

**Axial growth gradients across the post-protaspid ontogeny of the Silurian trilobite
*Aulacopleura koninckii***

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Appendix A

Calculation of the CCS-based holaspid stage

Assuming a constant per-stage growth rate of CCS across the whole ontogeny, OLS regression parameters (a and b) of $\ln(\text{CCS})$ vs. stage, estimated in the ontogenetic interval s9-s17, are used to calculate the putative stage ($\text{stage}_{\text{CCS}}$) of any given holaspid specimen i .

From the regression equation

$$\ln(\text{CCS}) = a + b * \text{stage}$$

solving for stage, for a specimen i , we can obtain

$$\text{stage}_{\text{CCS}}(i) = (\ln(\text{CCS}(i)) - a) / b = (\ln(\text{CCS}(i)) - 0.29329) / 0.08440$$

Appendix B

Fitting of meraspid cephalon growth data

Nonlinear least squares regression procedure was performed with the software Statgraphics Centurion ver. XVI, using Marquardt's algorithm as an estimation method.

The *TGexp* model (Fusco et al. 2014) set the local per-stage growth rate $g(x)$ at each point along the cephalon as a decaying exponential function from the anterior, defined in the closed interval of relative positions within the region $[0,1]$

$$g(x) = a + be^{-w(1-x)}$$

By integration of $g(x)$ and imposing the integral in $[0,1]$ to be equal to the average per-stage growth rate of the cephalon during meraspid period (r), the following function can be derived (Fusco et al. 2014)

$$Z(x) = x + \frac{-be^{-w} + be^{-w(1-x)} + bx(-1 + e^{-w})}{rw}$$

where, for a landmark at position x along the cephalon at a given stage, $Z(x)$ gives the relative position of the same landmark at the following stage. b and w are the fitting parameters, r is a fixed parameter equal to the meraspid average per-stage growth rate of CEL ($r = 1.08484$, estimated in the ontogenetic interval s9-s17).

Schematics of the fitting of meraspid cephalon data

Dependent variable: $RV(x)$

Independent variable: x

Fitting parameters: b, w

Fixed parameter: r

Fitting function: $RV(x) = Z(x)/x$

Observed data are pairs $(x, RV(x))$, where x is the average relative position within the cephalon of given positional marker (e.g., the posterior boundary of FAL) at a given meraspid stage, and $RV(x)$ is the relative variation in the position of the same marker at the following stage (see text).

Appendix C

Fitting of holaspid cephalon and trunk growth data

Nonlinear least squares regression procedure was performed with the software Statgraphics Centurion ver. XVI, using Marquardt's algorithm as an estimation method.

The *TGexp* model (Fusco et al. 2014) set the local per-stage growth rate $g(x)$ at each point along a given body region as a decaying exponential function (from the anterior in the cephalon, from the posterior in the trunk), defined in the closed interval of relative positions within the region $[0,1]$

$$g(x) = a + be^{-w(1-x)}$$

Imposing the integral of the function in $[0,1]$ (Fusco et al. 2014) to be equal to the average per-stage growth rate of the region during holaspid period (r), we obtain the following expression for $g(x)$

$$g(x) = \frac{b(-1 + e^{-w}) + rw}{w} + be^{-w(1-x)}$$

where b and w are the fitting parameters, and r is a fixed parameter ($r = 1.08864$ for CEL, $r = 1.10254$ for TRL, both estimated by RMA regressions vs. CCS-based stage on holaspid data).

Schematics of the fitting of holaspid cephalon and trunk data

Dependent variable: $GR(x)$

Independent variable: x

Fitting parameters: b, w

Fixed parameter: r

Fitting function: $GR(x) = g(x)$

Observed data are pairs $(x, GR(x))$, where for a given body part (e.g., a given thoracic segment), x is the average relative position of the center of that part within its region (e.g., the trunk), and $GR(x)$ is average per-stage growth rate of that part, estimated from its allometric coefficient with respect to CCS (see text).

Appendix D

Holaspid PYL size progression for an average morphotype t20 specimens under the hypothetical conservation of the trunk growth gradient during holaspis period

Starting values

Pygidial length at stage s20, $PYL(s_{20})$, is obtained from OLS regression of $\ln(PYL)$ vs. stage in the ontogenetic interval s9-s17 by extrapolation

$$PYL(s_{20}) = \exp(-0.7357+0.0098*20) = 0.5831$$

the same for trunk length at stage s20

$$TRL(s_{20}) = \exp(-0.3924+0.1091*20) = 1.7897$$

and from their ratio it is obtained the relative position within the trunk of the anterior border of the pygidium at stage s20,

$$RPP(s_{20}) = 1-PYL(s_{20})/TRL(s_{20}) = 0.9026$$

Progression of PYL from stage s20 to s32

First it is calculated the progression of the relative position of the anterior border of the pygidium from stage s21 to stage s32. Starting from $RPP(s_{20})$, the following RPP values have been calculated applying iteratively the function $Z(x)$ of the model *TGexp* in Fusco et al. (2014) for the meraspis trunk gradient

$$RPP(s_{x+1})=Z(RPP(s_x))$$

with

$$Z(x) = x + \frac{-be^{-w} + be^{-w(1-x)} + bx(-1 + e^{-w})}{rw}$$

where, for a landmark at position x along the trunk at a given stage, $Z(x)$ gives the relative position of the same landmark at the following stage. Parameters were set to $r = 1.11528$, $b = 0.29232$ and $w = 5.00009$, as obtained from least squares regression fittings in Fusco et al. (2014).

Then, from these values, the PYL at each stage s_x is obtained by multiplying the complement to 1 of RPP by TRL at the corresponding stage

$$PYL(s_x) = (1-RPP(s_x))*TRL(s_x)$$

where $TRL(s_x)$ is obtained from RMA regression of $\ln(TRL)$ vs. CCS-based stage on holaspis data

$$TRL(s_x) = \exp(-0.18107+0.09762*s_x)$$