

MODELLING SOMATIC CELL SCORES (SCS) IN CATTLE VIA LONGITUDINAL MIXED EFFECTS METHODOLOGY.

Christèle Robert-Granié, Jean-Louis Foulley*

INRA-SAGA, BP 27, 31326 Castanet-Tolosan, * INRA-SGQA, 78352 Jouy-en-Josas, France.

Mastitis in cattle is an important trait to consider in genetic improvement programmes. The aim of this study was to analyze somatic cell counts which is an indirect criterion to assess susceptibility to mastitis. Data analyzed are weekly records (6448 somatic cell scores) out of 159 primiparous pure and crossbred cows raised at the INRA “Le Pin”, experimental farm, France.

Given the longitudinal structure of this data set, the analysis consists of modelling both the mean and the individual profiles. This was achieved via the use of mixed models including fixed effects for the average profiles and random effects for the adjusted individual profiles.

As far as fixed effects are concerned, the main issue is to adjust the time trend. To that respect, we employed the technique of fractional polynomials described in Royston and Altman (1994) under several variance-covariance structures to make the procedure more robust. The best second degree polynomial involved an intercept plus the time at the power $(-1/3)$ and the latter times the logarithm of the time.

Regarding random effects, model comparisons involved random coefficient models, exponential stationary stochastic processes and heterogeneous variances. Models simultaneously including all these three structures seemed to be preferred. For instance, random coefficient models despite a high degree of polynomial adjustment were unable to fit properly the variance function. This phenomenon justified the introduction of heteroskedastic models. Further analyses are needed to include genetic and permanent environmental effects into the model and to predict mastitis occurrence based on SCS profiles.