, the genetic response were not different. The difference of genetic response were shown when the QTL effect was increased to 1.0 and 2.0. The conclusions of this research were: 1) there was non significant association between the trait and marker, however, it had possibility that there was the QTL located between 26 and 28 cM, 2) Either the data from only the first lactation or from all lactation can use for QTL analysis, 3) EBV was the suitable type of data for QTL analysis, 4) All statistical approaches can use for QTL analysis, 5) the minimum number suggested by simulation was 5 sires with 200 daughters per sire when QTL effect was low, and 6) the advantage of using QTL as MAS is the greatest when QTL had large effect on its trait and the frequency in population was low.