

## **Abstract**

To analyze the effect of genetic and environment interaction on the Somatic Cell Score (SCS), we used 579354 day test records from 201562 dairy cows from 4731 sires and 132652 dams gathered by Iran's animal breeding center from 1380-1389 (2001-2011). This data includes pedigree data and test day outcomes for milk SCS. In this study, different sires are used as different genetics. We also used average herd size, average milk production, average milk protein level and average milk fat level to act as our environments. Data analyses and (co)variance component estimation are done via ASReml software. Adding any of sire effects  $\times$  herd size average, sire effects  $\times$  milk production average, sire effects  $\times$  milk protein average or sire effects  $\times$  milk fat average to the additive genetic variance shows useful growth in the related LogL. The study shows that in addition to the meaningful effects of the interaction of genetic and environment among different herd size cattle, it also raises the additive genetic variance. So it is advised to use the sire effects  $\times$  herd size average as genetic and environment interaction in SCS model in order to provide animals genetic potential.

**Keywords:** somatic cell score, random regressions, the interaction of genetic and environment, dairy



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