Session G7.11, e-mail: jorgen.odegard@umb.no

Genetic analysis of survival data from challenge testing of furunculosis in Atlantic salmon: Model comparison using field survival data

Jørgen Ødegård[1], Ingrid Olesen[2], Bjarne Gjerde[2] and Gunnar Klemetsdal[1]

[1] Norwegian University of Life Sciences
[2] AKVAFORSK

Aims

- Analyze challenge-test data for furunculosis in Atlantic salmon
  - Comparison of various statistical models with respect to ability to predict field survival
- Models were compared at two different endpoints of recording
  - 66% overall mortality (original testing design)
  - 50% overall mortality (Gjøen et al., 1997)
    - Expected to be optimal for cross-sectional models for binary traits

Data

- Data consisted of challenge-test and field survival data
- Only challenge-test data was used in genetic evaluation of families

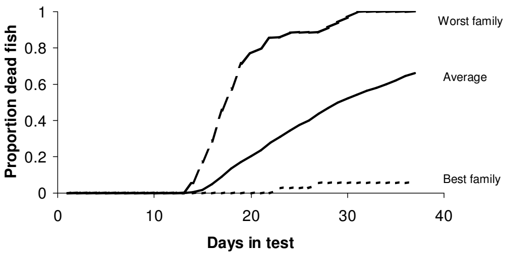
Challenge-test data

- Test conducted in 1991
- Infection by means of cohabitants
- Population consisted of 171 full-sib families
  - 171 dams, 93 sires
  - Number of test individuals per family averaged 33.5
  - Date of death recorded
- 30 d from first mortality to end of test
- Overall mortality = 66% (6 - 100%)
- All fish kept in the same tank
  - Families kept separate at earlier age

Field (sea) data

- Natural disease outbreak in 1992
- Population consisted of full-sibs of fish tested in 1991
  - 120 families
  - 40 tagged individuals per family
  - Date of death recorded
- 56 d from first mortality to end of test (antibiotic treatment)
- Overall mortality = 35% (0 – 75%)
- All fish kept in the same sea cage

Cumulative mortality in challenge-test



Statistical models

1. Linear cross-sectional
   - (μ, sire, dam, common environment)
2. Threshold cross-sectional
   - (μ, sire, dam, common environment)
3. Proportional hazards (Weibull frailty)
   - (baseline hazard, sire, dam)
4. Repeatability linear test-day
   - (time regression, sire, dam, common environment)

Sire and dam ~ $N(\mathbf{0},\mathbf{A}\sigma_{sd}^2)$
Common environment ~ $N(\mathbf{0},\mathbf{I}\sigma_c^2)$

Model comparison

- Models vary due to several factors:
  - Different trait definitions
  - Different distributions assumed
    - Parameters on different scales (observable scale, underlying scale)
  - Time perspective (early vs. late mortalities) may or may not be accounted for
- Parameters of the models cannot be compared directly

Comparison criteria

- Ability to predict rate of family rate of survival in the field (sea)
- Survival probably affected by additive genetic and common environmental effects in both field and challenge test data
  - Family effect used as predictor
    - sire + dam + common environment

Comparison criteria

- The predictive ability of the family effect was measured as:
  - Pearson correlation
    - Family effects – rate of field survival
  - Pearson goodness of fit statistic (χ^2)
    - Logistic regression of field survival on predicted family effects
    - Criteria based on deviance between expected and predicted number of failures and successes

Heritability

Model	**Type**	**h^2 (66% mort.)**	**h^2 (50% mort.)**
1	Linear	0.38 (0.095)	0.31 (0.09)
2	Threshold	0.59 (0.14)	0.46 (0.13)
3	Weibull	0.63	0.57
4	Repeatability	0.02 (0.007)	0.02 (0.007)

Predictive ability

Model	**Type**	**Correlation (66% mort.)**	**Correlation (50% mort.)**	**χ^2 (66% mort.)**	**χ^2 (50% mort.)**
1	Linear	0.7063	0.7091	422	427
2	Threshold	0.7345	0.7166	396	418
3	Weibull	-0.7199	-0.7189	410	411
4	Repeatability	0.7534	0.7332	386	409

Correlations family EBVs

Model	Type	1	2	3	4
1	Linear		0.991	-0.930	0.939
2	Threshold	0.999		-0.940	0.963
3	Weibull	-0.936	-0.935		-0.969
4	Repeatability	0.972	0.973	-0.976	

Pearson correlations above diagonal and Spearman rank correlations below diagonal

Conclusions

- The repeatability linear model for test-day survival had the best predictive ability for both scenarios
  - Advantageous to take time perspective into account
- The predictive ability of the Weibull survival model was probably reduced due to its lacking ability to predict common environmental effects

Conclusions

- High correlation between EBVs from different models
- Testing stopped at 50% vs. 66% mortality
  - Reduced heritability of cross-sectional models
    - Sampling effect?
    - Environment may change more rapidly during the initial phases of test-period
      - Infection by means of cohabitants
      - Cross-sectional models cannot account for environmental changes over time

Thanks