

Semi-quantitative scales for the assessment of the severity and genetic parameters of skeletal abnormalities in seabream larvae



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Introduction

Jaw abnormalities develop frequently in reared fish and have significant effects on both morphology and performance (Boglione *et al.*, 2013). So far the genetic basis of jaw abnormalities has been examined after a binary phenotypic categorization of juvenile or adult fish (Nguyen *et al.*, 2016). In the present study we developed a set of semi-quantitative scales for the early assessment of jaw abnormalities in Gilthead seabream larvae. Developed scales were used to estimate the heritability of jaw deformities at the end of the larval rearing phase (39 dph).

Materials and Methods

A sample of 1400 larvae (39 dph) was taken from a mass spawning of 64 males and 63 females. Larvae were reared according to the standard methodology of the commercial hatcheries. All specimens were examined for the presence of abnormalities in the maxillaries (Ma), pre-maxillaries (Pm) and rostral cartilage (Rc) (double stain for bone and cartilage, Fig. 1A). After their phenotypic examination, all specimens were subjected to DNA extraction and parentage analysis.

Results

Macroscopically, jaw abnormalities consisted of pugheadness (Fig. 1B), lateral displacement of the upper jaw (Fig. 1C-D') and crossbite (Fig. 2).

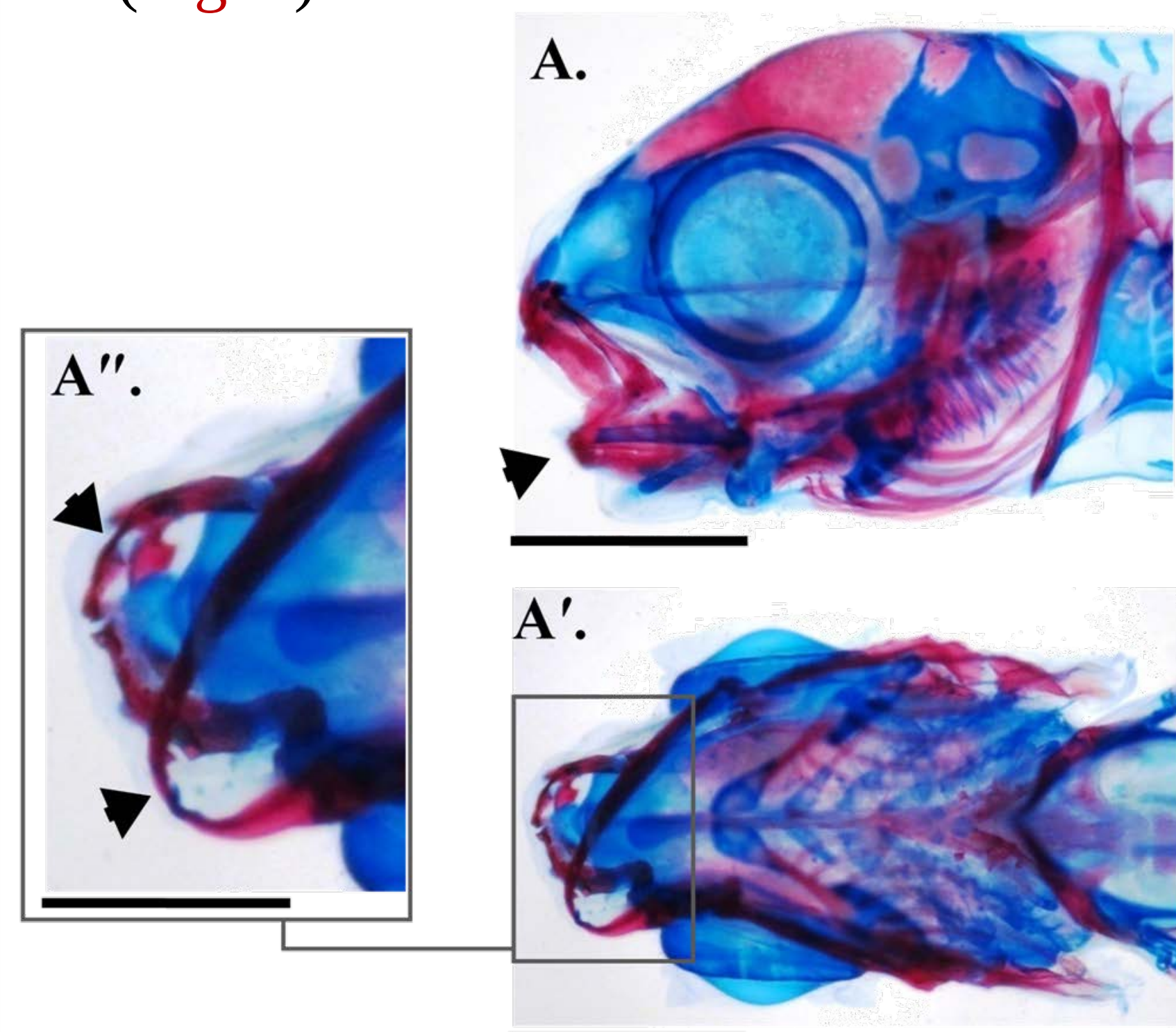


Fig. 2: Representative case of crossbite in a seabream larva of 10.6 mm TL. A, lateral view. A', A'', ventral view. Scale bars equal to 0.5 mm (A, A') and 0.25 mm (A'').

Upper jaw abnormalities were associated with abnormalities of the maxillaries, pre-maxillaries and rostral cartilage (*internal abnormalities*). The most frequent of them were the narrowing (n-Ma, 89.2±0.1%) and the inward bending of the maxillaries (b-Ma, 25.6±3.4%), the fusion of maxillaries with pre-maxillaries (f-Ma/Pm, 9.5±0.6%) and the partial to complete lack of the premaxillaries (a-Pm, 8.7±0.3%) (Fig. 3).

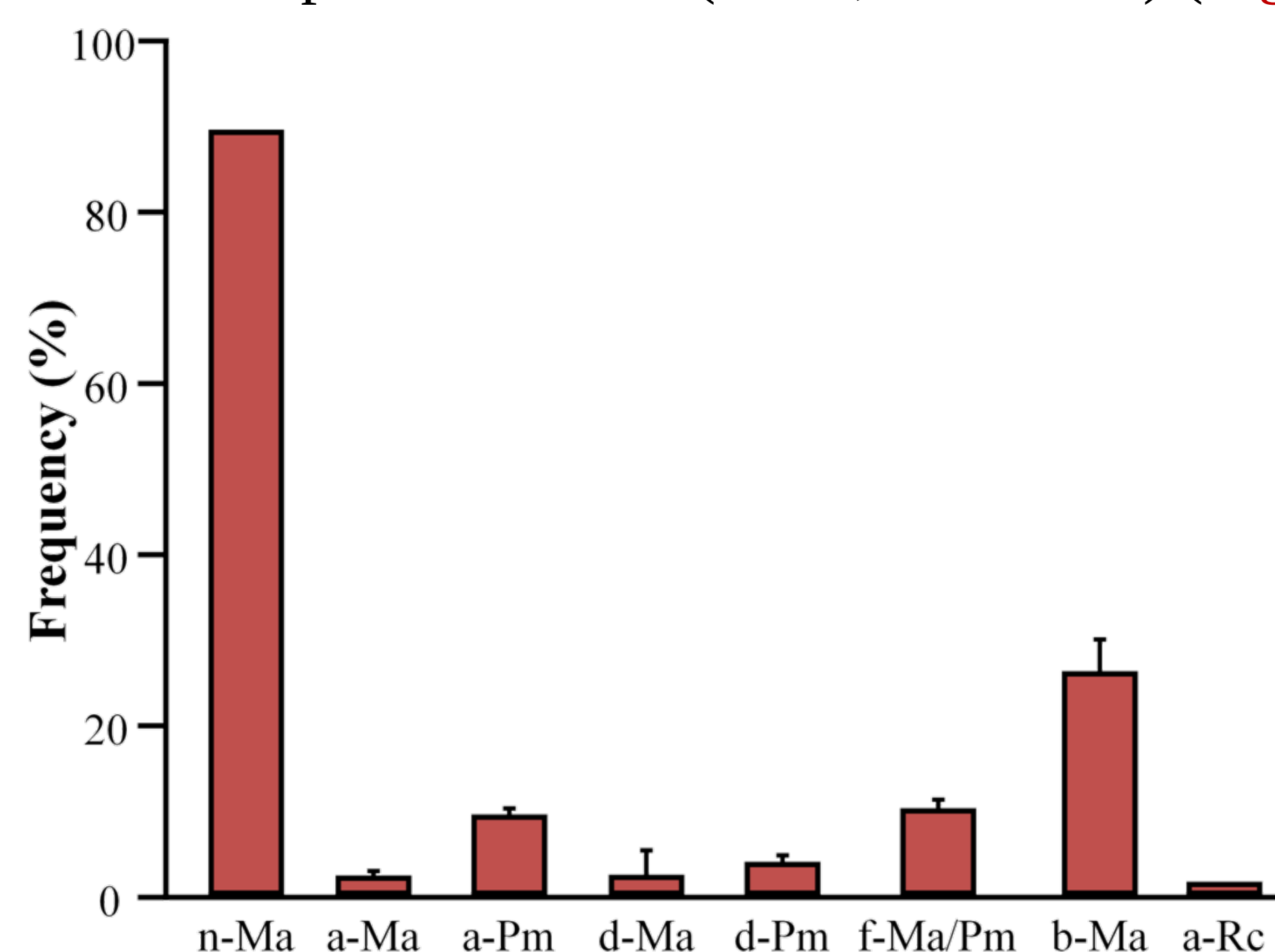


Fig. 3: Frequency of the different abnormalities affecting the skeletal elements of the upper jaws. n-Ma, narrowing of maxillaries. a-Ma, a-Pm, partial to complete lack of maxillaries and premaxillaries respectively. d-Ma, d-Pm, dorso-ventral curvature of maxillaries or premaxillaries respectively. f-Ma/Pm, fusion between maxillaries and premaxillaries. b-Ma, inwards bending of maxillaries. a-Rc, lacking of rostral cartilage.

Table	
Estimates (±SE) of heritabilities (h ²) for the different anatomical abnormalities.	
Abnormality	Mean h ² ±SE
n-Ma	0.13±0.04
a-Ma + a-Pm	0.02±0.02
d-Ma	0.01±0.02
d-Pm	0.00±0.02
f-Ma/Pm	0.23±0.06
b-Ma	0.06±0.03
a-Rc	0.00±0.02

Conclusions

- The first time where both qualitative and quantitative evaluation of skeletal abnormalities took place in fish larvae
- Full characterization of the phenotypic range of abnormalities during the phase of their development
- Tremendous potential of the approach for the selective breeding programs

Acknowledgements

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References

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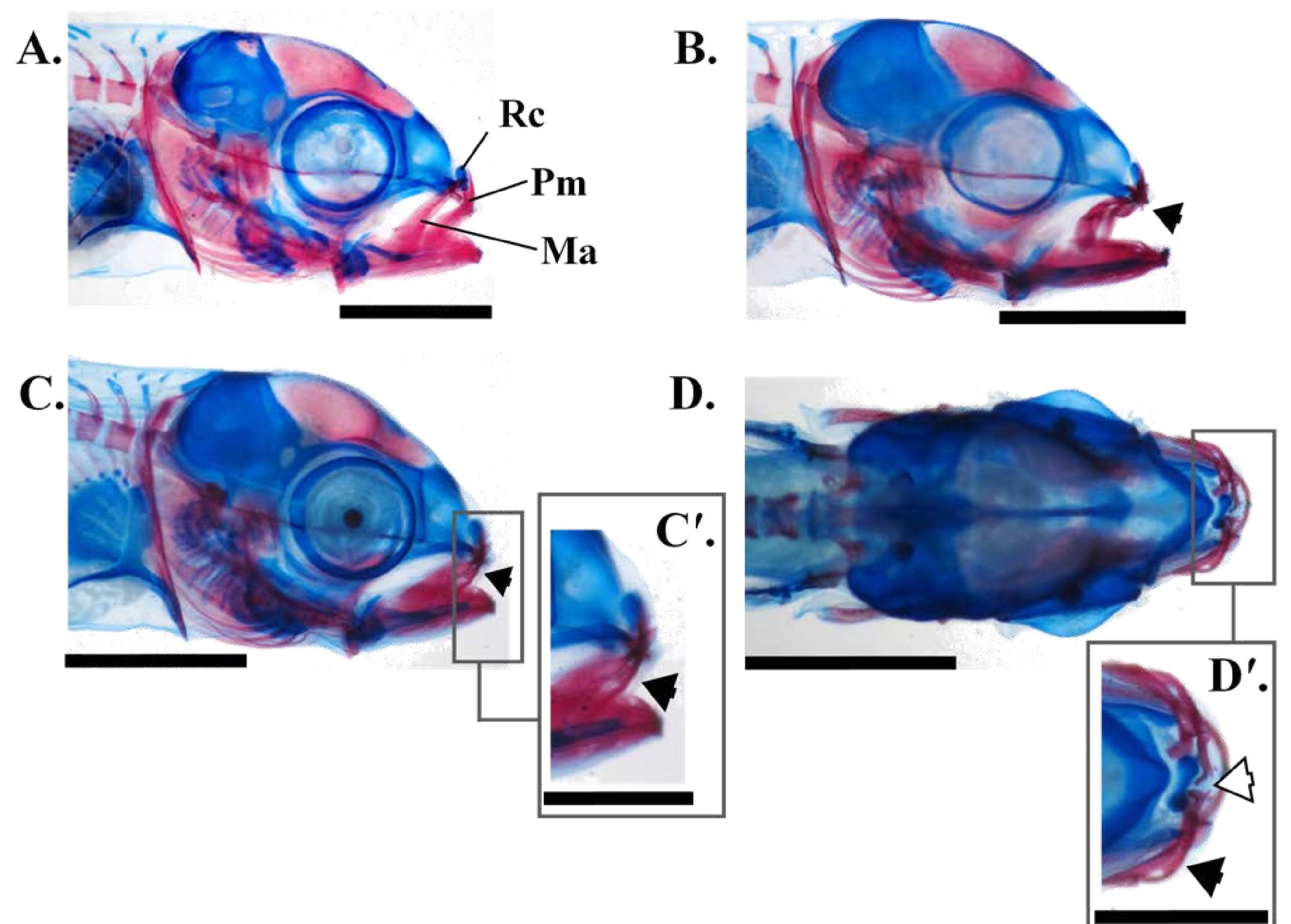


Fig. 1: Jaw abnormalities in larval samples. A. Normal. B. Pugheadness. C-C'. slight fusion of the left maxillary and premaxillary bones (black arrow). D-D'. Severe fusion of the left maxillary and premaxillary (black arrow), resulting to a lateral displacement of the upper jaw (white arrow). Rc, rostral cartilage. Ma, maxillary bone. Pm, premaxillary bone. Scale bars equal to 0.5 mm (A-D) and 0.25 mm (C'-D').

Based on the severity of the abnormalities, the examined larvae were categorized on a quality scale of 2 to 13 levels (depending on the index, Fig. 4). Genetic analysis revealed that the fusion of maxillaries with pre-maxillaries, and the narrowing of maxillaries presented significant heritabilities (0.23±0.06 and 0.13±0.04 respectively, Table).

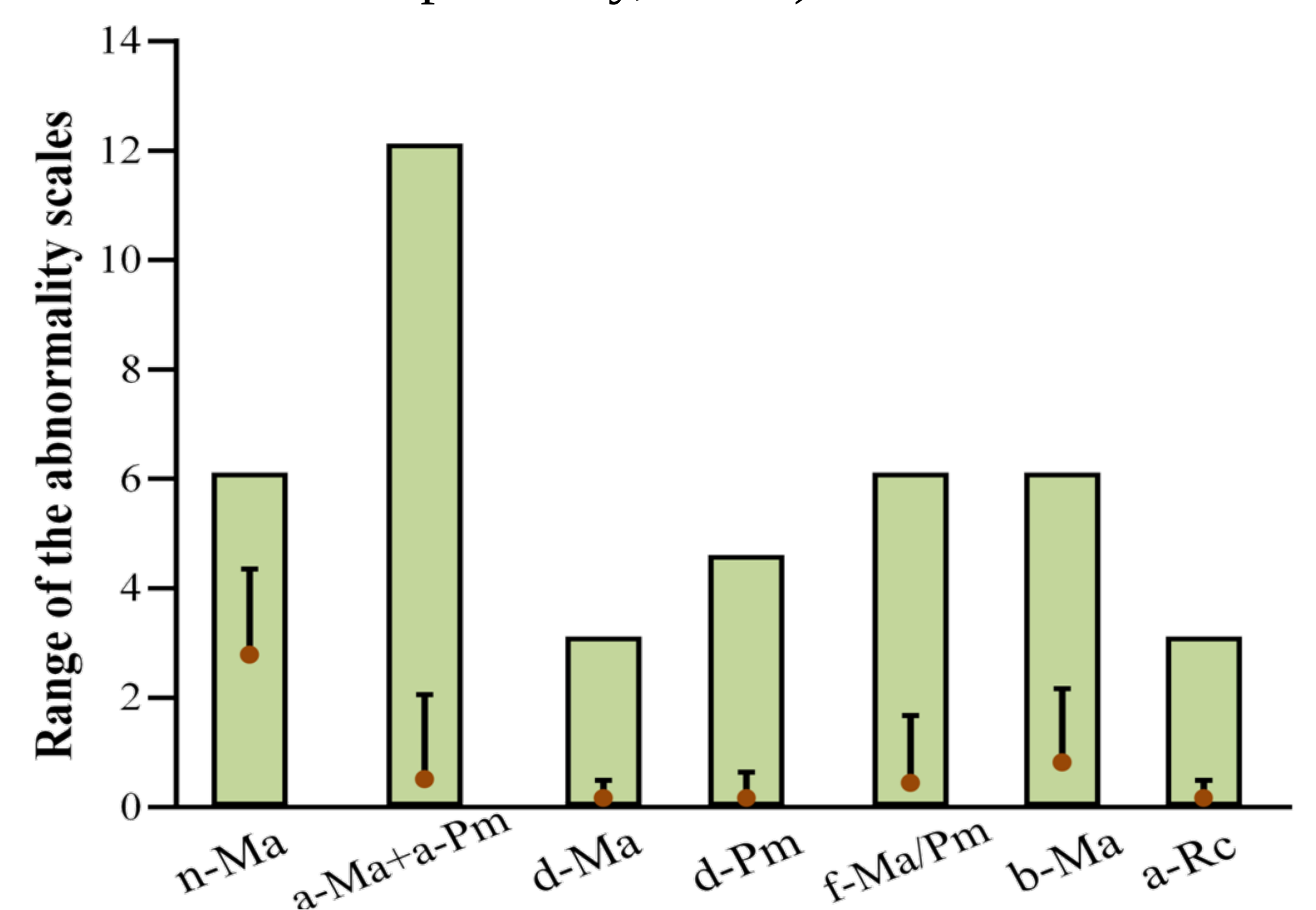


Fig. 4: Mean, SD (error bars) and range (columns) of the calculated abnormality scales. The mean indices are proportional to the severity of the abnormalities.