

Does Domestication in Upper Yakima River Spring Chinook Sires Effect Juvenile Growth, Maturation Threshold or Minijack Production?

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Larsen, et al. 2019. *Maintaining a wild phenotype in a conservation hatchery program for Chinook salmon: the effect of managed breeding on early male maturation*. PLoS Biol 14(5):e0216168.

Study design: Common garden experiment to estimate the effects of the number of generations of culture on growth and early male maturation.

The 3 broodlines: INT[0–1], SEG[1], and SEG[2]

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INT[0–1]: Progeny of natural origin parents that spawned in the wild. Have an adipose fin and no tags or marks. Some hatchery origin fish may have successfully spawned in wild and contributed to natural production.

SEG[1]: Progeny of INT parents that were artificially spawned at CESRF. Have a clipped adipose fin and unique tags/marks.

SEG[2]: Progeny of hatchery origin parents exposed to 2 consecutive generations of hatchery culture. Have clipped adipose fin and unique tag/mark.

Return Year	First generation ^a				Second generation ^b				Third generation ^c				Fourth generation			
	Brood Year:															
	1997	1998	1999	2000 ^d	2001	2002 ^e	2003	2004 ^f	2005	2006	2007 ^g	2008	2009	2010	2011	2012
2000	3															
2001	4	3														
2002	5	4	3													
2003		5	4	3												
2004			5	4	3											
2005				5	4	3										
2006					5	4	3									
2007						5	4	3								
2008							5	4	3							
2009								5	4	3						
2010									5	4	3					
2011										5	4	3				
2012											5	4	3			
2013												5	4	3		
2014													5	4	3	
2015														5	4	3
2016															5	4
2017																5

Taken from: Larsen et al. 2019. Table 1.

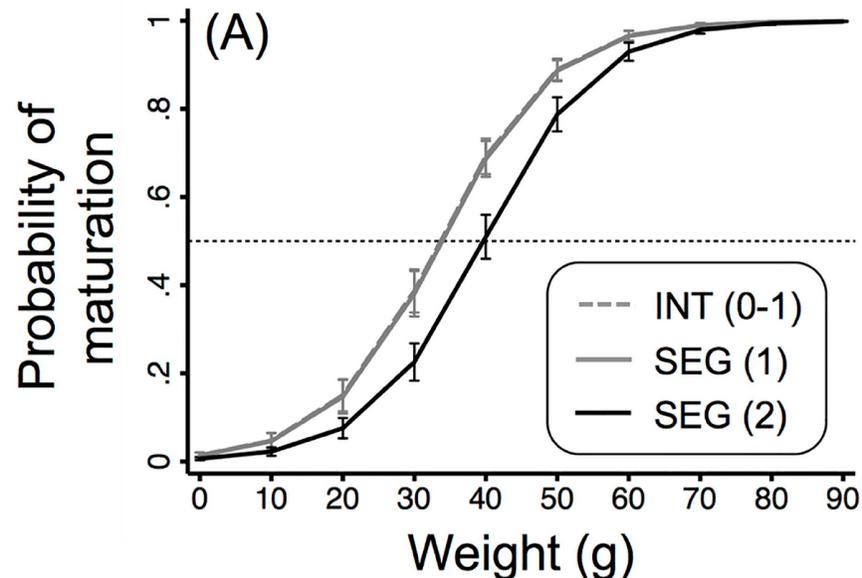
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Results:

1. Growth was not significantly different among the 3 broodlines.



Predictions based on the Larsen et al. (2019) results:

- 1. Growth during hatchery rearing should not significantly differ among broodlines: $INT[0-1] = SEG[1] = SEG[4]$.**
- 2. “50% maturation” threshold: $SEG[4] > SEG[1] = INT[0-1]$.**
- 3. Average age-2 minijack rates: $INT[0-1] = SEG[1] > SEG[4]$.**

Study Design

BY16 Factorial matings:

Return Year	First generation ^a				Second generation ^b				Third generation ^c				Fourth generation			
	Brood Year:															
	1997	1998	1999	2000 ^d	2001	2002 ^e	2003	2004 ^f	2005	2006	2007 ^g	2008	2009	2010	2011	2012
2000	3															
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2012											5	4	3			
2013												5	4	3		
2014													5	4	3	
2015														5	4	3
2016															5	4
2017																5

Taken from: Larsen et al. 2019. Table 1.

Study Design

	Females	Males (# gen culture)			
	SEG(1)	INT(0-1)	SEG(1)	SEG(4)	# Families
Factorial #1	S1 female 1	INT male 1	S1 male 1	S4 male 1	3

Study Design

BY16 Factorial matings:

Seven factorial matings.

One SH female crossed by 3 males;
one male from each of the 3 broodlines.

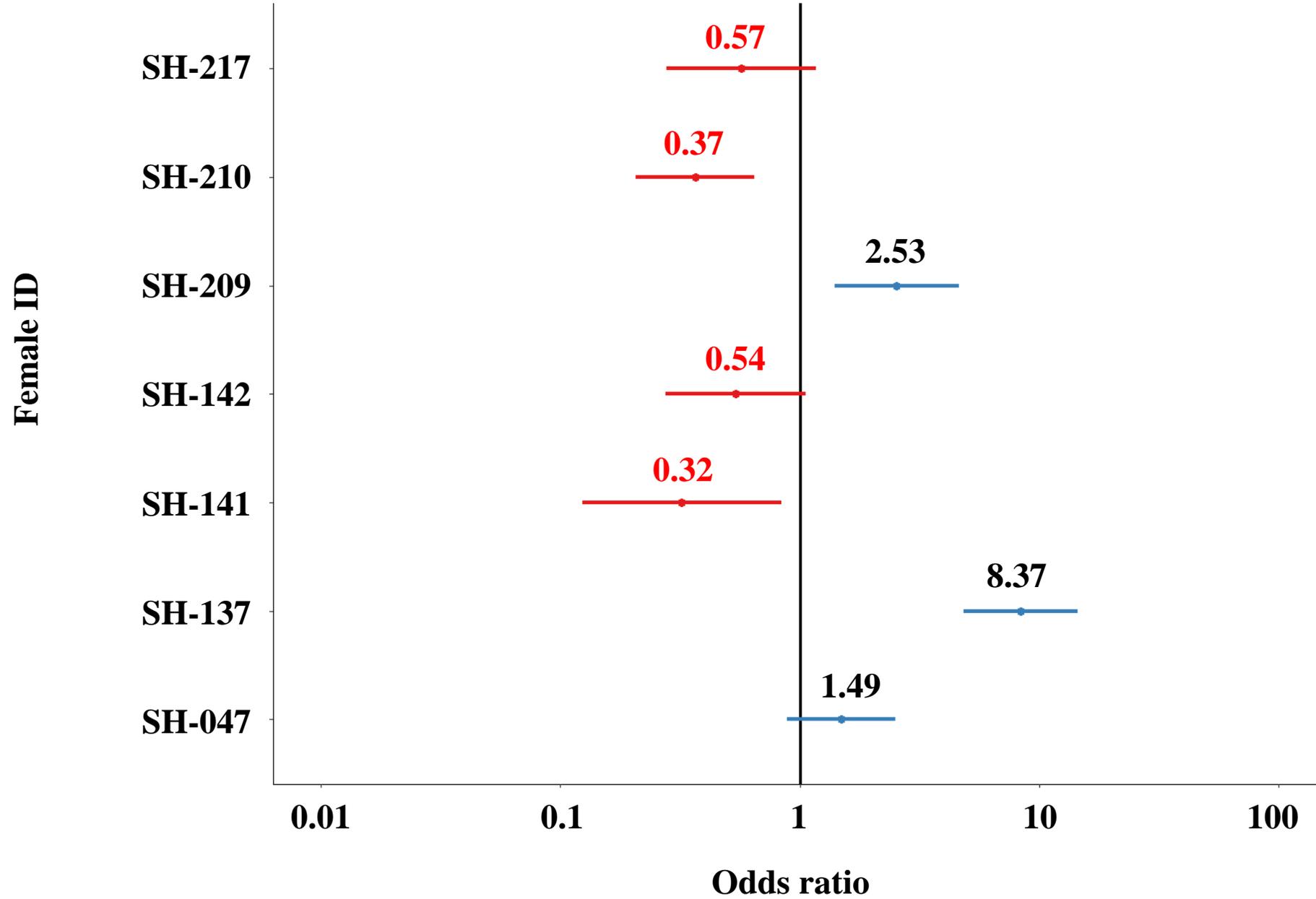
- BY16 Spawnings occurred in Sept. 2016.
- Fry were ponded in spring 2017 reared as a “common garden”.
- “Smolts” were sacrificed and sampled in April 2018.
11KT, FL and body weight and assigned to families via DNA pedigree analysis.

1. Growth not significantly different among INT, SEG[1], and SEG[4] broodlines.

Body Wt ~ SireBroodL + Maturity + (1 | FemaleID)

Fork Length ~ SireBroodL + Maturity + (1 | FemaleID)

Random Effects: Females (p<0.0001)



Model: Body Wt ~ SireBroodL + Maturity + (1 | FemaleID)

	<u>Estimate</u>	<u>Std. Error</u>	<u>df</u>	<u>t value</u>	<u>Pr(> t)</u>	
(Intercept)	0.3585	0.0171	8.6491	20.9533	<0.0001	***
INT	-0.0256	0.0106	506.7958	-2.4042	0.0166	*
SEG1	-0.0429	0.0107	506.8281	-4.0256	0.0001	***
Mature	0.1152	0.0108	488.3709	10.6650	<0.0001	***

Fork Length ~ SireBroodL + Maturity + (1 | FemaleID)

	<u>Estimate</u>	<u>Std. Error</u>	<u>df</u>	<u>t value</u>	<u>Pr(> t)</u>	
(Intercept)	0.3689	0.0157	9.2403	23.4921	0.0001	***
INT	-0.0293	0.0108	506.8978	-2.7166	0.0068	**
SEG1	-0.0381	0.0108	506.9357	-3.5246	0.0005	***
Mature	0.1102	0.0109	466.5120	10.1077	0.0001	***

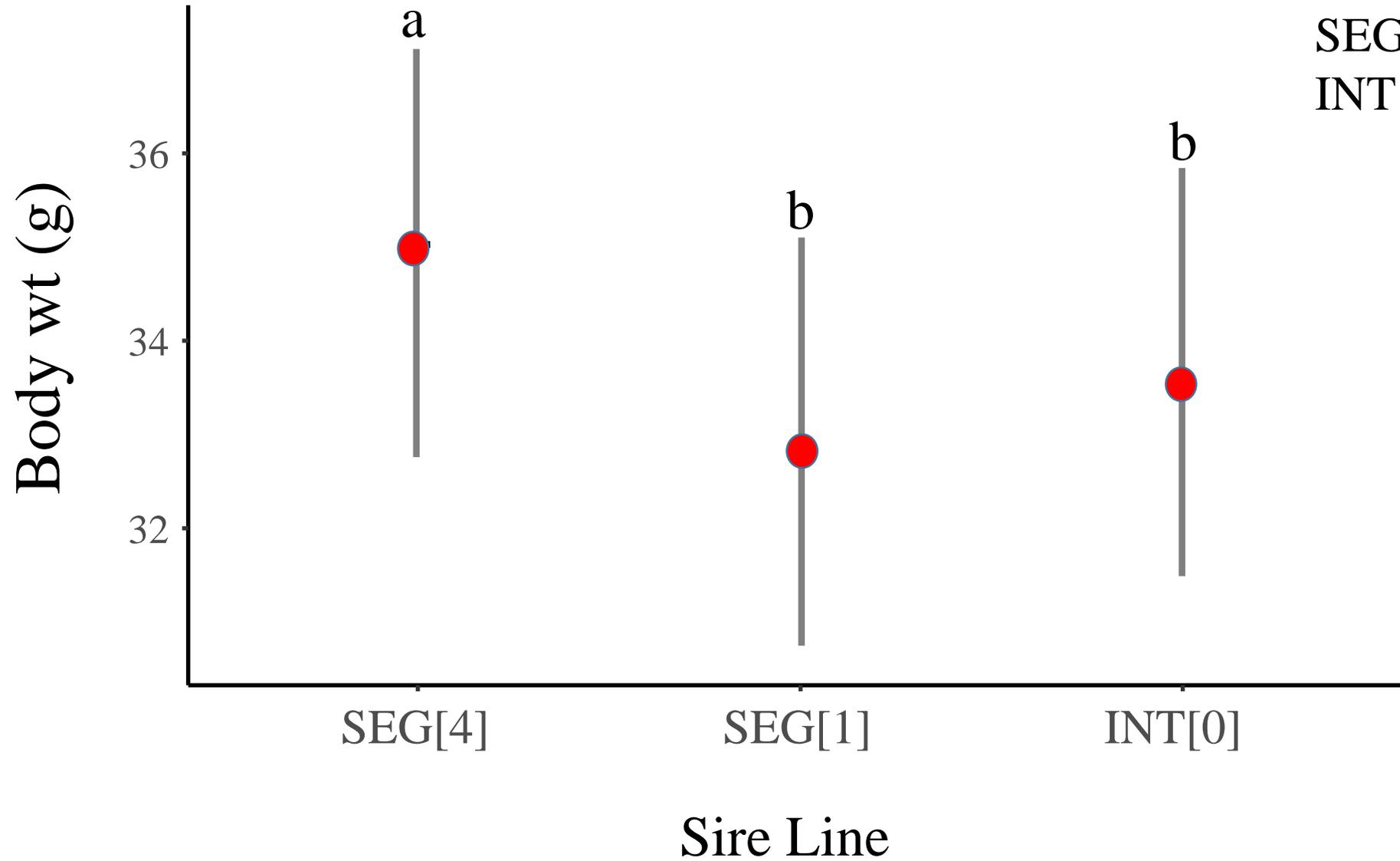
Body Weight

Paired differences

SEG4 - INT 1.5 g

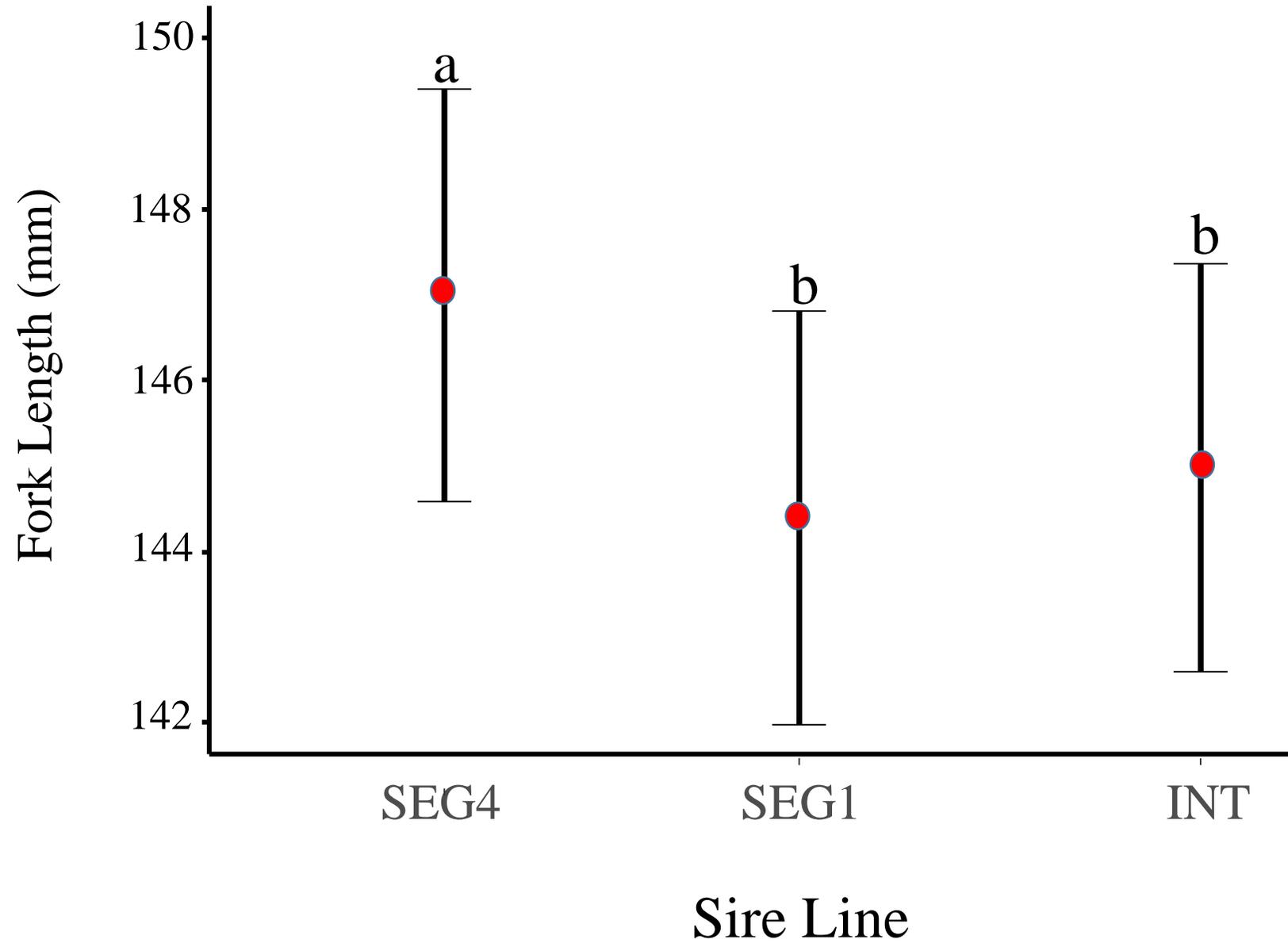
SEG4 - SEG1 2.2 g

INT - SEG1 0.7 g



Fork Length

Paired differences
SEG4 - INT 2.1 mm
SEG4 - SEG1 2.7 mm
INT - SEG1 0.8 mm



2. “50% *maturation*” threshold: $\text{INT} = \text{SEG}[1] < \text{SEG}[4]$.

Logistic model: Prob(MJ Maturity) ~ SireBroodL + lnBW + (1|FemaleID)

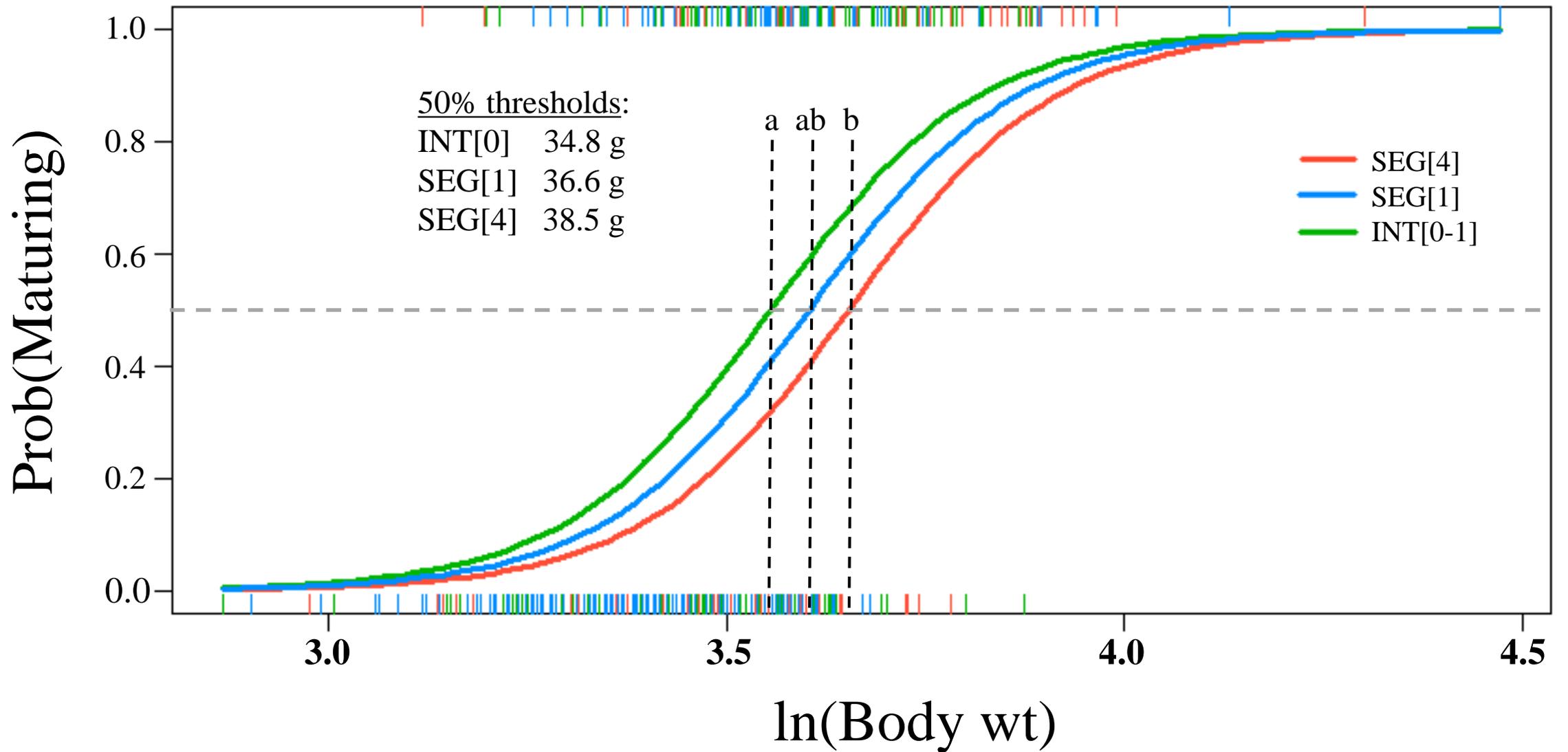
Random effects:

<u>Groups</u>	<u>Name</u>	<u>Variance</u>	<u>Std.Dev.</u>	<u>P-value</u>
FemaleID	(Intercept)	1.387	1.178	<0.0001 ***

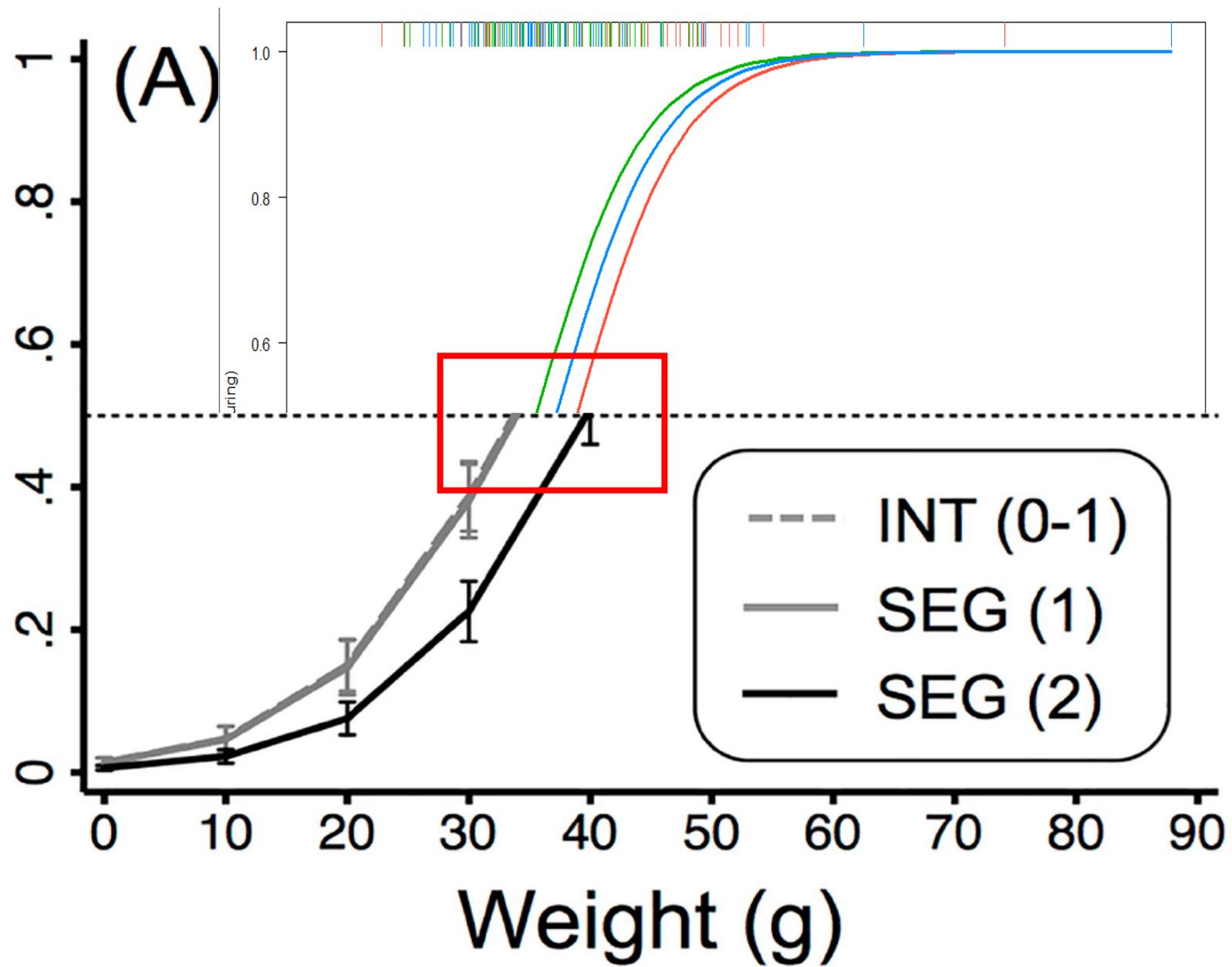
Number of obs: **516**, groups: **FCarcID, 7**

Fixed effects:

	<u>Estimate</u>	<u>Std. Error</u>	<u>z value</u>	<u>Pr(> z)</u>
(Intercept)	-6.0561	0.8164	-7.418	<0.0001 ***
INT (vs SEG4)	0.7565	0.3173	2.384	0.0171 *
SEG1 (vs SEG4)	0.3827	0.3185	1.202	0.2295
lnBW	12.3698	1.5371	8.048	<0.0001 ***

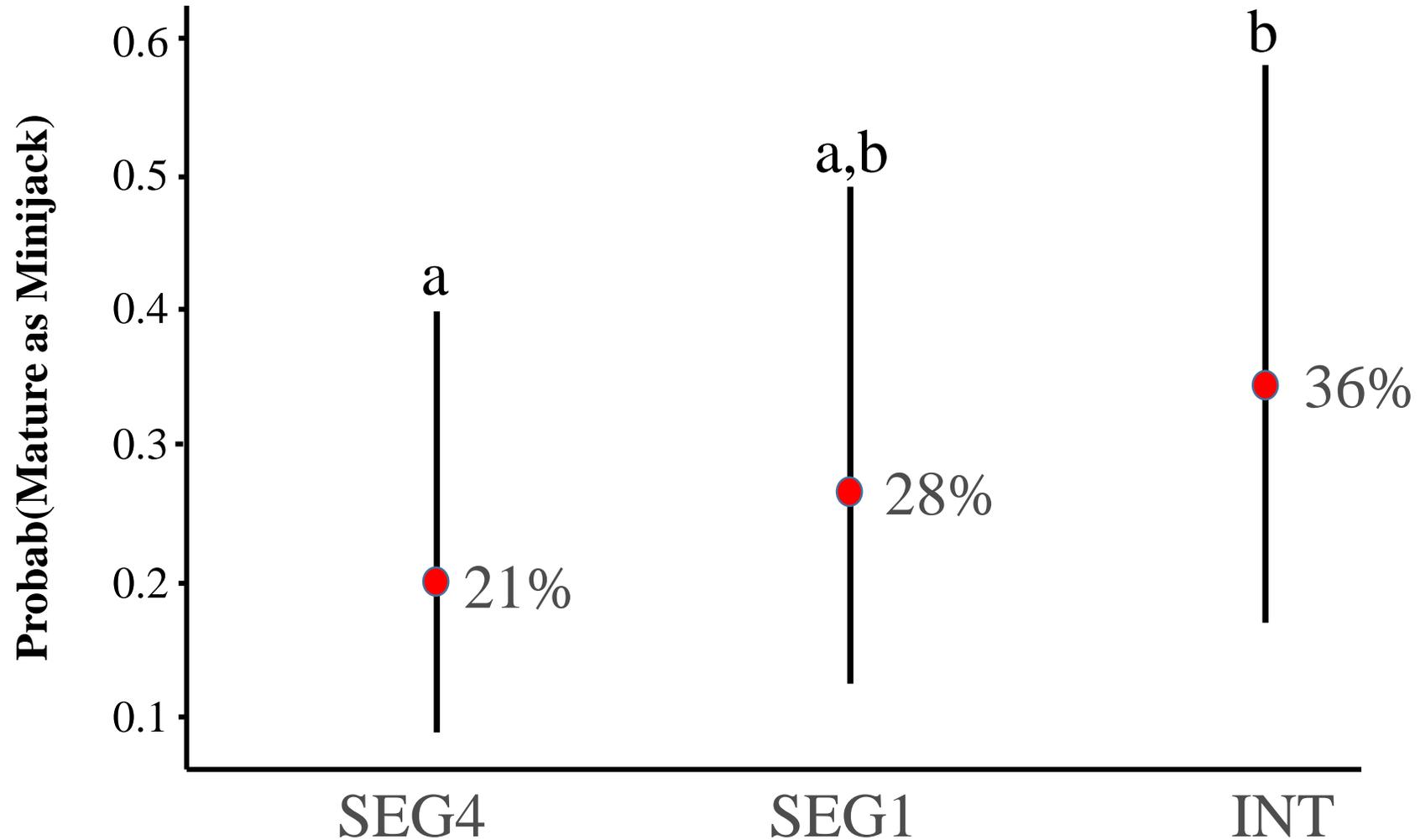


Probability of
maturation



2. “50% maturation” threshold: $INT = SEG[1] < SEG[4]$.

Estimated Minijack Proportions



Predictions based on the Larsen et al. (2019) results:

1. **Growth during hatchery rearing should not significantly differ among broodlines: $INT = SEG[1] = SEG[4]$.**

For both Body Wt and FL: $INT = SEG[1] < SEG[4]$

2. **“50% maturation” threshold: $INT = SEG[1] < SEG[4]$.**

$INT < SEG[4]$, $SEG[1]$ intermediate and not sign. different.

3. **Average age-2 minijack rates: $INT[0-1] = SEG[1] > SEG[4]$.**

$INT > SEG[4]$, but $SEG[1]$ intermediate and not sign. different.