# Updated GLM analyses of parasite data corroborate the sardine multi-stock hypothesis

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## Introduction

Results from GLM analyses of three indices of infection of sardine by a digenean "tetracotyle" type metacercarian parasite using data collected from commercial catch samples taken during 2011 and 2012 were presented at the SWG(PEL) meeting held on 19/03/2014 (van der Lingen and Hendricks 2014). Significant differences in the prevalence of infection, mean infection intensity and mean parasite abundance between sardine from the western stock and those from the southern stock have convincingly supported the multistock hypothesis of this species, with all indices being higher in western fish in comparison to southern fish. Initial results of analyses (not GLM) of parasite infection data collected during 2013 were also presented at that meeting, and the SWG(PEL) requested that the GLM analyses be updated to include the new data. This document presents those results.

## Methods and materials

Details of the GLM analyses are provided in van der Lingen and Hendricks (2014). A total of 2 317 commercially-caught sardine have now been examined, and the number of fish examined and the number of samples collected by putative stock and year are given in Table 1. The three indices of infection used were: infection prevalence (% of the sample infected), mean infection intensity (number of parasites.infected fish$^{-1}$) and mean parasite abundance (number of parasites.fish$^{-1}$).

**Table 1:** Number of fish examined (and number of samples) for "tetracotyle" type metacercariae parasites by putative stock, 2011-2013.

| Year | Western | Southern |
|---|---|---|
| 2011 | 268 (12) | 169 (7) |
| 2012 | 373 (16) | 508 (20) |
| 2013 | 358 (11) | 641 (23) |

Outputs from the updated GLMs are shown in Table 2.

**Table 2:** Outputs from the updated (2011-2013) GLMs for prevalence of infection, infection intensity and parasite abundance of "tetracotyle" type metacercariae in sardine; note that the three factors that explain the highest %s of variation in each index are given in bold.

| **GLM (and pseudo-$R^2$ value)** | **Model structure** | **AIC** | **Residual Dev.** | **Δ Dev.** | **% Dev. explained** | ***p*($c^2$)** |
|---|---|---|---|---|---|---|
| Prevalence of infection – Binomial GLM: (0.27) | | | | | | |
| | *Null* | 3135.6 | 3133.6 | | | |
| | ***+Stock*** | **2831.7** | **2827.7** | **-305.9** | **35.79** | **< 0.001** |
| | ***+Year*** | **2609.5** | **2601.6** | **-226.1** | **26.45** | **< 0.001** |
| | *+Season* | 2547.7 | 2533.7 | -67.9 | 7.94 | < 0.001 |
| | ***+CL*** | **2366.9** | **2350.9** | **-182.8** | **21.39** | **< 0.001** |
| | *+Stock*Season* | 2323.9 | 2301.9 | -49 | 5.73 | < 0.001 |
| | *+Year*CL* | 2304.9 | 2278.8 | -23.1 | 2.70 | < 0.001 |
| Infection intensity – truncated negative binomial GLM: (0.24) | | | | | | |
| | *Null* | 5011.8 | 1189.97 | | | |
| | ***+Stock*** | **4913.6** | **1068.16** | **-121.81** | **39.54** | **< 0.001** |
| | ***+Year*** | **4874.1** | **1005.31** | **-62.85** | **20.40** | **< 0.001** |
| | *+Season* | 4834.3 | 967.57 | -37.74 | 12.25 | < 0.001 |
| | ***+Log(CL)*** | **4796.6** | **925.89** | **-41.68** | **13.53** | **< 0.001** |
| | *+Stock*Season* | 4781.5 | 904.07 | -21.82 | 7.08 | < 0.001 |
| | *+Year*Log(CL)* | 4763.5 | 881.94 | -22.13 | 7.18 | < 0.001 |
| Parasite abundance – negative binomial GLM: (0.41) | | | | | | |
| | *Null* | 5011.8 | 3199.7 | | | |
| | ***+Stock*** | **4913.6** | **2646.5** | **-553.2** | **40.78** | **< 0.001** |
| | ***+Year*** | **4874.1** | **2455.4** | **-191.1** | **14.09** | **< 0.001** |
| | *+Season* | 4834.3 | 2274.7 | -180.7 | 13.32 | < 0.001 |
| | ***+Log(CL)*** | **4796.6** | **1969.4** | **-305.3** | **22.50** | **< 0.001** |
| | *+Stock*Season* | 4781.5 | 1903.6 | -65.8 | 4.85 | < 0.001 |
| | *+Year*Log(CL)* | 4763.5 | 1843.1 | -60.5 | 4.46 | < 0.001 |

The additional data corroborate previous results, but now show that *Stock* explains the majority of variation in the data for all three indices whereas previously *Year* had explained the majority of variation in the data in the Infection prevalence GLM and *Stock* the majority in the Infection intensity and Parasite abundance GLMs. Interannual variability in parasite loads is larger and the seasonal signal is weaker than previously estimated, and the *Year*CL* (or *Year*Log(CL)*) interaction has become a significant parameter indicating that there is a

difference in the pattern of infection at length by year within each stock. Results from the updated GLM for Infection prevalence are shown in Figure 1.

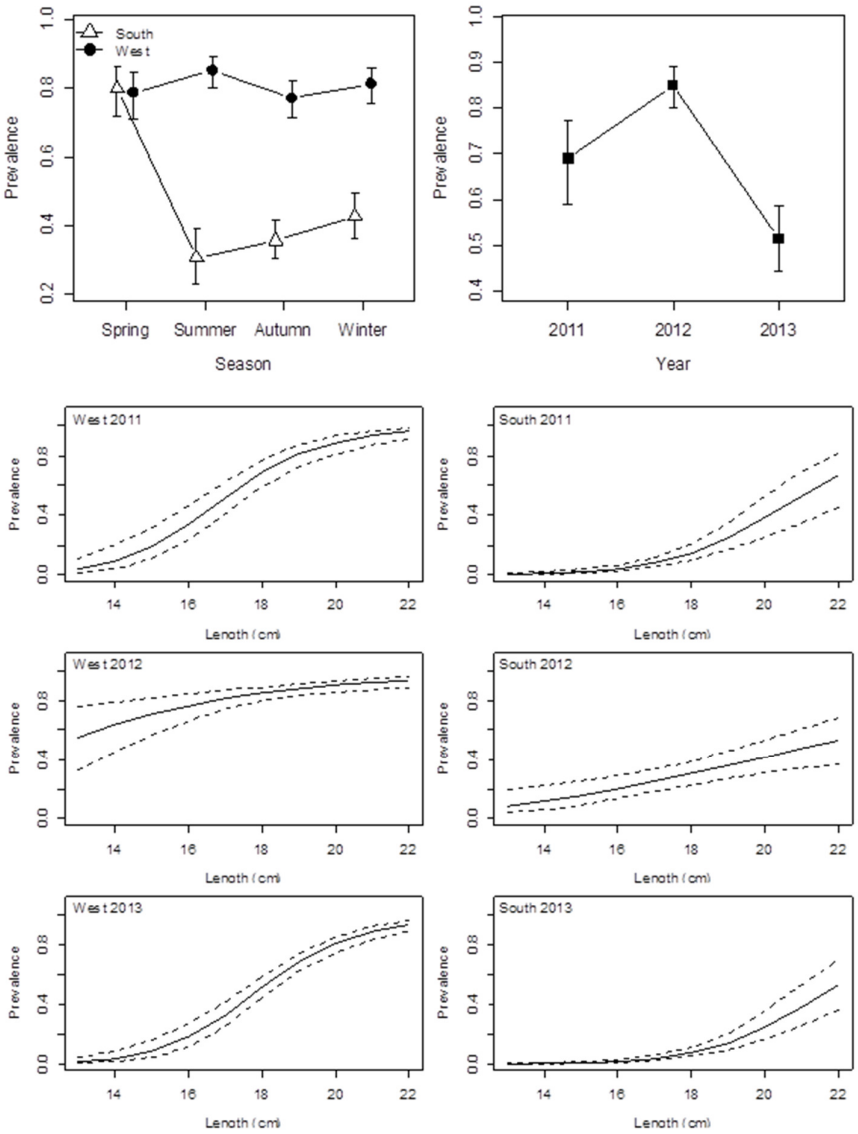


**Figure 1:** Outputs from the updated Infection prevalence GLM showing predicted prevalence (%) by *Stock* and *Season*, and by *Year* (upper plots, normalized for a fish of 18.1 cm *CL*), and predicted infection prevalence by *CL* for each stock during each year (with 95% confidence limits).

Analysis of the infection prevalence data using General Additive Modelling (GAM) showed virtually no difference in output plots (Figure 2) compared to GLM outputs.

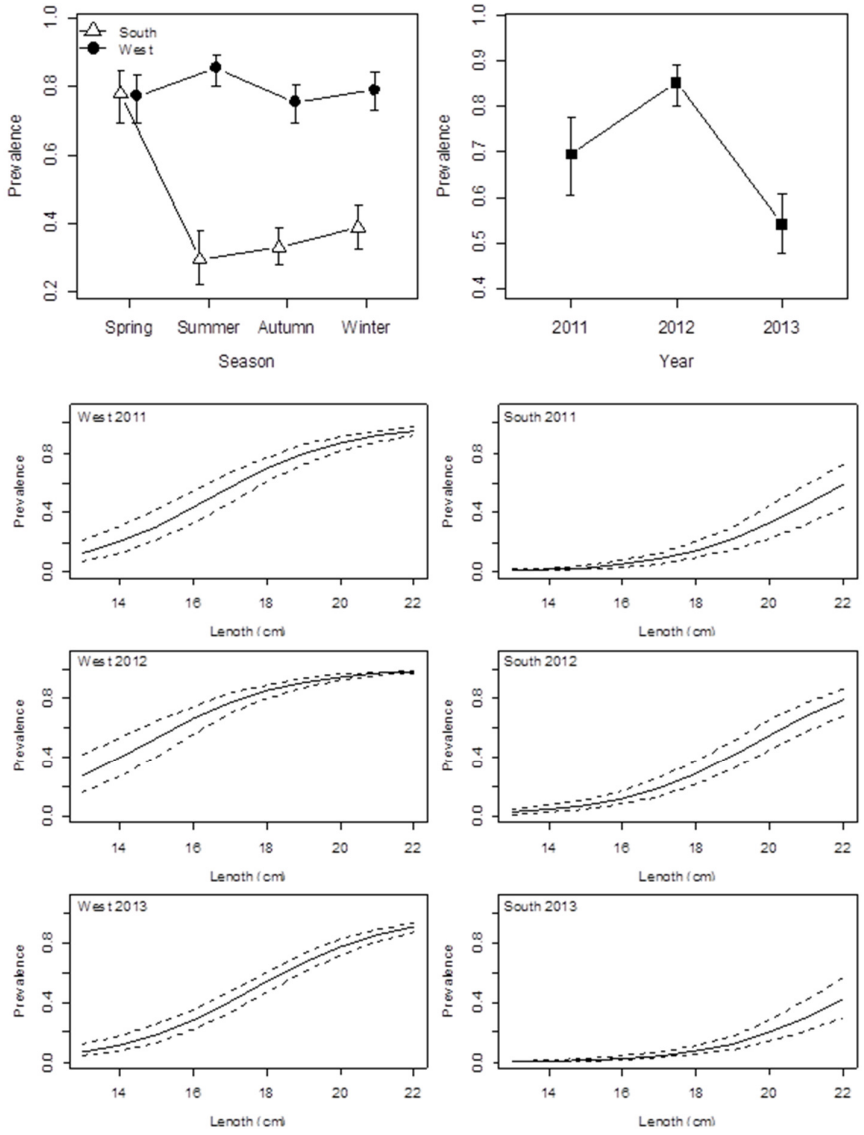


**Figure 2:** Outputs from a GAM of Infection prevalence (plots as for Fig. 1).

## References

van der Lingen, C.D. and Hendricks, M. (2014). Update on "tetracotyle" type metacercarian infection data and implications for sardine movement. FISHERIES/2014/MAR/SWG-PEL/08, 8P.