

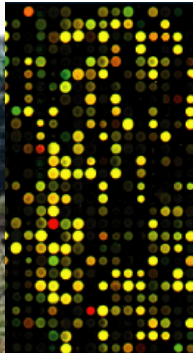
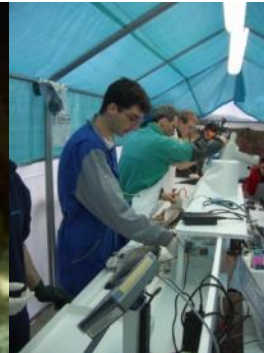
Does early growth play a role in the sex determination of European sea bass *Dicentrarchus labrax* ?

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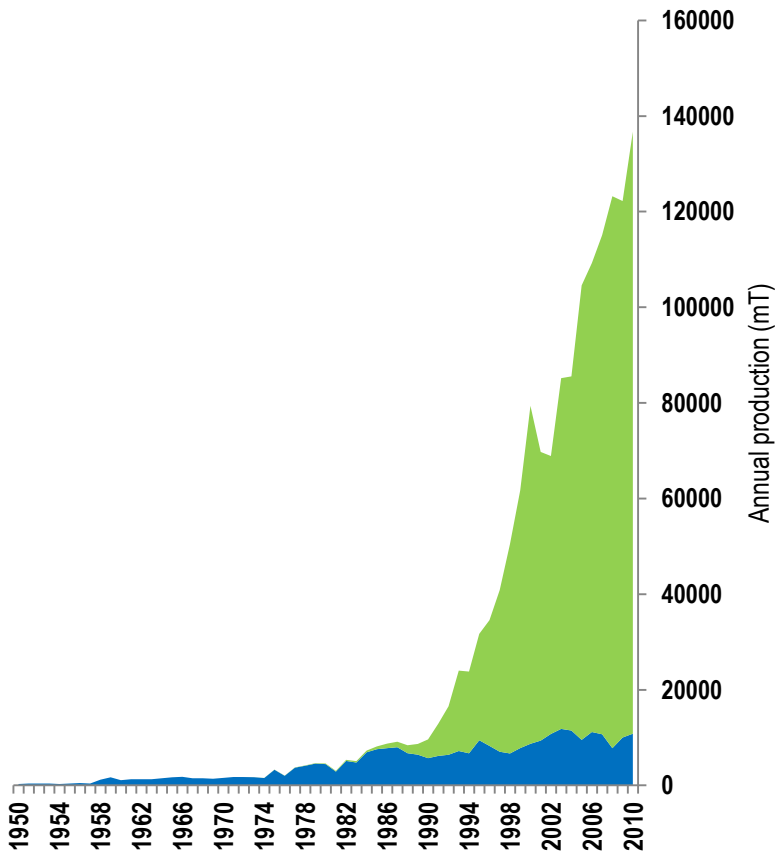
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² Ifremer UMR 110 INTREPID, Palavas les Flots, FR

³ Ifremer La Rochelle, FR



The sea bass: an important aquaculture species with unusual (polygenic) sex determination



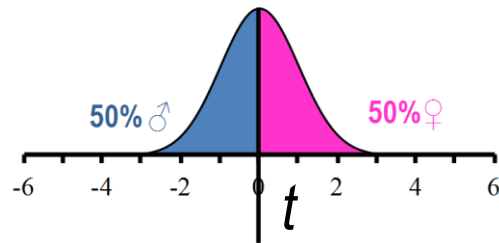
- 75-95% males in farmed populations
- Females 20-30% heavier → preferred
- Warm early rearing environment → males
- No protocol ensuring 50% females or more
- Polygenic sex determination postulated
Vandeputte et al. 2007, Genetics 176: 1049-1057

→ How to use it to manipulate sex-ratio ?

The polygenic threshold model for sex

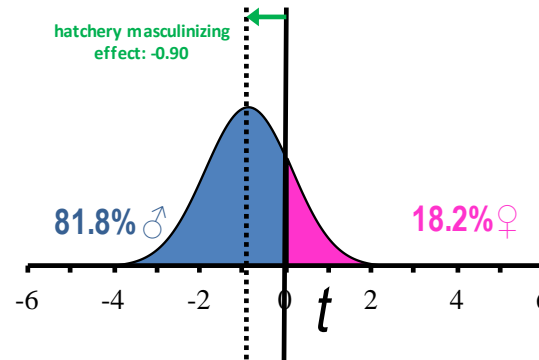
adapted from Bulmer and Bull, 1982

An underlying sex tendency $t = G + E$; if $t > 0$: female, else male



In nature

*Vandeputte et al. 2012,
Aquatic Living Resources 25: 77-81*



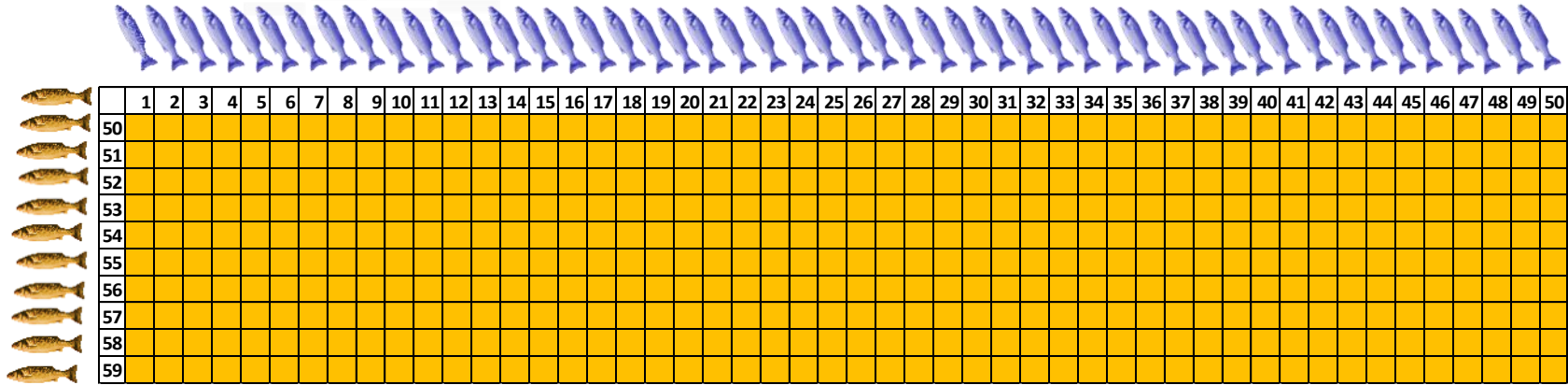
In hatchery

*Vandeputte et al. 2007
Genetics 176: 1049-1057*

t can be equally displaced by genetics and environment
 t is genetically correlated with BW at 1 yr ($r_A = +0.50$)

Is there variation in genetic correlations of t and growth?

Experimental design



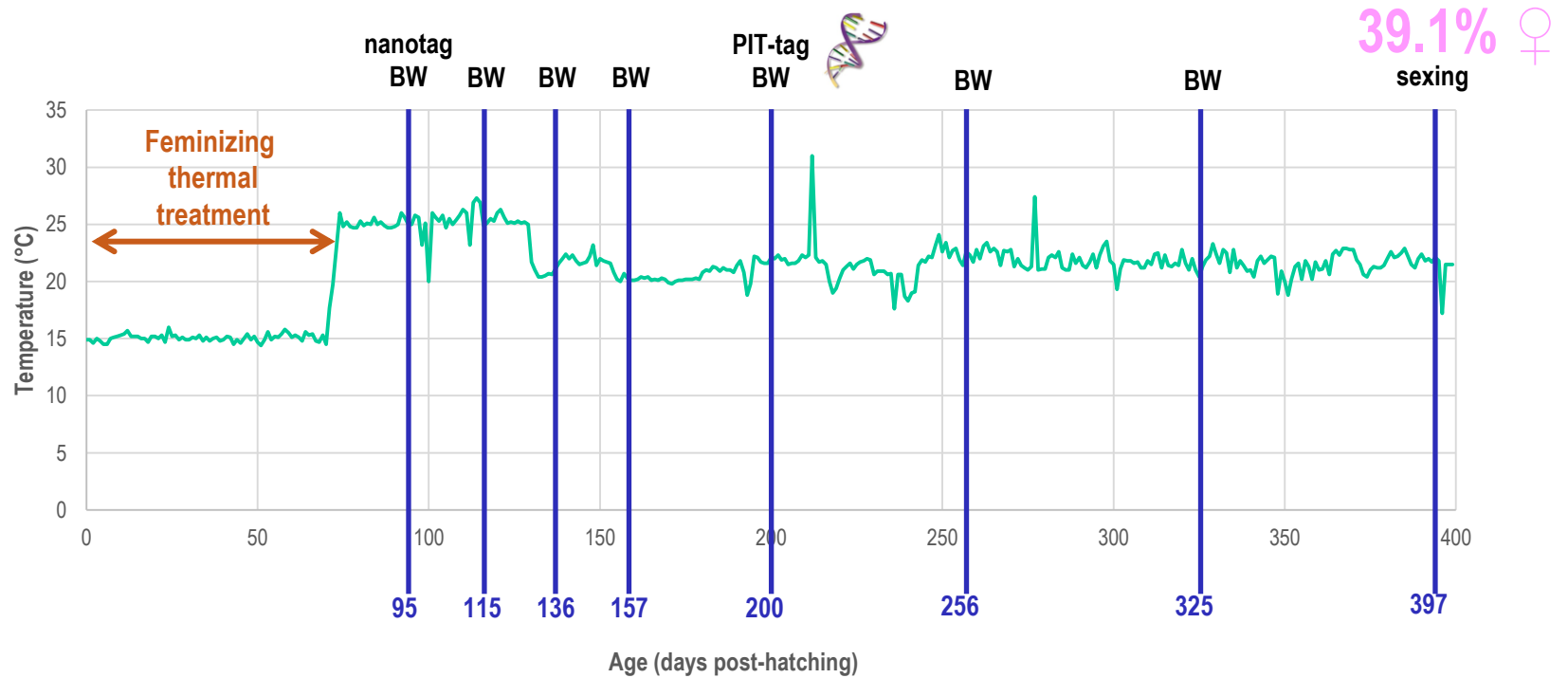
- 50 sires x 10 dams full factorial (G1 dom. WMED)
- All grouped in 1 batch
- 1938 tagged at 95 dph (0.57g) with nanotags

NONATEC™


Individual micro-tagging













Ferrari et al., 2014. Aquaculture 426-427: 165-171



Parentage assignment



	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	Total	
	50	9	12	1	1	1	7	4	11	5	10	4	3	6	4	3	0	7	9	10	9	12	1	2	4	3	13	4	1	7	10	10	0	5	6	4	2	2	4	4	6	7	6	2	0	13	3	2	7	8	0	264
	51	2	3	3	2	2	1	1	1	4	6	1	0	0	6	9	1	0	1	1	2	3	1	0	3	12	4	3	6	6	0	0	1	3	2	5	0	2	0	3	3	6	0	3	1	5	1	0	0	2	0	121
	52	1	2	8	4	3	6	8	3	6	1	1	2	3	0	6	1	5	5	1	6	4	8	7	2	7	4	4	3	13	2	2	1	0	3	14	4	6	2	2	8	3	1	4	8	6	2	0	2	1	0	195
	53	0	3	4	0	2	3	1	2	2	2	1	0	2	2	4	1	2	3	1	4	4	3	2	0	2	3	3	0	6	2	1	1	1	2	1	2	1	2	1	5	4	0	0	1	2	0	1	0	1	0	90
	54	0	1	0	3	2	2	7	0	2	0	2	0	4	2	3	2	0	0	1	3	3	2	1	5	0	0	0	1	4	2	2	3	5	2	4	4	2	0	1	6	2	0	3	0	3	3	2	1	0	0	95
	55	4	1	4	2	9	4	1	19	1	0	2	3	16	2	4	0	10	12	8	3	11	1	3	3	1	5	27	0	4	13	14	1	1	6	1	2	2	4	12	1	7	6	2	0	7	0	9	2	5	0	255
	56	0	0	0	0	1	0	7	1	1	0	1	1	1	0	1	2	1	0	1	0	1	1	0	0	0	0	0	0	2	2	1	0	1	2	0	2	1	0	0	3	0	0	0	0	0	0	0	0	0	0	39
	57	0	1	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	5	
	58	0	0	1	0	0	0	0	2	0	0	0	0	0	0	1	0	2	1	0	0	0	0	0	0	0	0	0	1	0	1	2	0	0	0	0	1	0	0	0	3	0	0	0	3	0	0	1	0	0	19	
	59	2	2	0	2	1	0	1	1	2	1	0	1	1	1	0	0	2	2	1	4	0	0	1	1	2	2	4	1	1	0	0	1	0	3	0	2	2	1	0	0	0	0	0	0	0	2	0	0	0	51	
		18	25	21	15	21	23	30	40	22	21	13	9	34	17	32	7	27	33	25	28	42	17	15	18	26	31	43	16	44	33	32	7	17	23	32	17	18	15	24	32	32	13	14	10	44	10	16	15	17	0	1134

- Genotyped for 12 microsatellites **LABOGENA**
- 98.0% assignment (VITASSIGN, 2 mismatches tolerated)
- 1134 individuals with complete phenotypes and pedigree



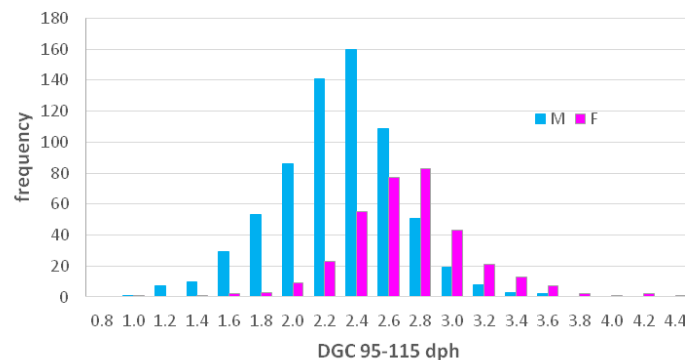
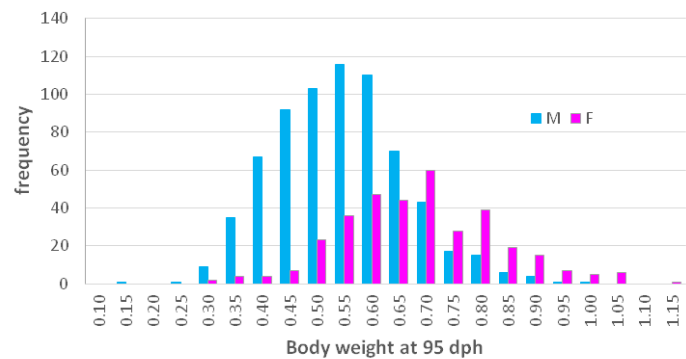
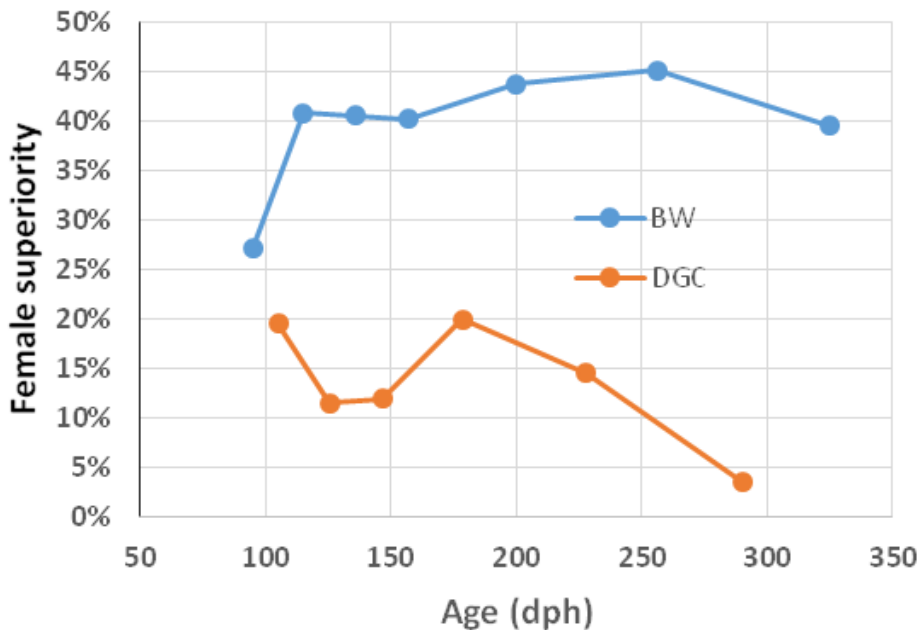
Models used

➤ Multivariate sire models in VCE 6.0

$$\left\{ \begin{array}{ll} \text{Sex } (0,1) = \text{Sire} + \varepsilon & \\ BW_x \text{ or } DGC_{x-y} = \text{sex} + \text{Sire} + \varepsilon & \text{(if growth= consequence of sex)} \\ BW_x \text{ or } DGC_{x-y} = \text{Sire} + \varepsilon & \text{(if growth= cause of sex)} \end{array} \right.$$

Dempster & Lerner (1950) correction for h^2_U

Sex dimorphism for BW & DGC



Heritability of sex tendency

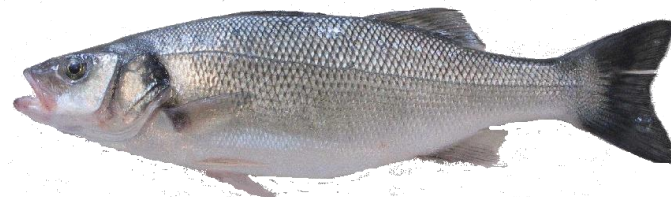
$$h^2_u = 0.39 \pm 0.12$$



WEM

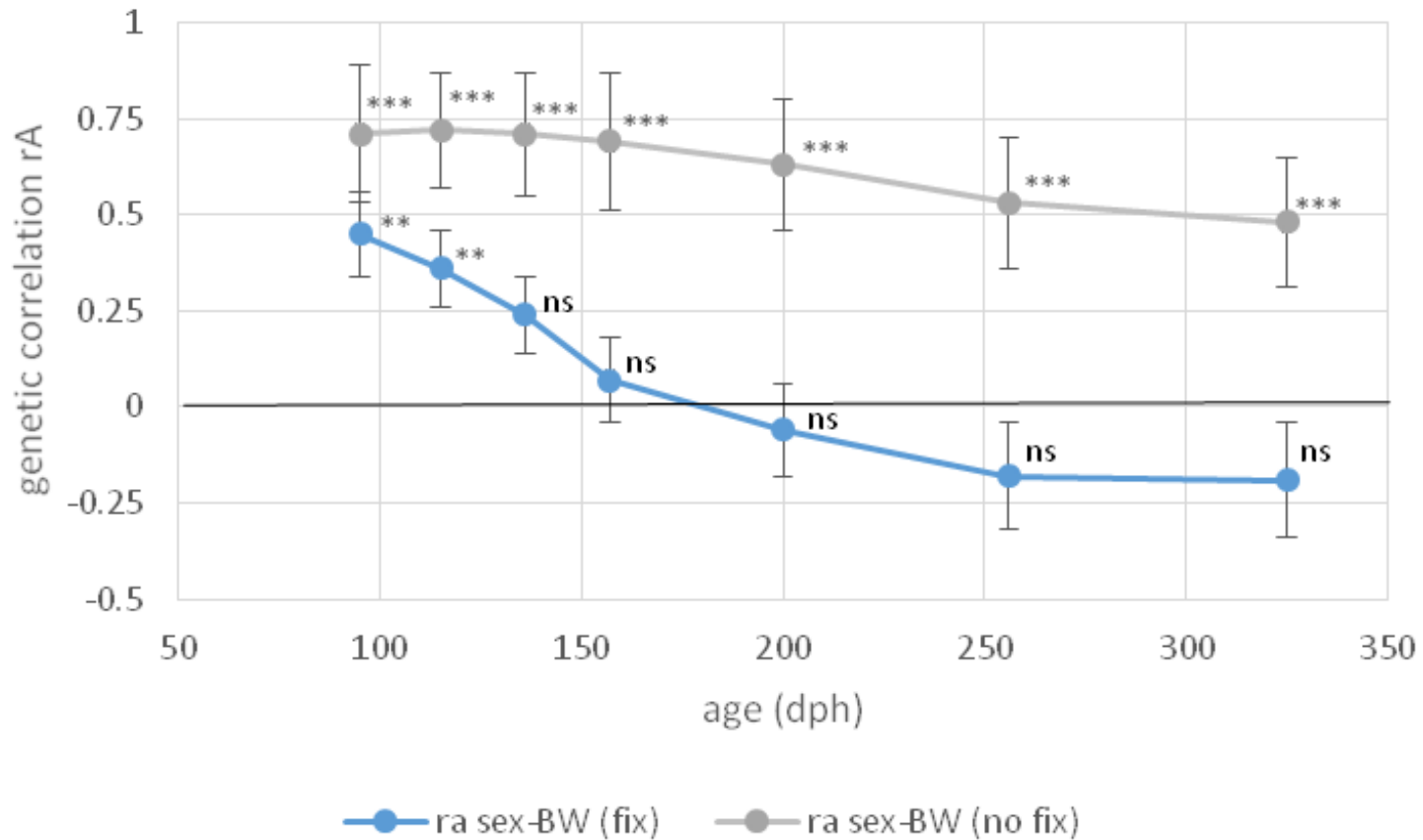
Lower than previous estimate :

$$h^2_u = 0.62 \pm 0.12$$

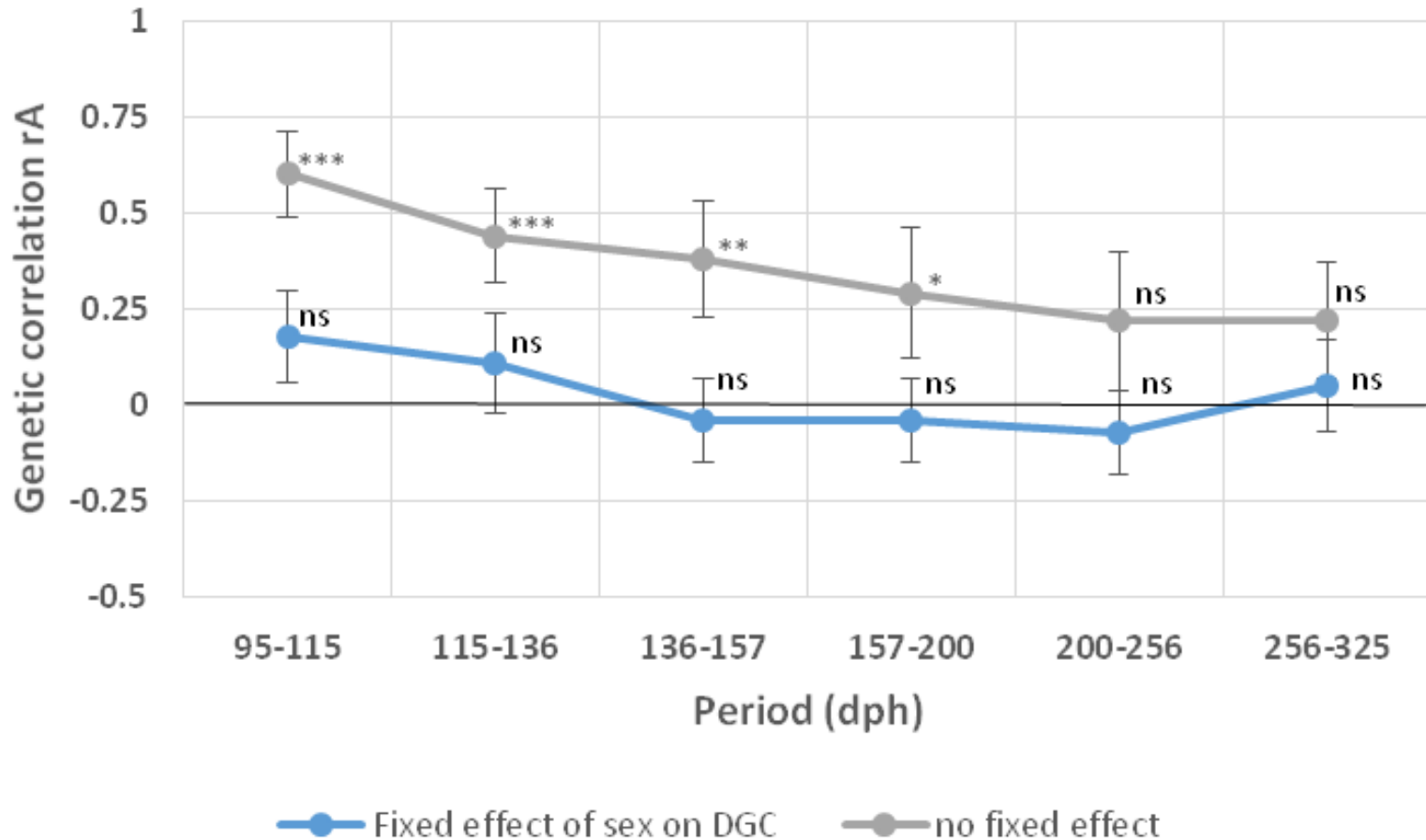


NAT

Sex tendency – BW genetic correlations

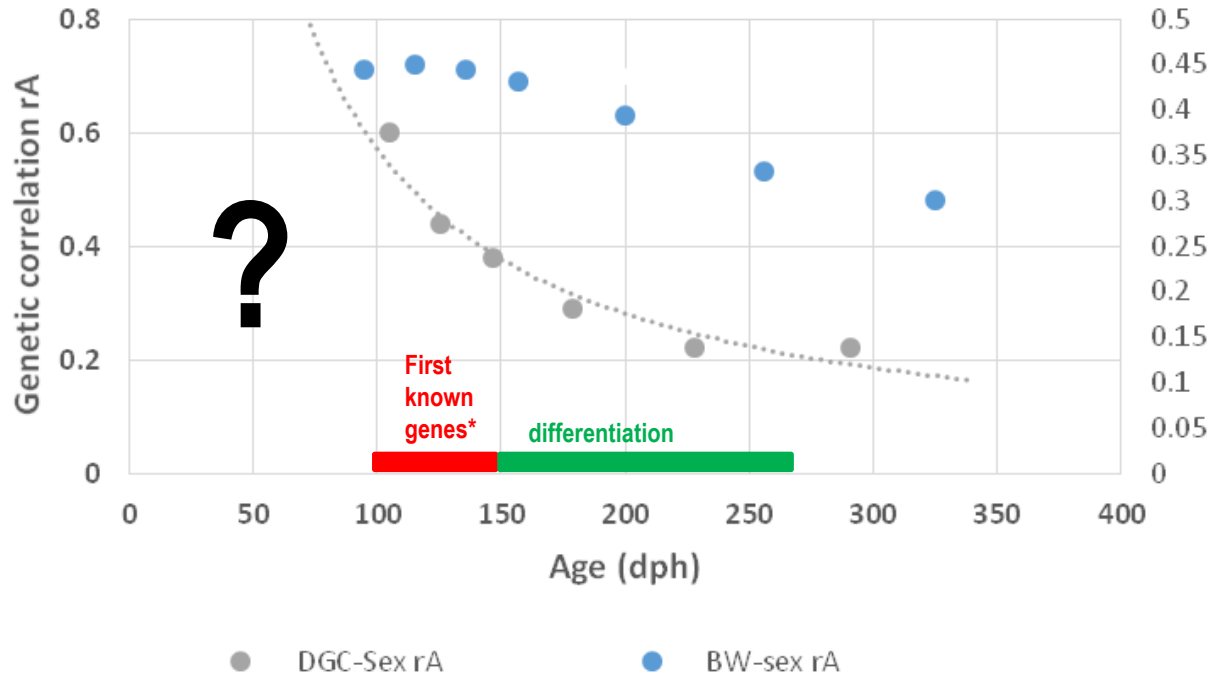


Sex tendency – DGC genetic correlations





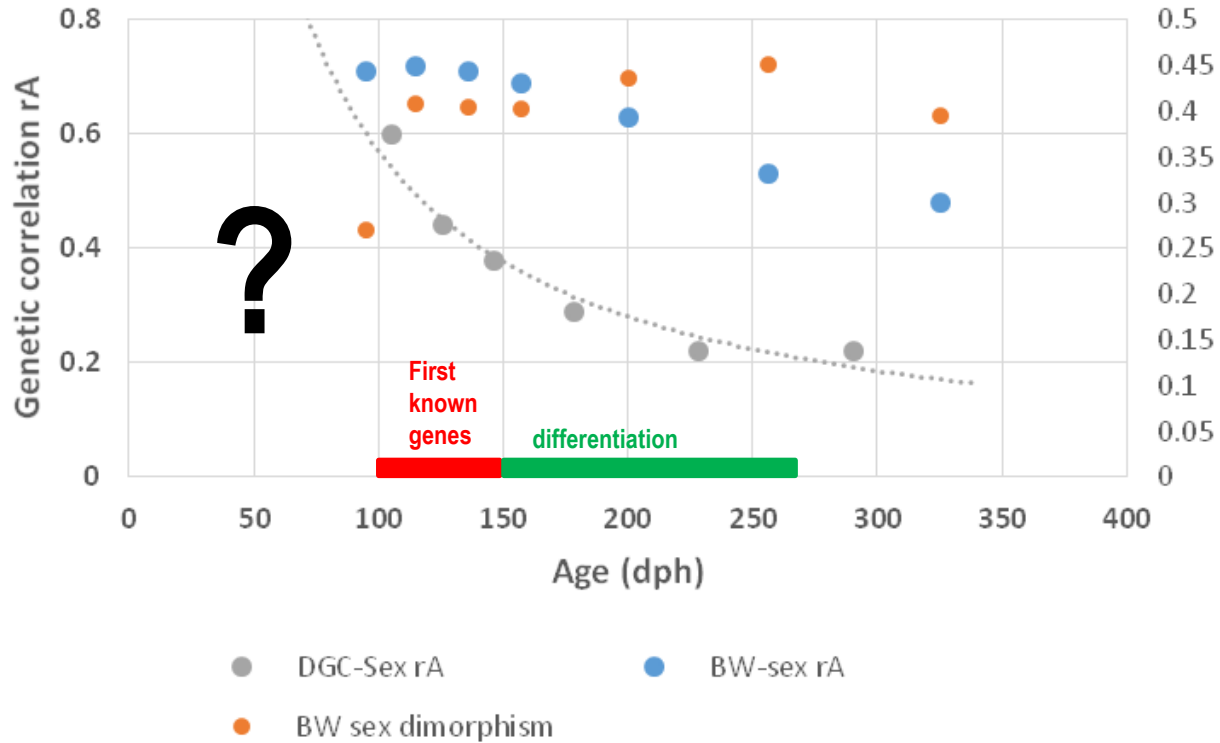
So what happens ?



**cyp19a, Blazquez et al, 2009*

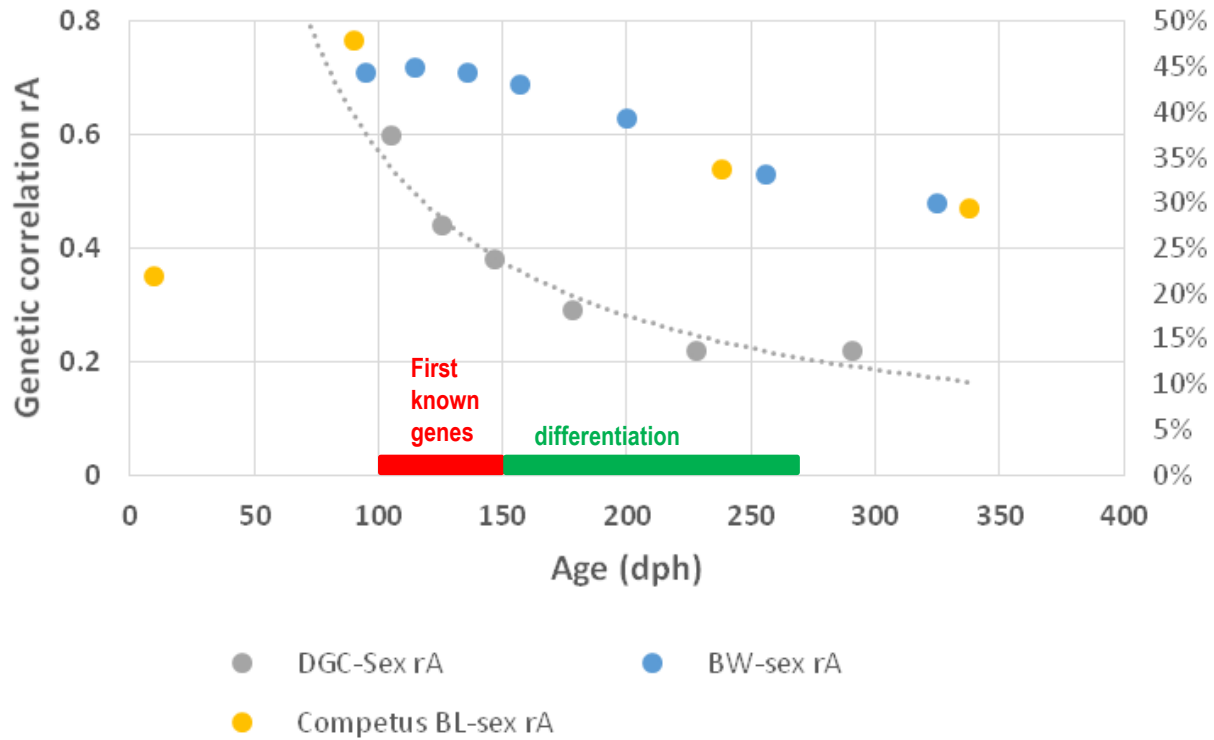


So what happens ?



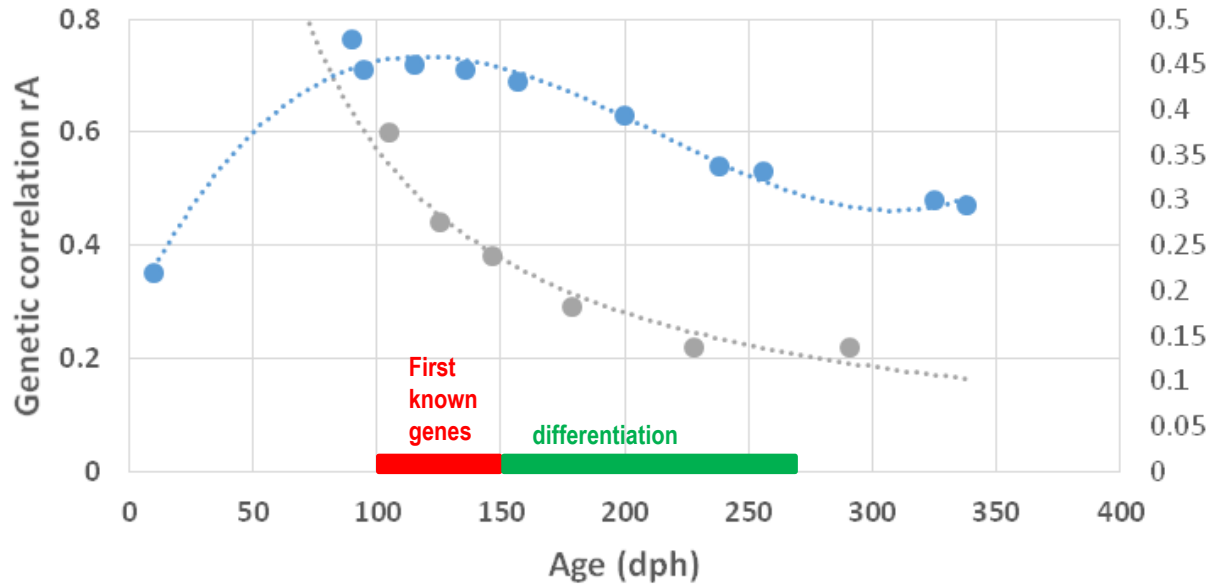


So what happens ?





So what happens ?

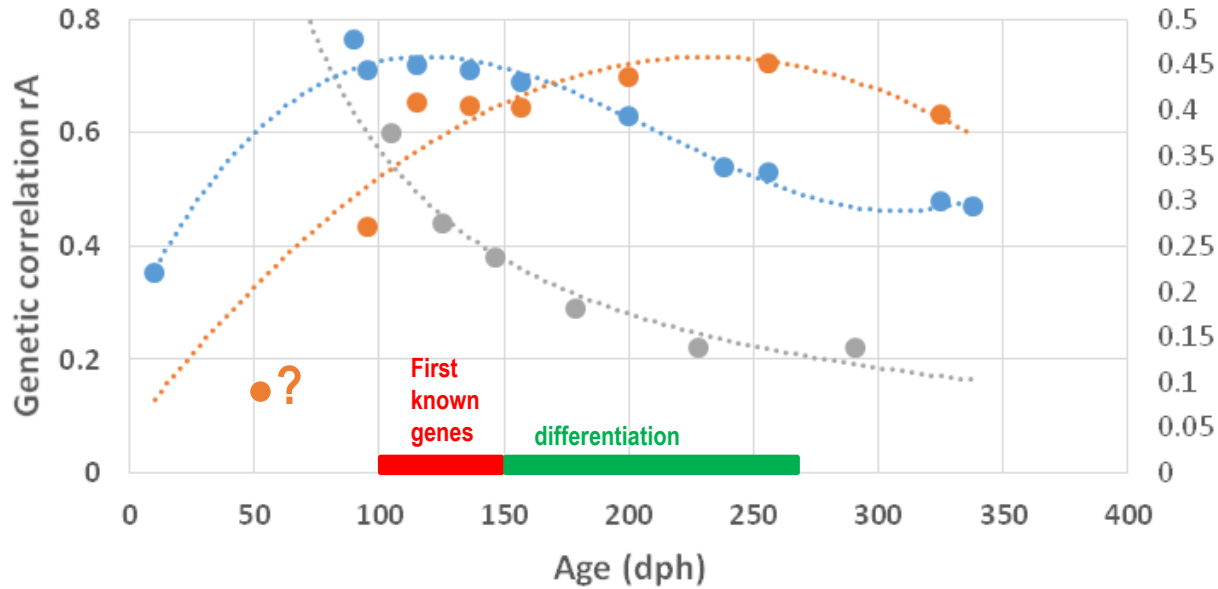


- DGC-Sex rA
- BW-sex rA
- Competus BL-sex rA



So what happens ?

sex tendency-DGC genetic correlations



- DGC-Sex r_A
- BW-sex r_A
- Competus BL-sex r_A
- BW sex dimorphism



In summary

- With micro-tagging and genotyping, we could obtain genetic parameters of sex and growth in sea bass starting at 570 mg (95 dph)
 - Sex-ratio is heritable in WMED sea bass ($h^2u=0.39$)
 - Genetic correlation of growth with sex tendency is highest at 95 dph
 - Future females are already 27% heavier than males at 95 dph
 - This is before the first published signs of differential gene expression
 - We hypothesize that differential growth around 70-120 dph can be a cause rather than a consequence of female differentiation
- ➔ Possible new approaches to manipulate sea bass sex-ratios ?



Questions ?

