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Reaction norm model analysis for heat stress tolerance of growth performance in purebred pigs

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Introduction

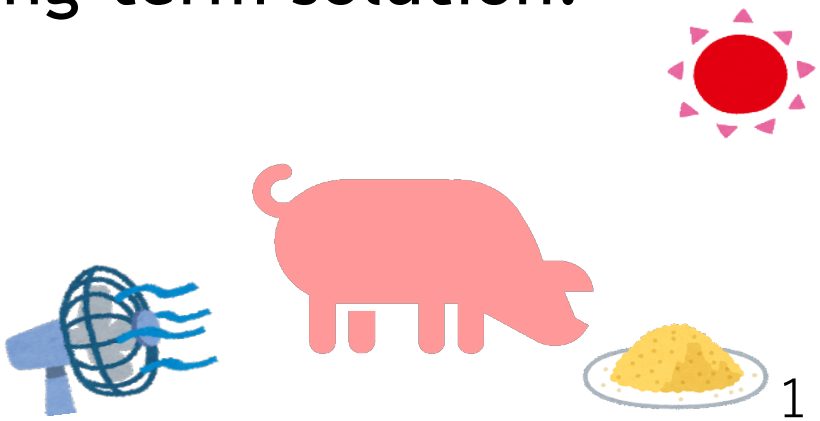
Heat stress due to global warming has increased the loss of productivity among essential livestock such as pigs.

Takada *et al.*(2008) estimated that global warming will reduce average daily weight gain of pigs in most parts of Japan by 2060, particularly by up to 30% in some areas.

Until now, heat stress countermeasures have focused on rearing management such as feed and equipment.

However, genetic improvement may provide a long-term solution.

Is it possible to evaluate heat-tolerant pigs using a reaction norm model?



Objectives

- **Identify an indicator to evaluate heat stress.**
  - To evaluate heat stress of pigs, identify threshold temperatures and critical periods from the average daily maximum temperature.
  - As an indicator of heat stress, calculate the Thermal Load.

- **Find out if genetic improvements for heat tolerance are possible.**
  - Estimating genetic parameters using a reaction norm model.

Data

Animals & Trait

- Breed: Landrace, Large White and Duroc (L, W, and D)
- Number of animals: 50,000 records on each breed
- Trait: Lifetime average daily gain (ADG) (g/ day)

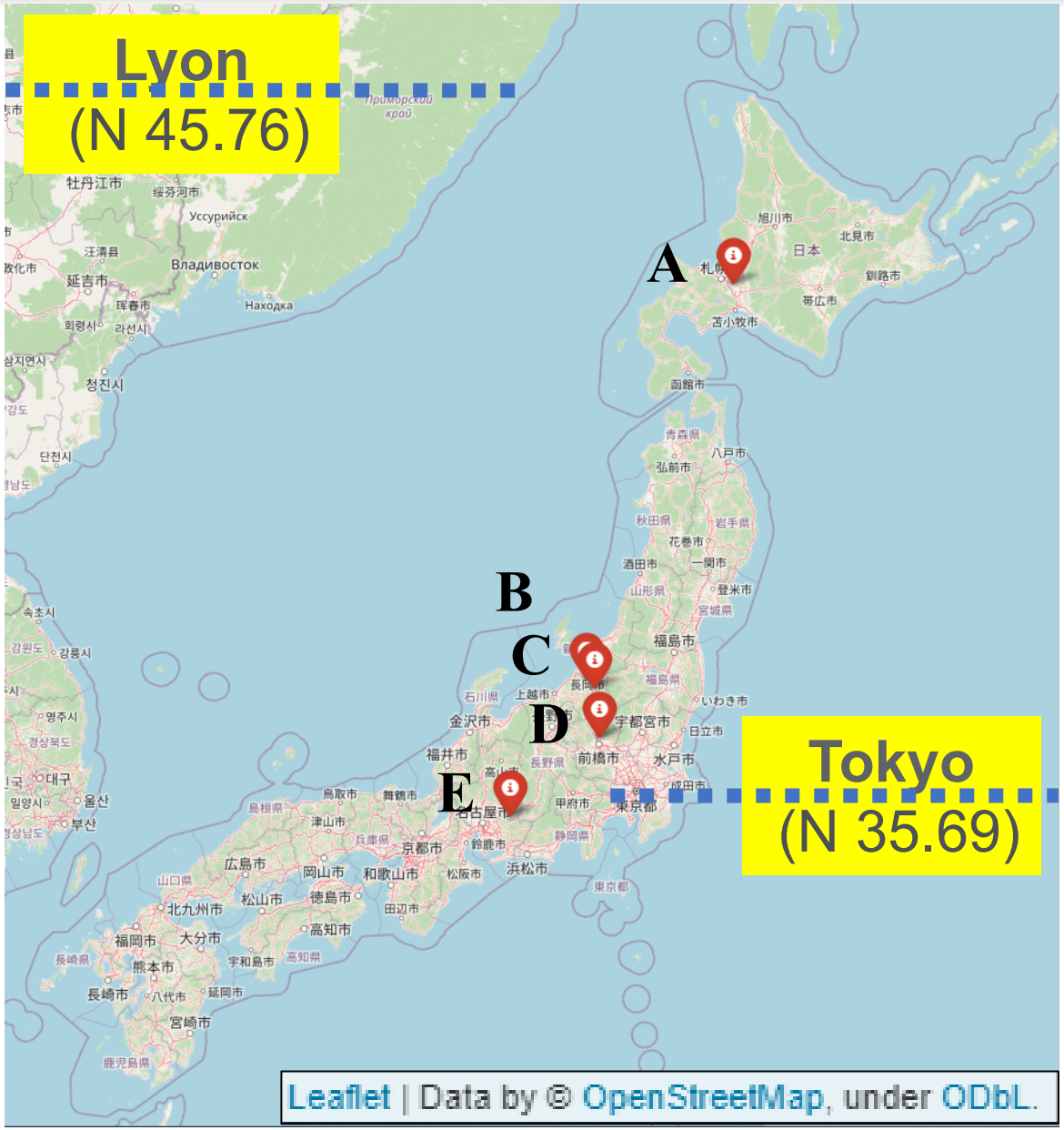
  = Body weight / Age

  ※ Range of body weight (BW): 70-148 kg

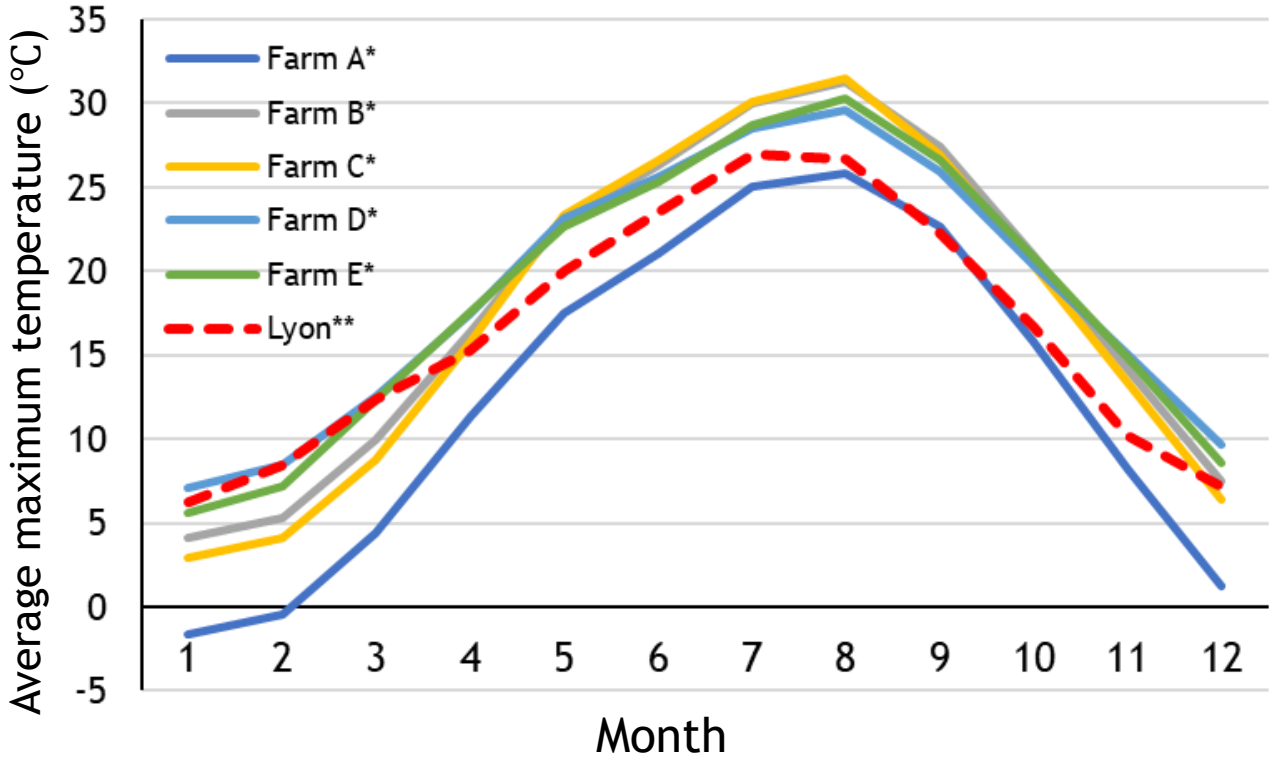
Weather records: Daily maximum temperature

- Estimated ambient weather records on the farm were taken from the Agro-Meteorological Grid Square Data, NARO in Japan.

Locations of farms and weather conditions



Records were collected from five farms of one breeding company.
Most farms were lower latitude and warmer than Lyon.

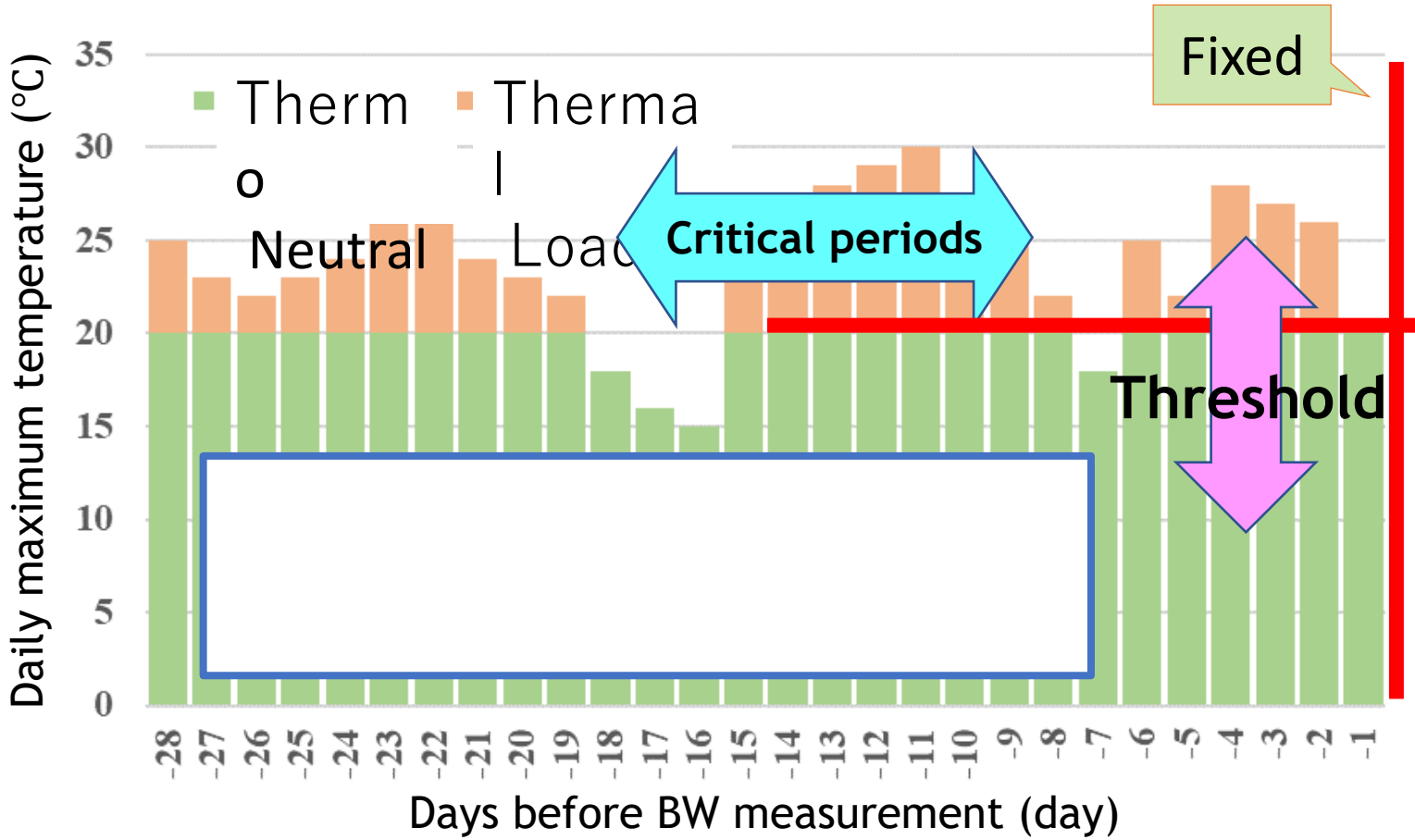


* Estimated ambient weather record on the farms (NARO)
** Prévisions météo de Météo-France

Search for TL threshold and critical periods

- Thermal Load (TL): The amount of heat above the thermal neutral zone

$$TL = \frac{1}{\text{Range}} \sum_{\text{start}}^{\text{end}} \max(0, \text{Max Temp.} - \text{Threshold Temp.})_{\text{day}}$$



■ Grid Search

Varying range of critical periods and threshold temperature to search optimal TL.

- Range of critical periods:
  1 to 16 weeks
  before BW measurement
  (in 1 week increments)
- Threshold temperature:
  No threshold or 11-30℃
  (in 1 ℃ increments)

Search for TL thresholds and critical periods

- Statistical model

$$y_{ijk} = FYS_i + Sex_j + b_0 * BW_k + b_1 * TL_k + e_{ijk}$$

y_{ijk} : Observations

FYS_i : Farm × Year × Season (Fixed effect)

Sex_j : Sex (Fixed effect)

$b_0 * BW_k$: Linear regression of Body Weight (covariate)

$b_1 * TL_k$: Linear regression of TL (covariate)

e_{ijk} : error

- Indicators of model fit

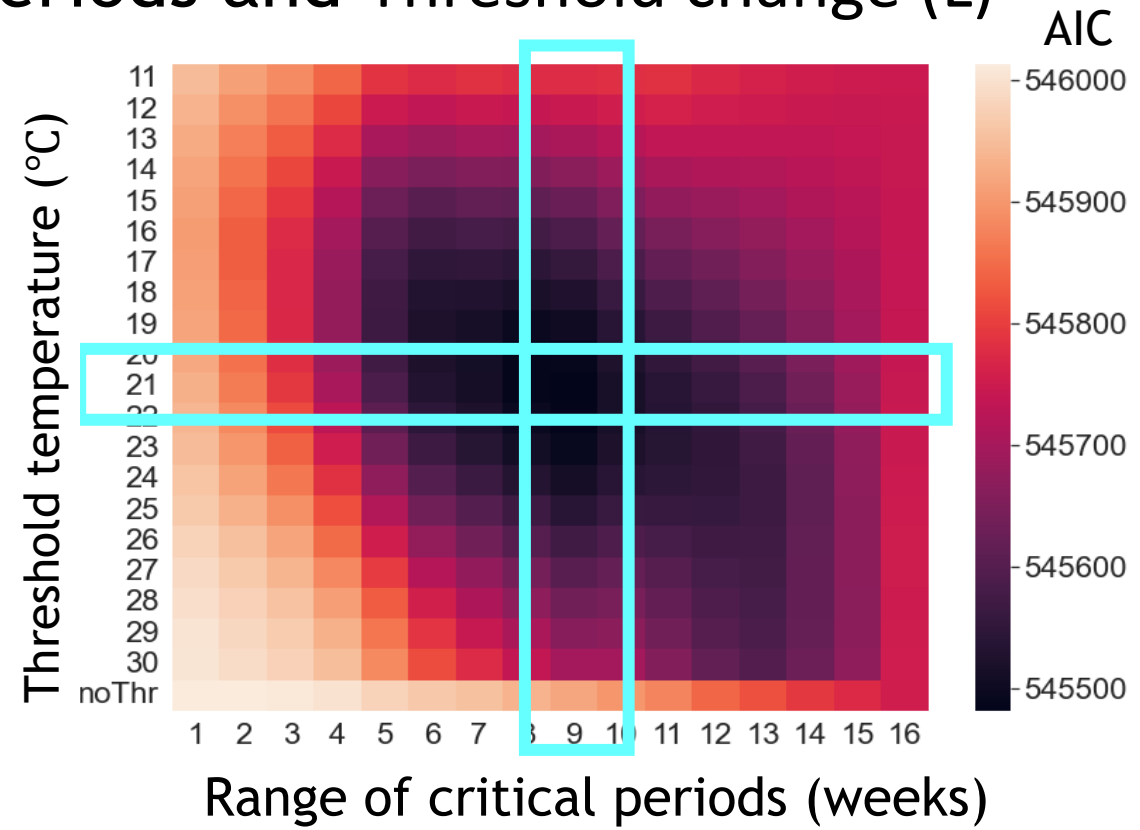
Akaike's Information Criterion (AIC)

TL thresholds and critical periods

	Breed		
	L	W	D
※Thre. Temp. (℃)	21	23	25
Critical periods (weeks)	9	8	8

※ Threshold Temperature

How AIC change as Range of critical periods and Threshold change (L)



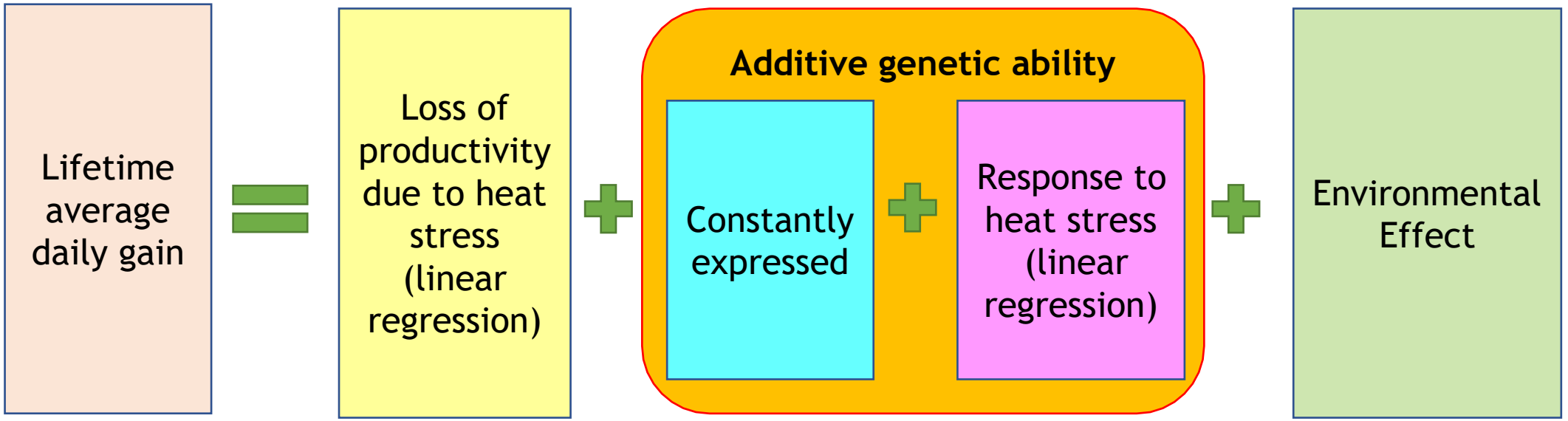
- Different TL criteria were obtained for different breeds.
  - ➢ These were used to calculate TL and analyze genetic parameters.

Reaction Norm Model

We estimated genetic parameters of heat tolerance by reaction norm models (RNM). RNM is a first order random regression model.

It is often used in analyses that consider genetic and environmental interactions.

In the RNM, the genetic ability of an individual is analyzed separately in terms of its ability to be constantly expressed and its ability to response to heat stress.



Model for estimating genetic parameters

$$y_{ijk} = FYS_i + Sex_j + b_0 * BW_k + b_1 * TL_k + a_{0k} + a_{1k} * TL_k + e_{ijk}$$

a_{0k} : Constantly expressed additive genetic effect (random)

$a_{1k} * TL_k$: Additive genetic effect expressed in response to TL (random) and TL

e_{ijk} : error

$$E\begin{bmatrix} a_0 \\ a_1 \\ e \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \\ 0 \end{bmatrix}, \quad \mathrm{Var}\begin{bmatrix} a_0 \\ a_1 \\ e \end{bmatrix} = \begin{bmatrix} \sigma^2_{a_0}\mathbf{A} & \sigma_{a_0a_1}\mathbf{A} & 0 \\ \sigma_{a_0a_1}\mathbf{A} & \sigma^2_{a_1}\mathbf{A} & 0 \\ 0 & 0 & \sigma^2_e\mathbf{I} \end{bmatrix}$$

σ^2_a : additive genetic variance, σ^2_e : error variance,
$\mathbf{A}$: additive relationship matrix, $\mathbf{I}$: design matrix

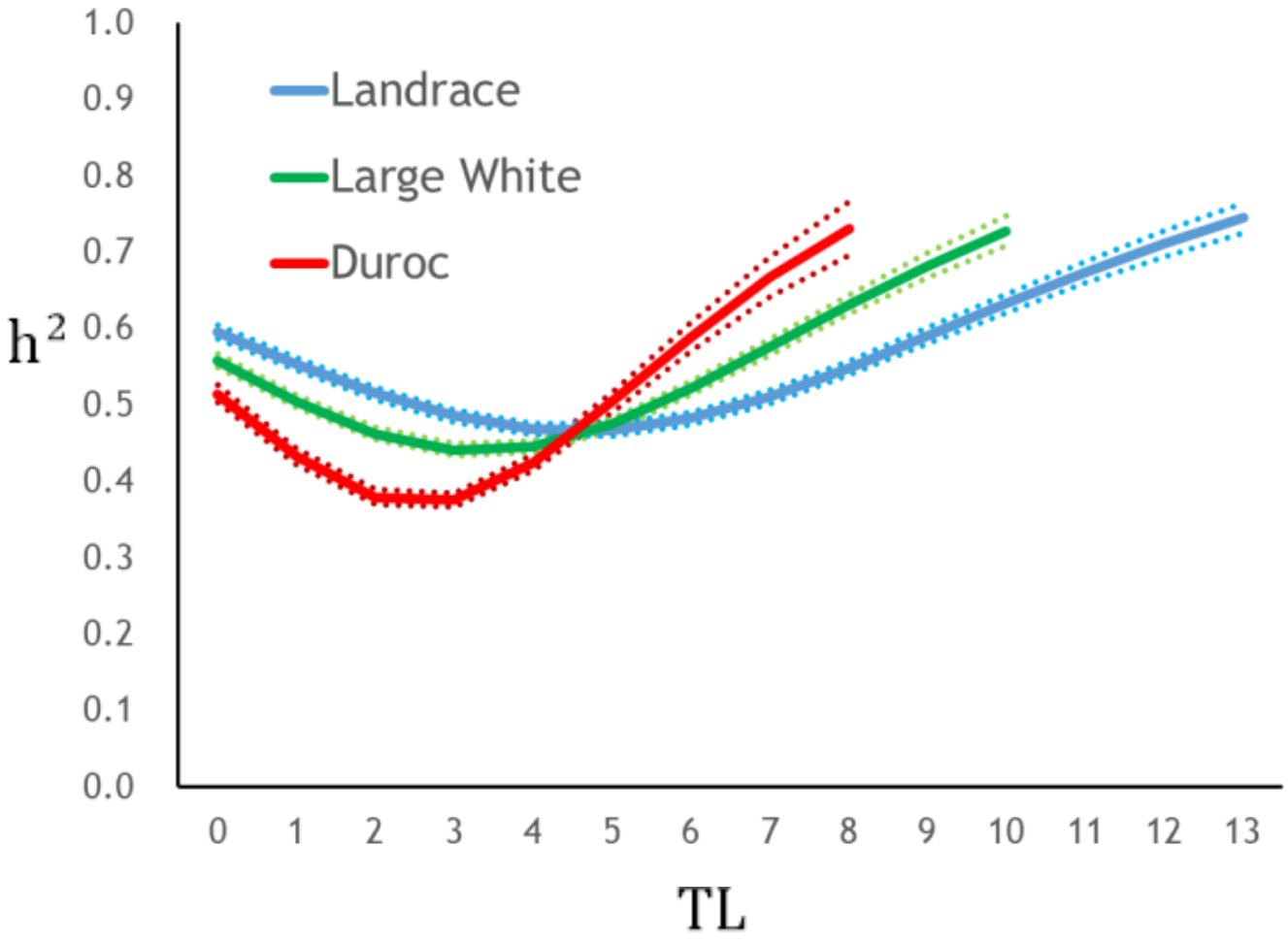
Estimated by AI-REML method using BLUPF90+ program.

Estimates of genetic parameters

	Landrace	Large White	Duroc
$\sigma^2_{a_0}$	597.22	646.48	536.65
$\sigma_{a_0a_1}$	-53.20	-72.82	-93.32
$\boldsymbol{\sigma^2_{a_1}}$	**11.66**	**21.86**	**36.44**
σ^2_e	404.75	513.0	505.24
$\mathbf{r_{a_0a_1}}$	**-0.64**	**-0.61**	**-0.67**

- Variations in genetic ability to response to TL ($\boldsymbol{\sigma^2_{a_1}}$) were observed
  - ➢ Potential for heat tolerance improvement.
- Genetic correlations between the constantly expressed and TL responsive genetic ability ($\mathbf{r_{a_0a_1}}$) is NEGATIVE.
  - ➢ Difficulty of simultaneous improvement.

Change in estimated heritability with TL



Formula for heritability on TL_k

$$h^2_{TL_k} = \frac{var(a_0 + a_1 TL_k)}{var(a_0 + a_1 TL_k) + \sigma^2_e}$$

- Estimated heritability varied with TL.

※ The upper limit of TL is the maximum value of the data set.

- Similar trends were observed for all three breeds.

- Heritabilities in response to TL were confirmed.
- Moderate heritabilitis were observed even at high TLs.

Summary

- The novel **indicators for evaluating heat stress** on purebred pigs reared in Japan **were identified.**
  - ➢ **Thermal load (TL) on pigs can be calculated.**
- Genetic variances in response to TL were identified and heritabilities were confirmed.
  - ➢ **Possibility of improving heat tolerance**.
- Genetic ability constantly expressed and response to TL has an undesirable relationship.
  - ➢ **Difficulty of simultaneous improvement.**

Acknowledgments

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Related Research in Poster Session 55

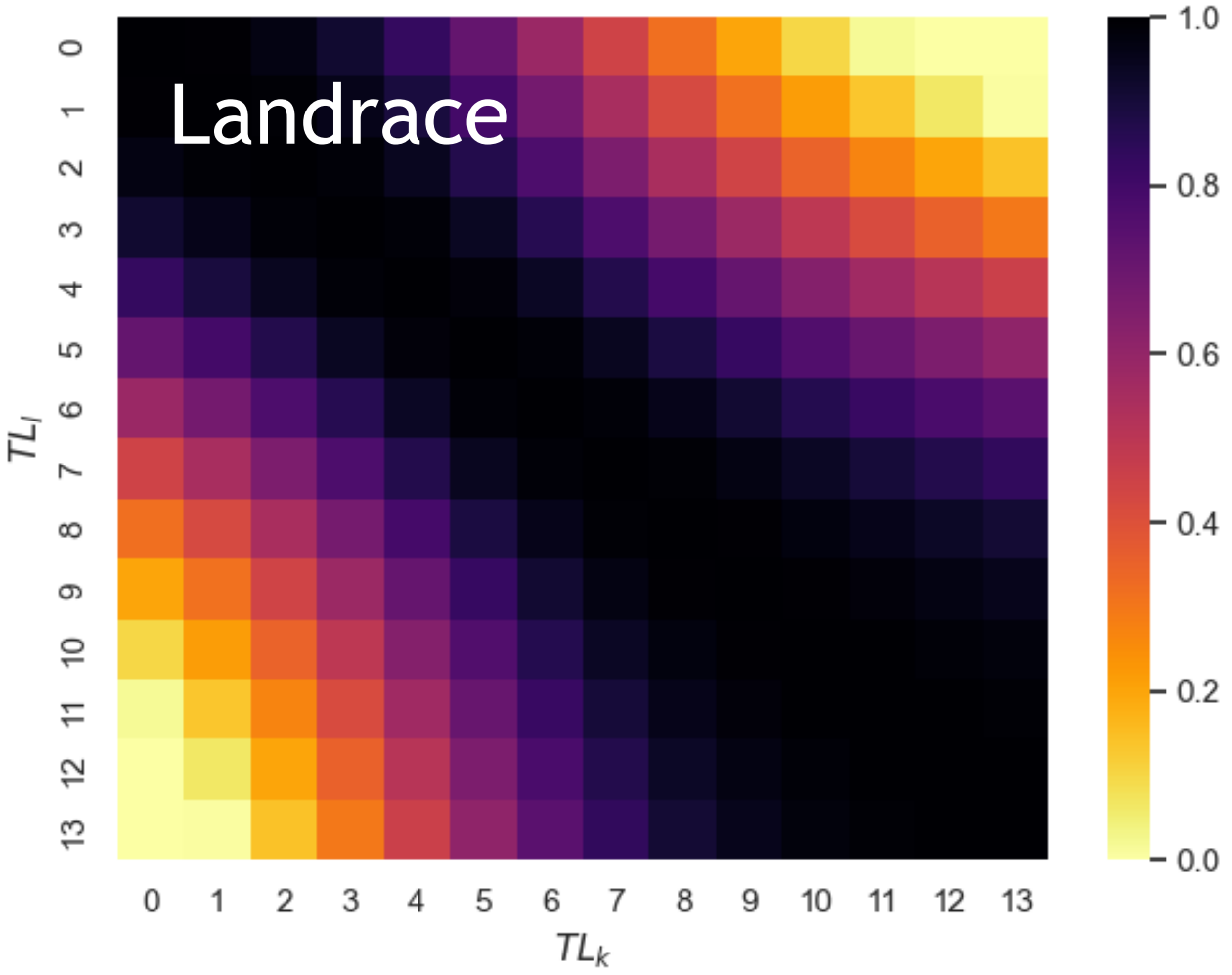
55.13 Plateau-linear regression analysis of farrowing records on temperature data for pigs reared in Japan (Ogawa et al.)

55.14 Genetic parameter of heat tolerance for reproductive traits in Landrace, Large White and Duroc pigs (Okamura et al.)

Formula for Calculating Genetic Parameters

- **Breeding value(BV)**
- BV in environment TL_k: $BV_k = a_0 + a_1 TL_k$
- BV in environment TL_l: $BV_l = a_0 + a_1 TL_l$
- **Genetic variance**
- $\mathrm{var}(a_0 + a_1 TL_k) = \mathrm{var}(a_0) + \mathrm{var}(a_1 TL_k) + 2\,\mathrm{cov}(a_0, a_1 TL_k)$
  $= \sigma^2_{a_0} + TL_k^2\ \sigma^2_{a_1} + 2TL_k\sigma_{a_{01}}$
- **Genetic covariance**
- $\mathrm{cov}(a_0 + a_1 TL_k, a_0 + a_1 TL_l)$
  $= \mathrm{var}(a_0) + \mathrm{cov}(a_0, a_1 TL_l) + \mathrm{cov}(a_1 TL_k, a_0) + TL_k TL_l \mathrm{var}(a_1)$
  $= \sigma^2_{a_0} + TL_l\sigma_{a_{01}} + TL_k\sigma_{a_{01}} + TL_k TL_l\sigma^2_{a_1}$
  $= \sigma^2_{a_0} + (TL_k + TL_l)\,\sigma_{a_{01}} + TL_k TL_l\sigma^2_{a_1}$
- **Genetic correlation**
- $$\frac{\sigma^2_{a_0} + (TL_k + TL_l)\,\sigma_{a_{01}} + TL_k TL_l\sigma^2_{a_1}}{\sqrt{(\sigma^2_{a_0} + TL_k^2\ \sigma^2_{a_1} + 2TL_l\sigma_{a_{01}}) * (\sigma^2_{a_0} + TL_l^2\ \sigma^2_{a_1} + 2TL_l\sigma_{a_{01}})}}$$

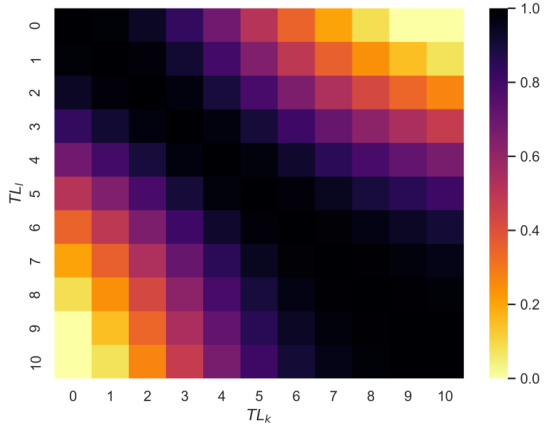
Changes in estimated genetic correlation with TL



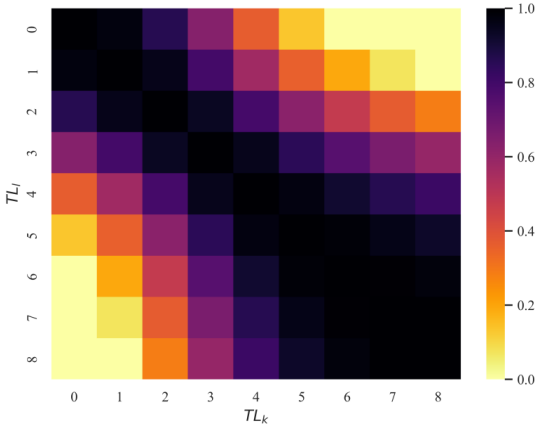
Formula for estimated genetic correlation between TL_k and TL_l

$$r_{g_{TL_k\_TL_l}} = \frac{Cov(a_0 + TL_k * a_1, a_0 + TL_l * a_1)}{\sqrt{Var(a_0 + TL_k * a_1) * Var(a_0 + TL_l * a_1)}}$$

Large White



Duroc



- The values of estimated genetic correlation suggest a genotype-TL interaction effect.