



Updated results for candidate MP using CK and GT data only

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In 2018, we explored the performance of a candidate management procedure (MP) that uses only gene-tagging (GT) and close-kin (CK) data (MP “D25” in 2018). The “D25” MP has been renamed “A49” and re-tuned to the reference set of updated operating models. This reference set of operating models, for MP testing, includes the “UAM1” scenario for additional sources of unaccounted mortality.

The underlying model and operation of the “A49” MP is the same as the “rh12” MP described in Hillary et al, 2019, but the CPUE component is excluded. Weighting and gain parameters differ from “rh12”, to allow the “A49” MP to meet the tuning objective. As was the case in 2018, it is more difficult to get this MP to tune to the B30% by 2035 tuning objective, and the preliminary results below are for the 35% by 2040 tuning objective only (Figure 1). Additional results will be provided to the meeting when available.

The median TAC trends for this initial tuning of a GT and CK-only MP (“A49”) are more conservative in the early years than the “rh12” MP results in Hillary et al., 2019. Average annual variation (AAV) in TAC is low, and the probability of TAC increases followed by a decrease (P(2up1down)) is very low. The probability of SSB being above 20%SSB₀ by 2035 is very high.

Figure 1 Violin plot, TAC and relative SSB. Preliminary results for “A49” MP, which uses gene-tagging and close-kin data only, tuned to B35% by 2040.



