

# GxE Interactions Of Body Weight For Broilers Raised In Bio-secure And Commercial Environments

*Hélène Romé, Think T. Chu, Elise Norberg, Danye Marois, John Henshall, Just Jensen*

# INTRODUCTION - G<sub>x</sub>E FOR BROILERS

highly bio-secure breeding (B) env.

vs

commercial production (C) env.

Better

*Hygienic conditions*

Worse

Better

*Litter management*

Worse

Minimum

*Transportation of 1-day-old chick*

Long distance

G<sub>x</sub>E between B and C for broilers

- Only 1 large-scale study in literature (Kapell *et al.* 2012):  $r_{B,C} = 0.46-0.69$

Need G<sub>x</sub>E parameters for designing breeding programs to ensure maximum genetic gain under commercial conditions

# AIMS

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**Explore GxE for BW in broilers raised in B vs C environments**

**Model heterogeneous variances between sexes**

# Methods - Experimental Design

Bio-secure environment

Commercial environment

Same line => No crossbreeding

Each bird would have full and half sibs in both environments

BW at 5 and 6 weeks of age for males and females

Decision of selection

# Methods - Experimental Design

BW at week	Sex	B environment			C environment		
		Number of records	Mean	Standard deviation	Number of records	Mean	Standard deviation
5	Male	10117	2183	213	7455	1735	302
5	Female	10801	1882	180	7922	1550	248
6	Male	18651	2758	269	3975	2231	364
6	Female	22020	2329	217	4217	1940	290

# Methods - Model

**Step 1** : For each trait (by week, sex, & env.) => estimate  $\sigma_p$

**Step 2** : Standardize phenotypic records for each trait:  $y^0 = y/\sigma_p$

**Step 3** : Use standardized phenotypic records for multi-trait PBLUP model

$$\begin{bmatrix} y_{5B}^{m0} \\ y_{5B}^{f0} \end{bmatrix} = \begin{bmatrix} X_{5B}^m & 0 \\ 0 & X_{5B}^f \end{bmatrix} \begin{bmatrix} b_{5B}^m \\ b_{5B}^f \end{bmatrix} + \begin{bmatrix} Z_{5B}^m & 0 \\ 0 & Z_{5B}^f \end{bmatrix} a_{5B} + \begin{bmatrix} W_{5B}^m & 0 \\ 0 & W_{5B}^f \end{bmatrix} c_{5B} + \begin{bmatrix} e_{5B}^m \\ e_{5B}^f \end{bmatrix}$$
$$\begin{bmatrix} y_{6B}^{m0} \\ y_{6B}^{f0} \end{bmatrix} = \begin{bmatrix} X_{6B}^m & 0 \\ 0 & X_{6B}^f \end{bmatrix} \begin{bmatrix} b_{6B}^m \\ b_{6B}^f \end{bmatrix} + \begin{bmatrix} Z_{6B}^m & 0 \\ 0 & Z_{6B}^f \end{bmatrix} a_{6B} + \begin{bmatrix} W_{6B}^m & 0 \\ 0 & W_{6B}^f \end{bmatrix} c_{6B} + \begin{bmatrix} e_{6B}^m \\ e_{6B}^f \end{bmatrix}$$
$$\begin{bmatrix} y_{5C}^{m0} \\ y_{5C}^{f0} \end{bmatrix} = \begin{bmatrix} X_{5C}^m & 0 \\ 0 & X_{5C}^f \end{bmatrix} \begin{bmatrix} b_{5C}^m \\ b_{5C}^f \end{bmatrix} + \begin{bmatrix} Z_{5C}^m & 0 \\ 0 & Z_{5C}^f \end{bmatrix} a_{5C} + \begin{bmatrix} W_{5C}^m & 0 \\ 0 & W_{5C}^f \end{bmatrix} c_{5C} + \begin{bmatrix} e_{5C}^m \\ e_{5C}^f \end{bmatrix}$$
$$\begin{bmatrix} y_{6C}^{m0} \\ y_{6C}^{f0} \end{bmatrix} = \begin{bmatrix} X_{6C}^m & 0 \\ 0 & X_{6C}^f \end{bmatrix} \begin{bmatrix} b_{6C}^m \\ b_{6C}^f \end{bmatrix} + \begin{bmatrix} Z_{6C}^m & 0 \\ 0 & Z_{6C}^f \end{bmatrix} a_{6C} + \begin{bmatrix} W_{6C}^m & 0 \\ 0 & W_{6C}^f \end{bmatrix} c_{6C} + \begin{bmatrix} e_{6C}^m \\ e_{6C}^f \end{bmatrix}$$

# Methods - Model

**Step 1** : For each trait (by week, sex, & env.) => estimate  $\sigma_p$

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**Step 3** : Use standardized phenotypic records for multi-trait PBLUP model

**Step 4** : Rescaling of parameters to original scale

$$\begin{aligned} \mathbf{V}_a &= \mathbf{T}_2 (\mathbf{T}_1 \mathbf{V}_a^0 \mathbf{T}_1') \mathbf{T}_2' \\ \mathbf{V}_c &= \mathbf{T}_2 (\mathbf{T}_1 \mathbf{V}_c^0 \mathbf{T}_1') \mathbf{T}_2' \\ \mathbf{V}_e &= \mathbf{T}_2 \mathbf{V}_e^0 \mathbf{T}_2' \end{aligned}$$

$$\mathbf{T}_1 = \begin{bmatrix} 1 & 0 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{bmatrix}$$

$$\mathbf{T}_2 =$$

8x8 matrix

- Off-diagonal elements are zero
- Diagonal is vector of phenotypic standard deviations

# Results

BW at week	Sex	B environment			C environment		
		$\sigma_a^2$	$h^2$	$c^2$	$\sigma_a^2$	$h^2$	$c^2$
5	Male	10454	0.274	0.033	24984	0.358	0.037
5	Female	7614	0.278	0.033	17469	0.366	0.038
6	Male	17301	0.301	0.034	39544	0.312	0.028
6	Female	11651	0.298	0.034	23831	0.305	0.027
Standard errors in range			0.022–0.024	0.007–0.008		0.033–0.037	0.011–0.013



# Results

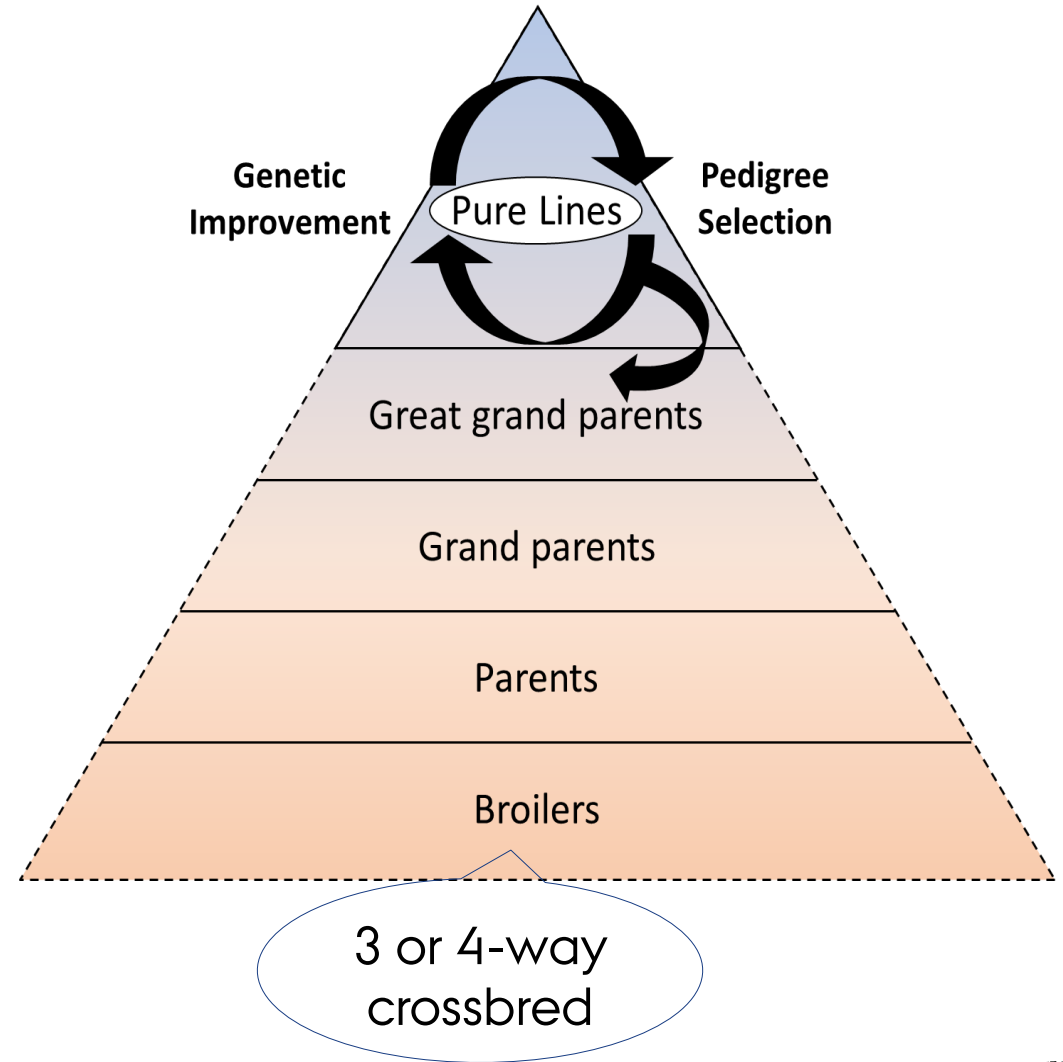
Environment		B		C		
	BW at week	5	6	5	6	
B	5	1	0.956	0.535	0.490	} Genetic correlation
	6		1	0.497	0.479	
C	5			1	0.989	
	6				1	

**Strong GxE interaction found**

# DISCUSSIONS - CROSSBRED OR PUREBRED IN C?

Why GxE between B and C in purebred broilers?

- Low GxG (purebred vs crossbred same environment):  $r_g = 0.90-0.96$  for BW5 (Duenk *et al.* 2019)
- Relationships between selection candidates in B and tested birds in C: purebred (full-sibs and half-sibs), crossbred (half-sibs, progeny or distant descendants) -> higher relationship -> higher accuracy
- A shorter generation interval of selection based on purebred records from C
- Difficult for tracing pedigree of crossbred



# CONCLUSIONS

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Strong GxE found for BW of broilers measured in B and C:

- Genetic cor. between B & C relatively low
- Heterogeneous variances between B and C traits.
- $h^2$  of C traits higher than B traits
- Difference in performances

-->> We do need records obtained in C env.

Sib-testing in C very beneficial for genetic gains of C traits:

- Explore re-ranking of EBVs between B and C traits
- Unlock significant new sources of genetic variations as genetic variances of C traits more than 2 times higher than those of B traits



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