Update on the Phase 7 Main Bay Model (MBM)

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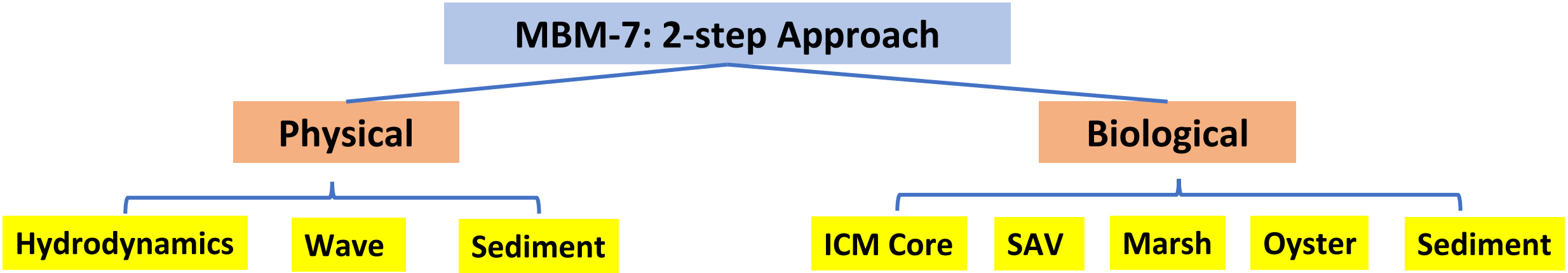
Outline

- ❑ Overview on the phase-7 MBM status
  - MBM incorporated pure P7 loading (beta version)
  - Skill is comparable with CH3D-ICM
- ❑ Improvement on MBM-7 nutrient simulation on systematic biases
  - ❑ POM (POC/PON/POP) simulation is improved
  - ❑ DOC simulation is greatly improved
  - ❑ DON/POP are also improved, but more improvement is needed
  - ❑ NH4/NO3 are also improved compared to baseline

Phase-7 MBM Structure

- **Phase-7 MBM includes physical and biological components.**
- **Each component also comprise several sub-modules. Note sediment module is activated at both steps**
- **We has established a compressive and streamlined modeling workflow.**



- Watershed flow
- Shoreline erosion
- Boundary conditions of elevation, velocity, TS and wave inputs
- Initial conditions of hydrodynamics and sediment
- Atmospheric Forcing: ERA5

- Watershed nutrient loading
- Shoreline erosion for sediment and nutrients
- Atmospheric nutrient deposition

Overview On Phase-7 MBM Status

- ❑ The hydrodynamics of MBM was well calibrated. Our current calibration focuses on the ICM simulation.

- ❑ MBM has completely switched to pure phase-7 nutrient loading (July 2025 beta): watershed nutrient inputs, atmospheric nutrient deposition, and shoreline erosion. We greatly thank WSM team (Gopal, Richard, et. al) for providing the MBM loadings.

- ❑ We has established a MBM baseline (RUN14v) with model skill comparable to phase-6 CH3D-ICM.

- ❑ Preliminary Internal review on the MBM performance was conducted (Thank Carl). We got many constructive comments/suggestions. Based on these comments, we further improved the MBM.

Overview: Assessment of Watershed Loading between P6 and P7: Major Rivers

- ❑ We assessed nutrient concentrations from watershed loadings against nearby downstream CBP observations
- ❑ P7 (beta) nutrient concentrations match better with observations at RIM stations than P6
- ❑ Note: P6 refers to the hybrid loading (20250101_P7beta_Hybrid).

RMSE between WSM nutrient conc. and the nearby CBP observations

Worse | Close | Better

Regions	NH4	NO3	PO4	TN	TP	TSS ✓
Susquehanna	(0.0432,0.0437)	(0.2875,0.2991)	(0.0089,0.0106)	(0.3310,0.3425)	(0.0280,0.0243)	(11.5428,13.6488)
Patuxent	(0.1483,0.1814)	(0.6331,0.9060)	(0.0455,0.0680)	(0.7464,1.1992)	(0.0866,0.1336)	(35.6555,32.6645)
Potomac	(0.0963,0.0931)	(0.5480,0.5792)	(0.1282,0.1275)	(0.7700,0.5674)	(0.0637,0.1044)	(16.6087,14.0334)
Rappahannock	(0.0334,0.0430)	(0.2594,0.3228)	(0.0178,0.0133)	(0.6914,0.5231)	(0.2182,0.1911)	(104.7578,97.1951)
James	(0.0370,0.0414)	(0.2161,0.1410)	(0.0683,0.0488)	(0.3482,0.3166)	(0.1287,0.1314)	(66.3107,73.1921)
Choptank	(0.0424,0.0491)	(0.7703,0.3458)	(0.0272,0.0211)	(0.6864,0.3682)	(0.0919,0.0719)	(20.3460,8.3691)
Mattaponi	(0.0344,0.0404)	(0.1240,0.1050)	(0.0145,0.0215)	(0.3505,0.2198)	(0.0650,0.0682)	(15.3698,17.6690)
Pamunkey	(0.0298,0.0534)	(0.1702,0.1721)	(0.0209,0.0356)	(0.3722,0.2859)	(0.0548,0.0755)	(47.7405,53.3133)
Appomattox	(0.0343,0.0345)	(0.1621,0.1739)	(0.0076,0.0094)	(0.3941,0.2013)	(0.0292,0.0291)	(15.6633,13.1813)

In brackets, the 1st number is P6 error, and 2nd number is P7 error.

Overview: comparison between CH3D-ICM (MBM-6) and MBM-7 simulations

❖ MBM-7 results are mostly comparable to MBM-6.

- ❑ For most variables, the RMSEs are very close between two MBM results.
- ❑ Compared to MBM-6, MBM-7 has slightly larger errors for TP and PO4. On the other hand, NO3, DOC and DON has some improvements.

In brackets, the 1st number is MBM (P6) error, and 2nd number is current MBM (P7) error.

Major Variables

RMSE	temp	salt	chla	DO	TN	TP
surface	(0.770, 0.770)	(1.082, 1.082)	(12.776, 12.637)	(1.192, 1.175)	(0.334, 0.319)	(0.044, 0.047)
bottom	(0.987, 0.987)	(1.602, 1.602)	(12.296, 12.595)	(1.510, 1.504)	(0.365, 0.370)	(0.060, 0.063)

Bias	temp	salt	chla	DO	TN	TP
surface	(-0.212, -0.212)	(-0.372, -0.372)	(0.174, 0.606)	(-0.210, -0.153)	(-0.095, -0.005)	(0.002, 0.007)
bottom	(0.085, 0.085)	(-0.781, -0.781)	(1.493, 2.211)	(0.469, 0.375)	(-0.079, 0.021)	(-0.011, -0.004)

MBM-7 better

Close (<5%)

MBM-6 better

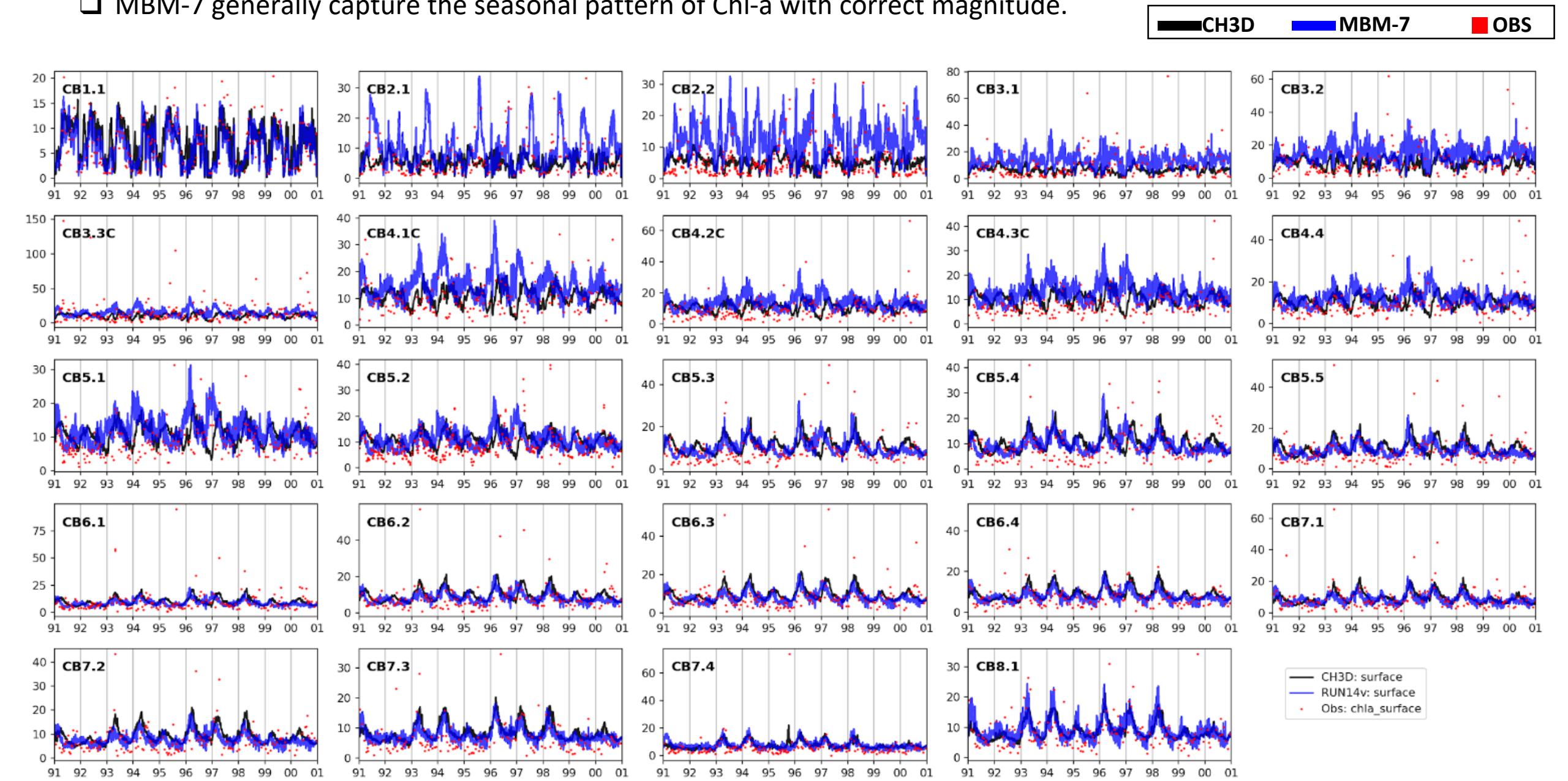
Nutrients

RMSE	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(0.234, 0.221)	(0.059, 0.059)	(0.020, 0.020)	(2.016, 1.908)	(0.170, 0.149)	(0.012, 0.012)	(1.506, 1.467)	(0.176, 0.173)	(0.036, 0.038)
bottom	(0.222, 0.216)	(0.085, 0.088)	(0.022, 0.023)	(1.932, 1.819)	(0.176, 0.155)	(0.012, 0.012)	(1.906, 1.929)	(0.220, 0.222)	(0.058, 0.058)

Bias	NO3	NH4	PO4	DOC	DON	DOP	POC	PON	POP
surface	(-0.082, -0.022)	(-0.013, -0.010)	(0.003, 0.004)	(-1.518, -1.552)	(-0.065, -0.053)	(-0.002, -0.002)	(-0.330, 0.177)	(-0.078, -0.061)	(-0.013, -0.010)
bottom	(-0.052, 0.006)	(-0.015, -0.002)	(0.003, 0.006)	(-1.395, -1.417)	(-0.067, -0.056)	(-0.003, -0.002)	(-0.474, 0.142)	(-0.089, -0.070)	(-0.026, -0.023)

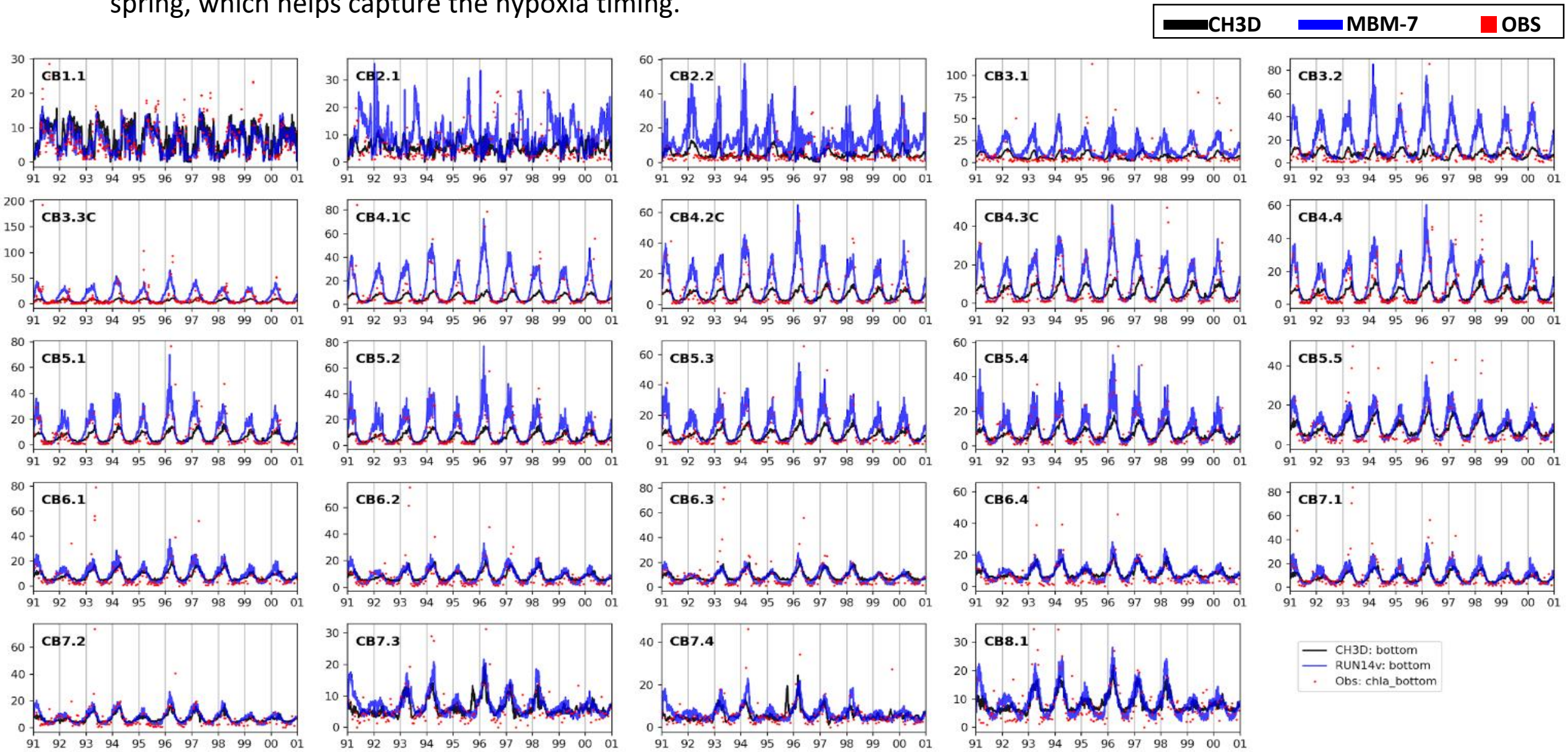
Baseline: Surface Chl-a Simulation Along Main-Bay Channel

- MBM-7 generally capture the seasonal pattern of Chl-a with correct magnitude.



Baseline: Bottom Chl-a Simulation Along Main-Bay Channel

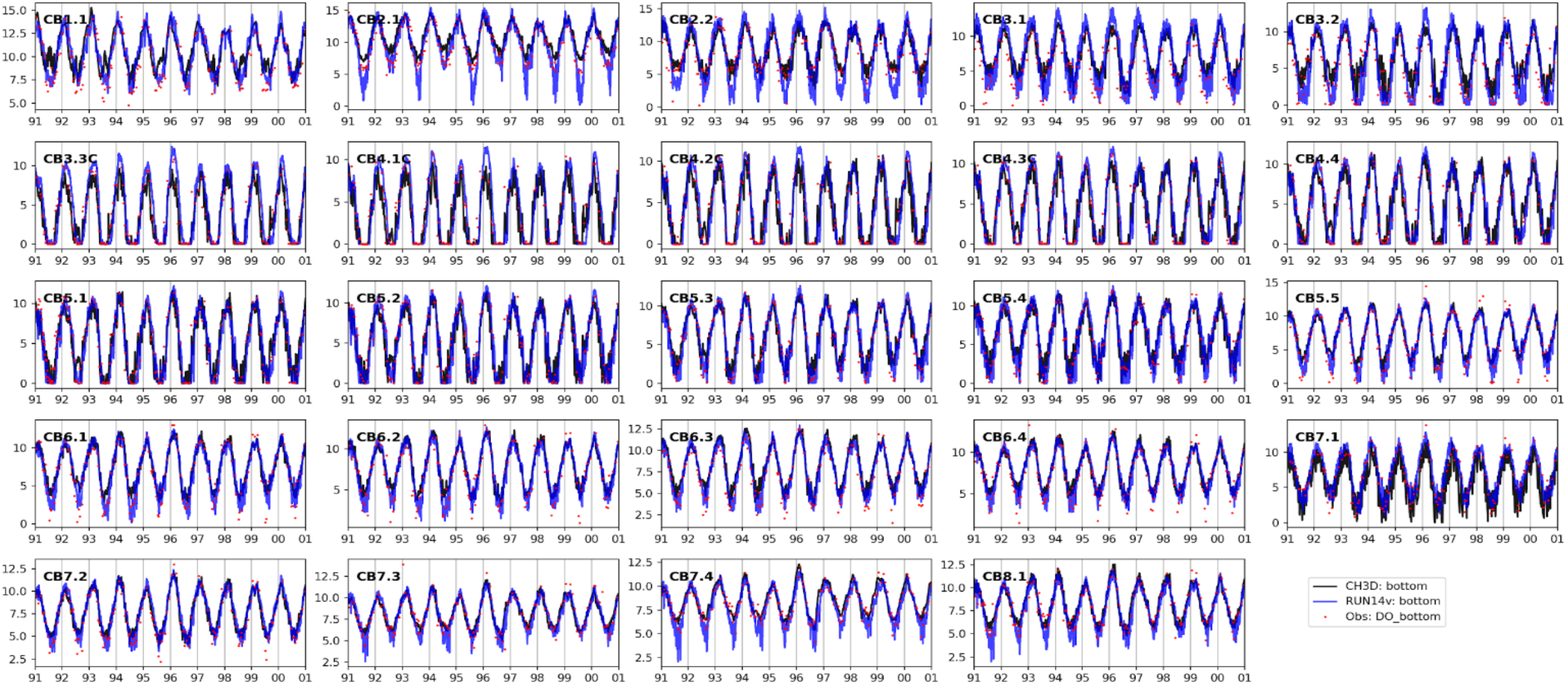
- MBM-7 did a good job in capturing the high Chl-a concentrations in the bottom during spring, which helps capture the hypoxia timing.



Baseline: Bottom DO Simulation Along Main-Bay Channel

- MBM-7 also did a good job in capturing the hypoxia events.
- In upper bay, lower DO was caused by DOC export from SAV bed, which is fixed now.

CH3D MBM-7 OBS



Problems in Baseline (RUN14v)

- ❑ Although the baseline MBM generally achieved comparable model skill to CH3D, there exists some systematic biases in addition to local problems.
- ❑ Based on the Carl's comments, we further tuned the model parameters to address the issues (ongoing).

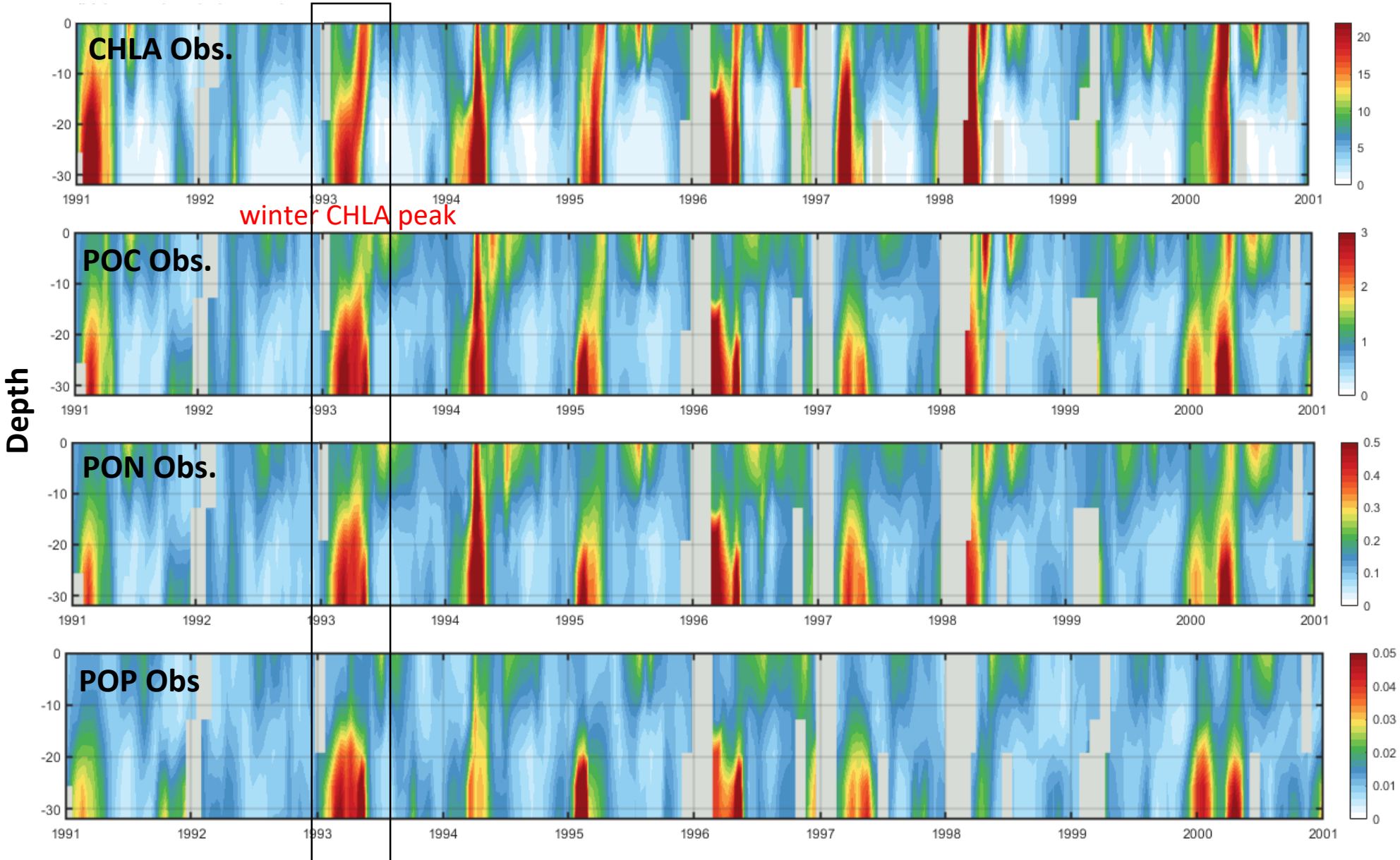
Snapshot of Carl's review

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	Station		Chl	DO	DOC	DON	DOP	POC	PON	POP	PO4	NH4	NO3	TN	TP
2	CB1.1	Surface	ok	ok	low	low		ok	low	low	ok	ok	ok	ok	ok
3		Bottom													
4	CB2.1	Surface	high	low				high			ok	ok	low	ok	ok
5		Bottom		low											
6	CB2.2	Surface	high	low	low	low		high	ok	ok		ok	ok	ok	ok
7		Bottom	high	ok											
8	CB3.1	Surface	ok	low	low	low	ok	high	ok	ok	ok	low	ok		
9		Bottom	high	good											
10	CB3.2	Surface	high	low	low	ok	ok	high	ok	ok	high	high		ok	high
11		Bottom	high											ok	high
12	CB3.3C	Surface	ok	low	low	ok	ok	ok	ok		high	high		ok	high
13		Bottom	ok	ok	low	low	ok				high	high	high		
14	CB4.1C	Surface	high	low	low	ok	ok	high	ok	high	high	high		ok	high
15		Bottom	okay	okay				ok		high				high	high
16	CB4.2C	Surface	high	low	low		ok	high	ok	high	high	high	ok	ok	high
17		Bottom	okay	okay	low	low	ok	high	ok	high	high	high	high	high	high
18	CB4.3C	Surface	high	low	low	low	ok	high	ok	high	high	high	ok	ok	high
19		Bottom	okay	ok	low	low	low	high	high	high	high	high	high	high	high
20	CB4.4	Surface	high	low	low	ok	ok	ok	ok	high	high	high	ok	ok	high
21		Bottom	good	okay	low	low	low	high	high	high	high	high	high	ok	high
22	CB5.1	Surface	high	low	low	ok	ok	ok	high	high	high	high	ok	ok	high
23		Bottom	ok	ok	low	low	low	ok	ok		ok	high	high	ok	high
24	CB5.2	Surface	high	low	low	low	low	ok	ok	high	high	high	ok	ok	high
25		Bottom	okay	ok	low	low	ok	high	high	high	high	high	high	ok	high
26	CB5.3	Surface	okay	ok	low	ok	ok	ok	ok	high	high	high	low	ok	high
27		Bottom	okay	ok	low	low	low	high	high	high	ok	ok	ok	ok	high
28	CB5.4	Surface	high	ok	low		ok	low	ok	high	high	high		ok	high
29		Bottom	ok	ok	low		ok	ok	ok	ok	ok	ok		ok	high
30	CB5.5	Surface	ok	ok	low		ok	low	ok	high	high	high	low	ok	high
31		Bottom	ok	ok	low		ok	ok	ok	ok	ok	ok	ok	ok	high
32	CB6.1	Surface	ok		low		ok	low	ok	high	high	high	low	ok	high
33		Bottom	ok		low		ok	ok	ok	high	ok	ok	ok	ok	high
34	CB6.3	Surface	ok	ok	low		ok	ok	ok	high	high	high	low	ok	high
35		Bottom	ok	ok	low		ok	ok	ok		ok	ok		ok	ok
36	CB7.4	Surface	ok	ok	low	ok	ok	ok	ok	high	ok	high	ok	high	high
37		Bottom	ok	ok		high	ok	ok	ok	ok	ok	ok	ok	high	ok

- Surface Chl-a bias high
- Dissolved Organic Matter bias low
- Particulate Organic Matter bias high
- NH4/PO4 bias high

Seasonality and vertical structure of POM (POC/PON/POP): Observation

- Observations show that POM shares a similar seasonal variation and vertical structure with Chl-a.



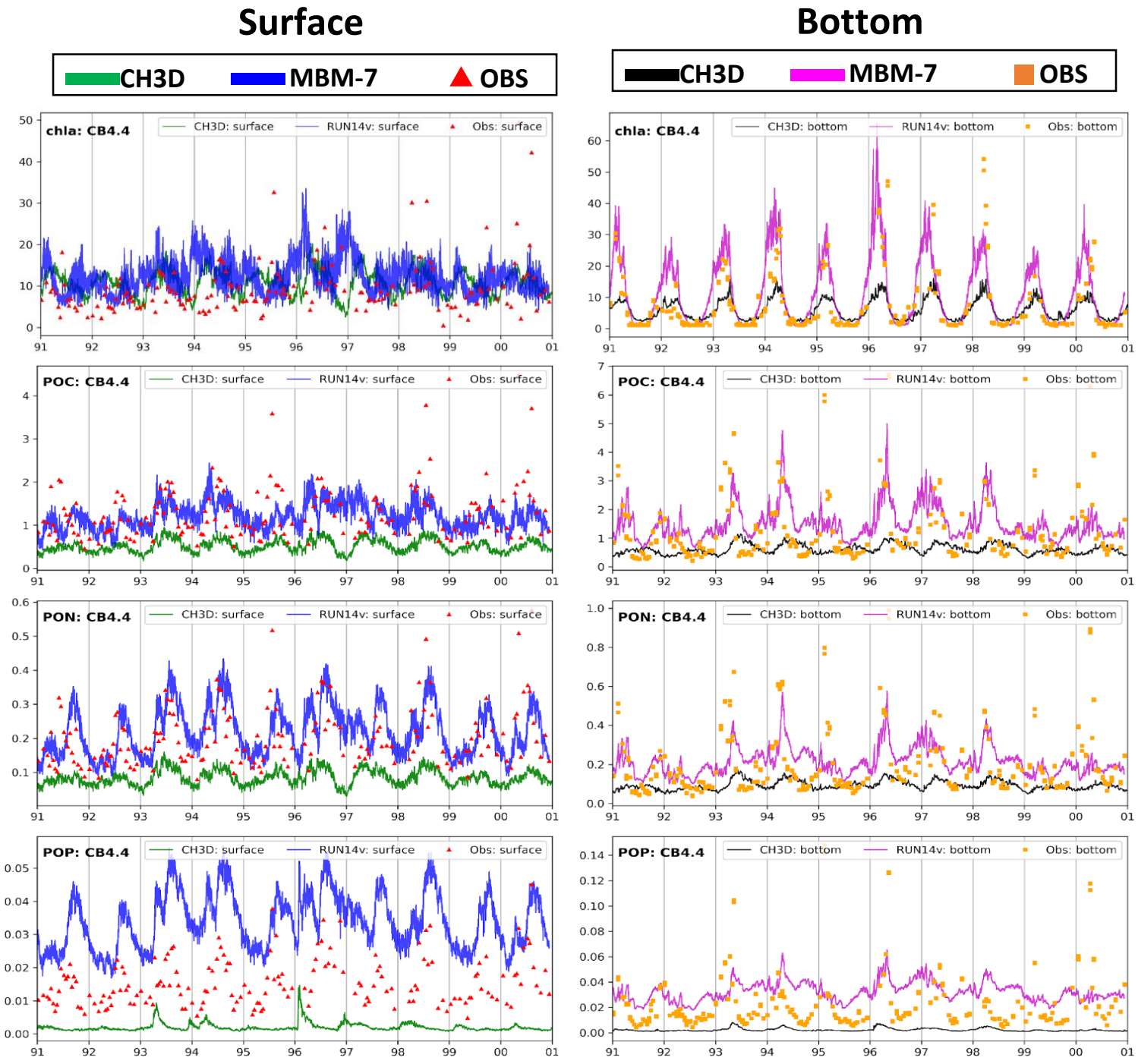
Station: CB4.4

CHLA

⇩

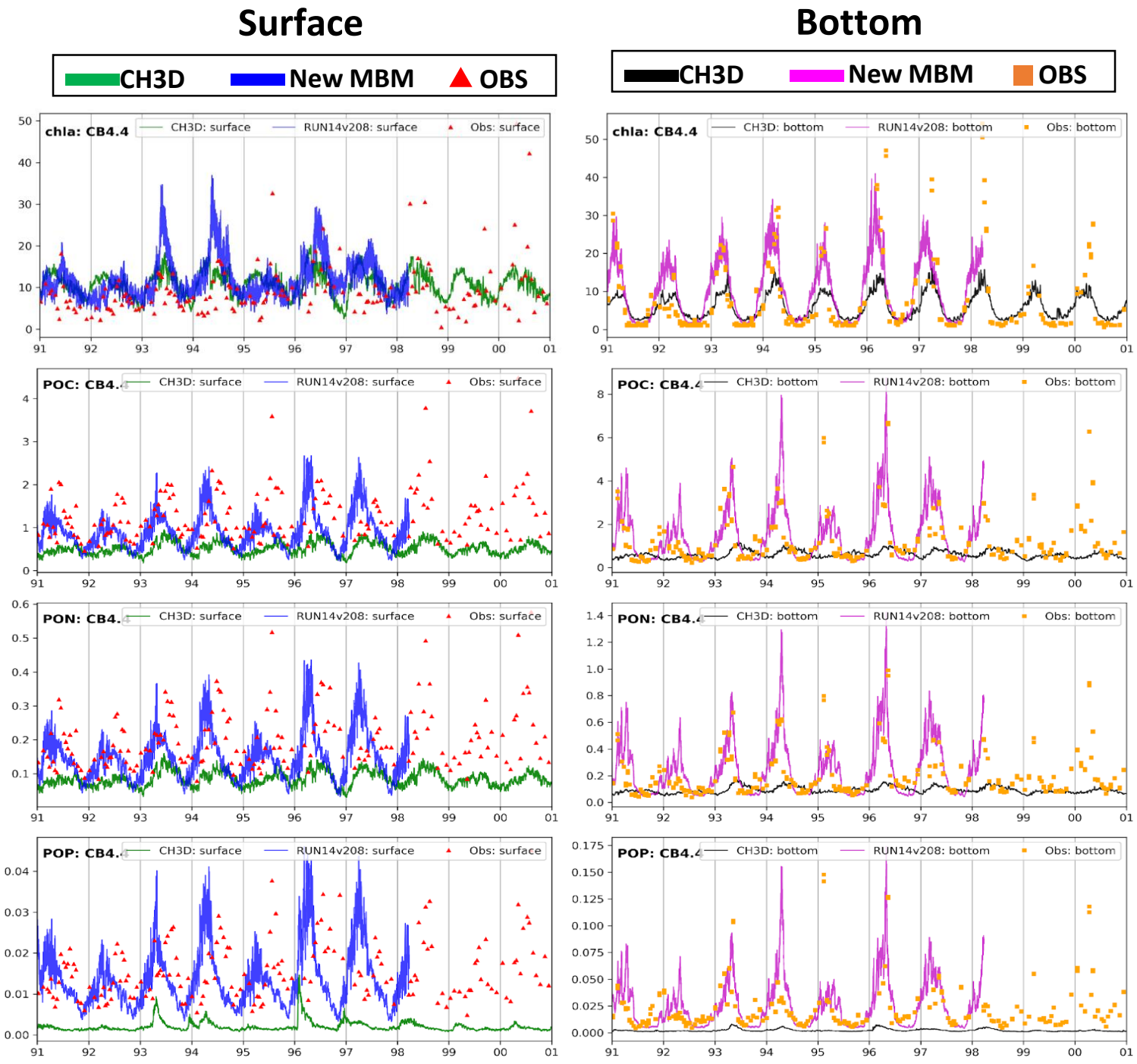
POC/PON/POP

- ✔ POC/PON/POP show highly similar behaviors
- ✔ POC/PON/POP came from the decay of CHLA



Seasonal variation of Baseline POM (POC/PON/POP)

- CH3D has large errors in simulating POM (POC/PON/POP)
- Baseline MBM can capture some seasonal variabilities of POM, but it has large biases for POP. Also, the correlation between Chla-a and POM is not very good.

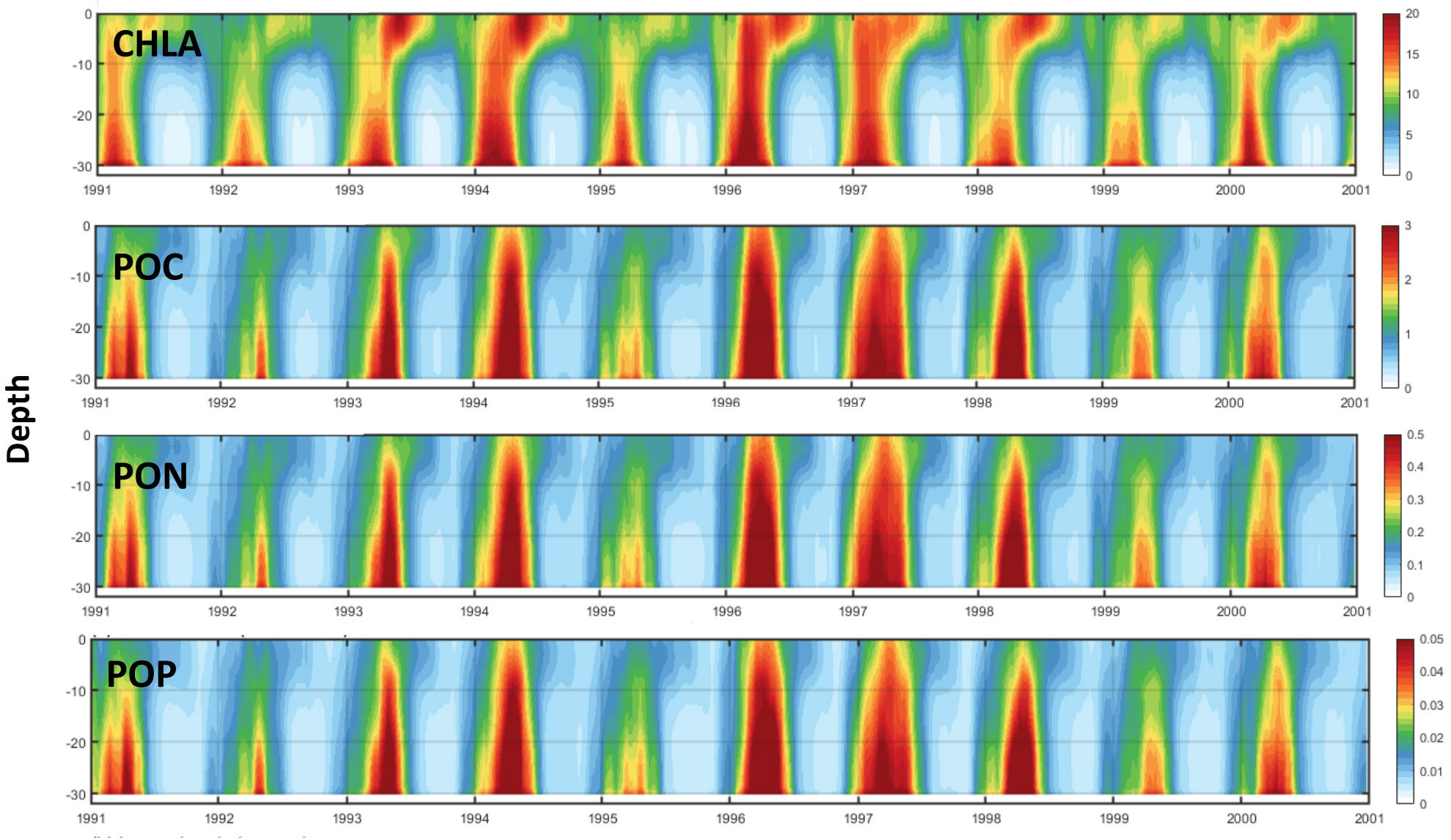


Improvement:
Seasonal pattern of POM (POC/PON/POP)

- By using consistent partition coefficient from phytoplankton biomass to POM among all POM, the seasonal variation of POM now closely follows that of Chl-a. The improvements on the bottom POM is evident.

Improvement: vertical structure of POM (POC/PON/POP)

- The simulated POM now also shares a similar seasonal variation and vertical structure with Chl-a



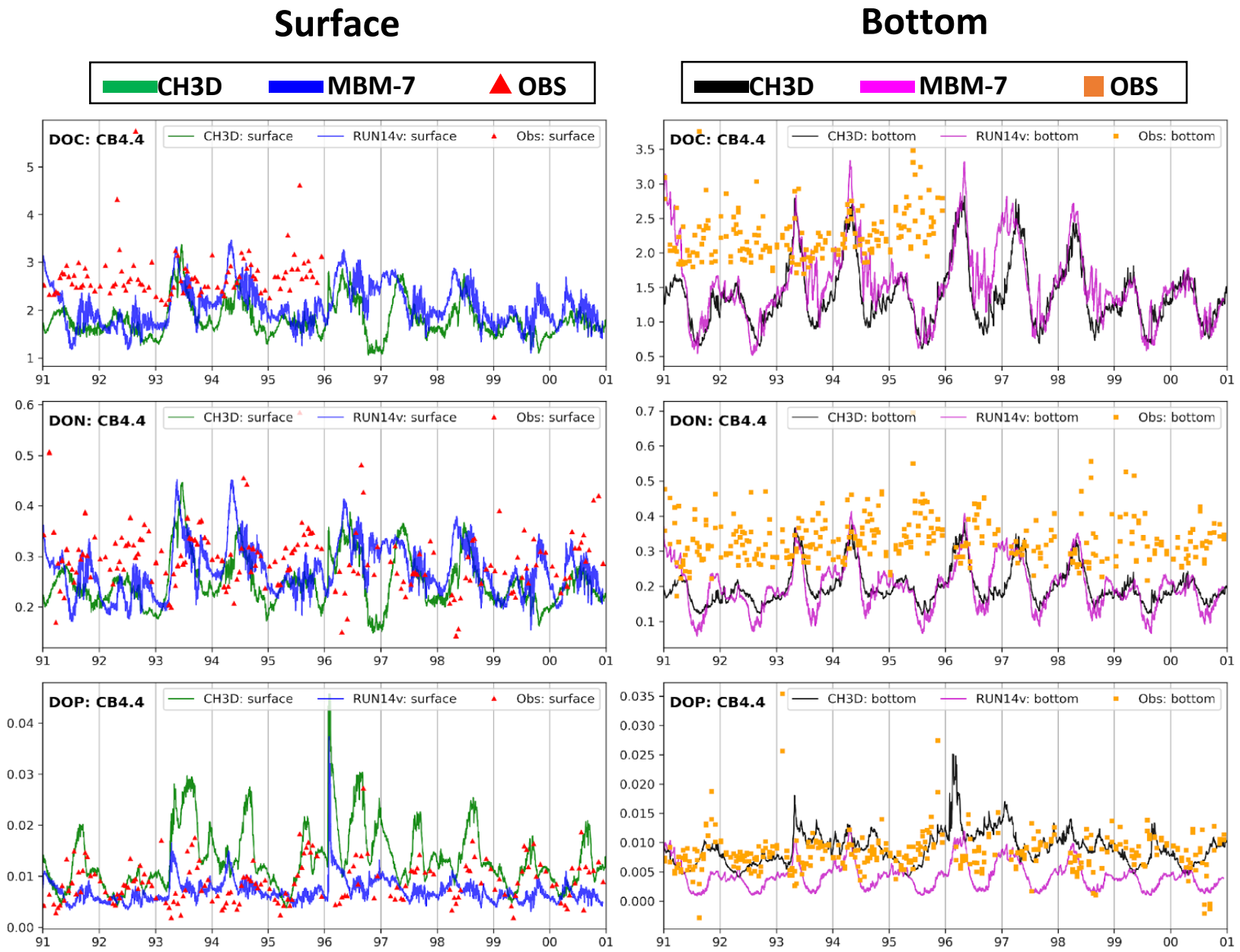
Station: CB4.4

CHLA

⇩

POC/PON/POP

Problems in Baseline DOM (DOC/DON/DOP)



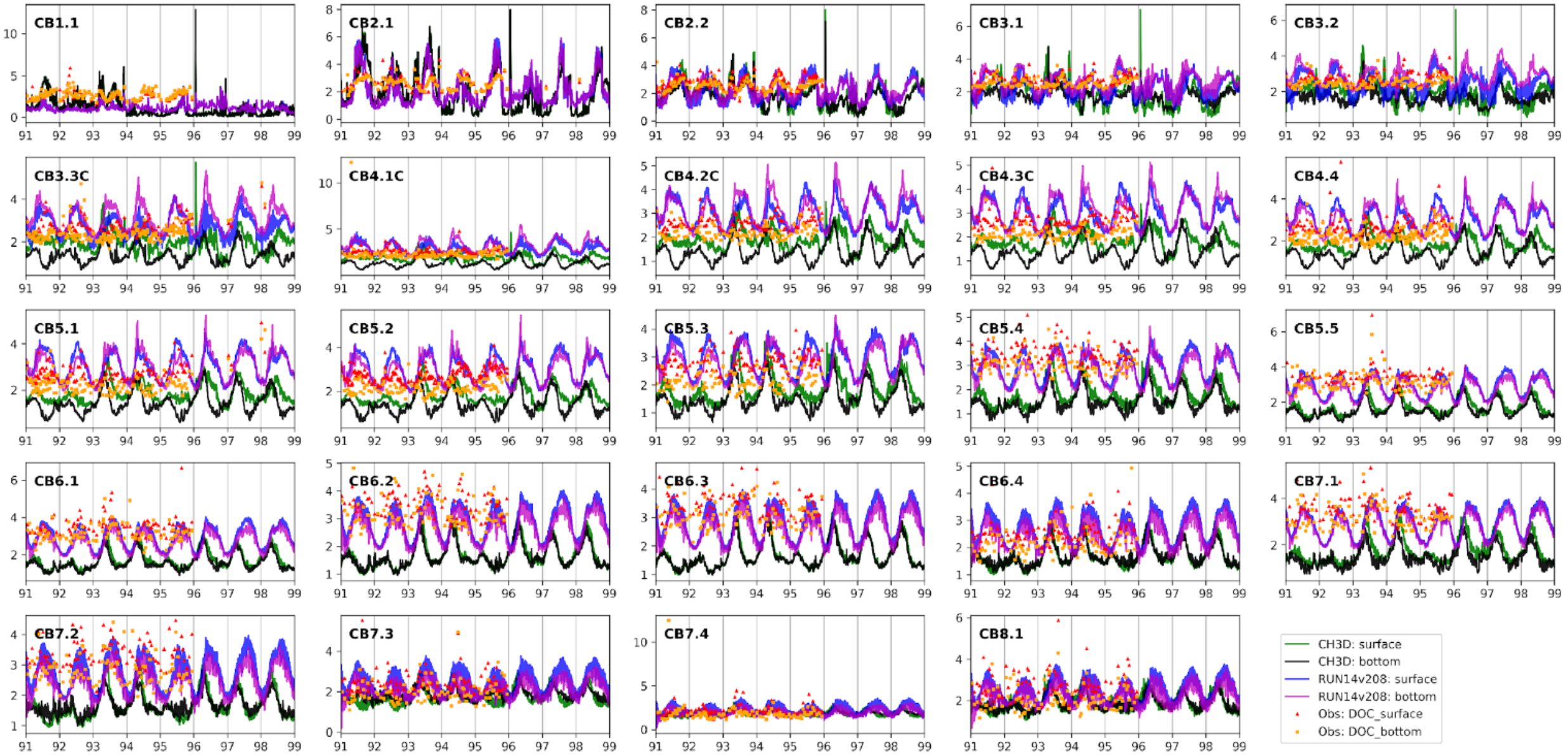
- Both CH3D and baseline MBM have difficultly in reproducing the seasonal variation of DOC/DON/DOP.
- DOM decay rate used to rely only on temperature. Our experiments show shat algal effect seems to play a role on the decay rate of DOM.

Improvement on DOC along main-bay channel

- By modifying the decay rates of DOC, we are able to improve both on the seasonal variation and magnitude of DOC.

surface CH3D MBM-7 OBS

bottom CH3D MBM-7 OBS

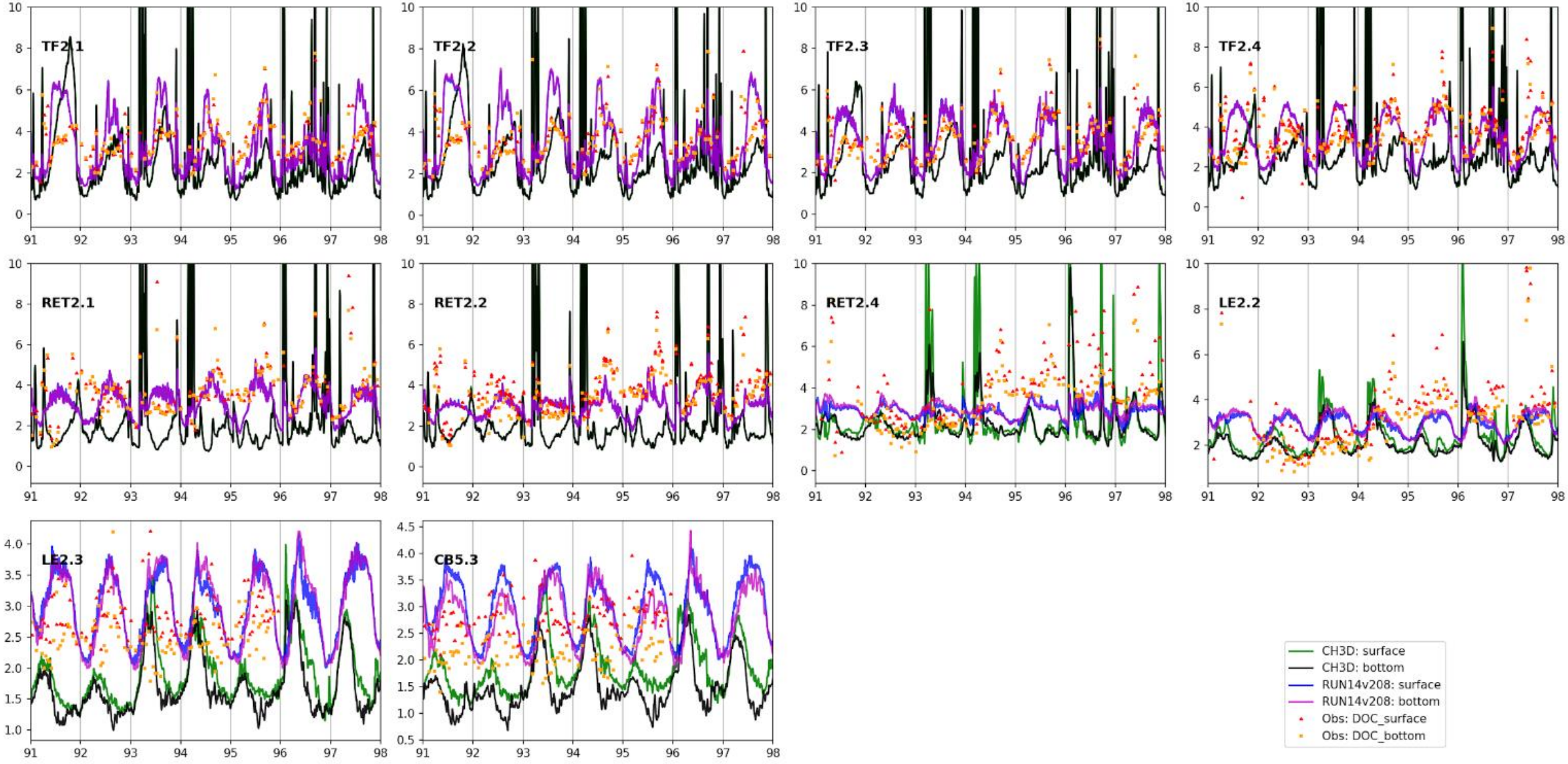


Improvement on DOC in Potomac River

- DOC simulation is also greatly improved in tributaries.

surface — CH3D — MBM-7 — OBS

bottom — CH3D — MBM-7 — OBS

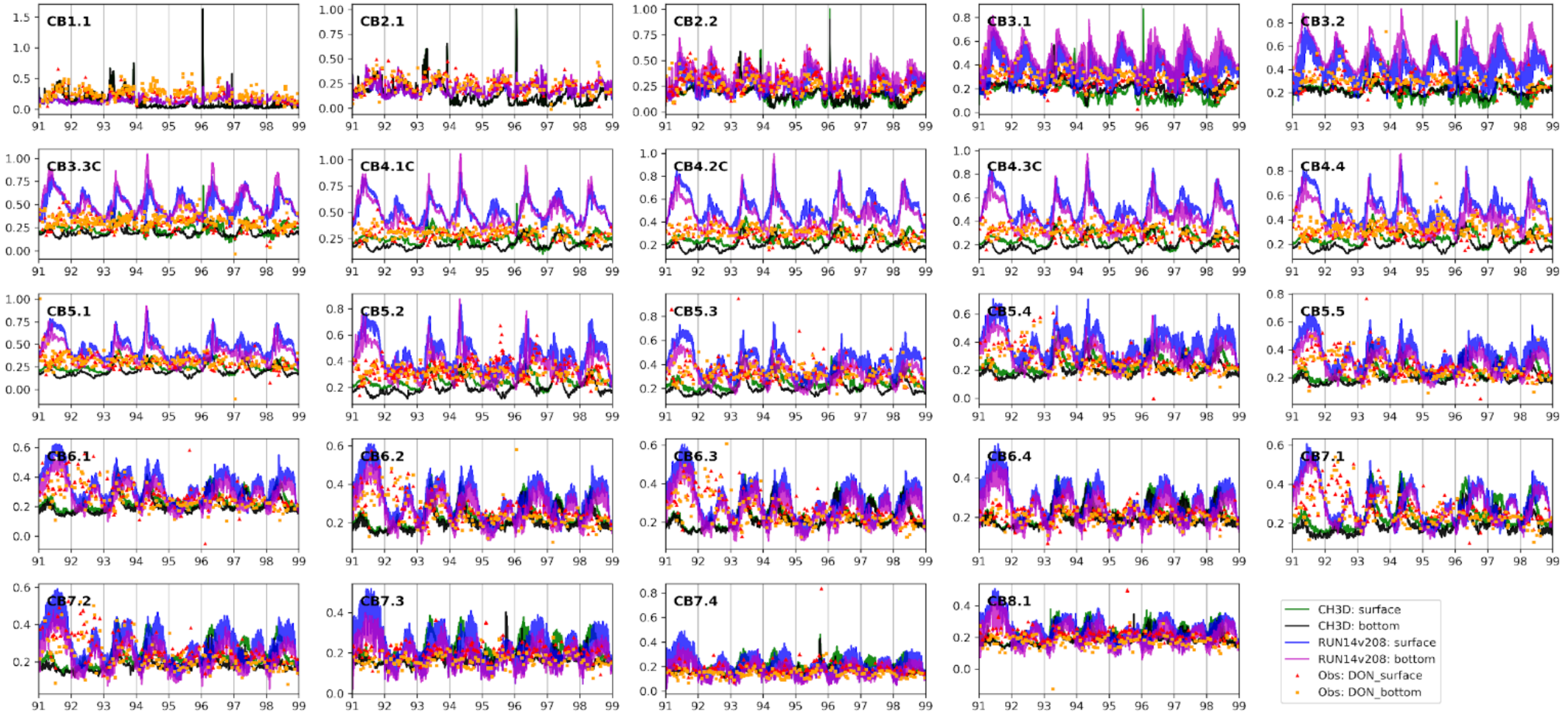


Improvement on DON/DOP along main-bay channel

- The seasonal variations of DON/DOP are improved. However, their magnitude is overestimated (todo for us).

surface — CH3D — MBM-7 — OBS

bottom — CH3D — MBM-7 — OBS

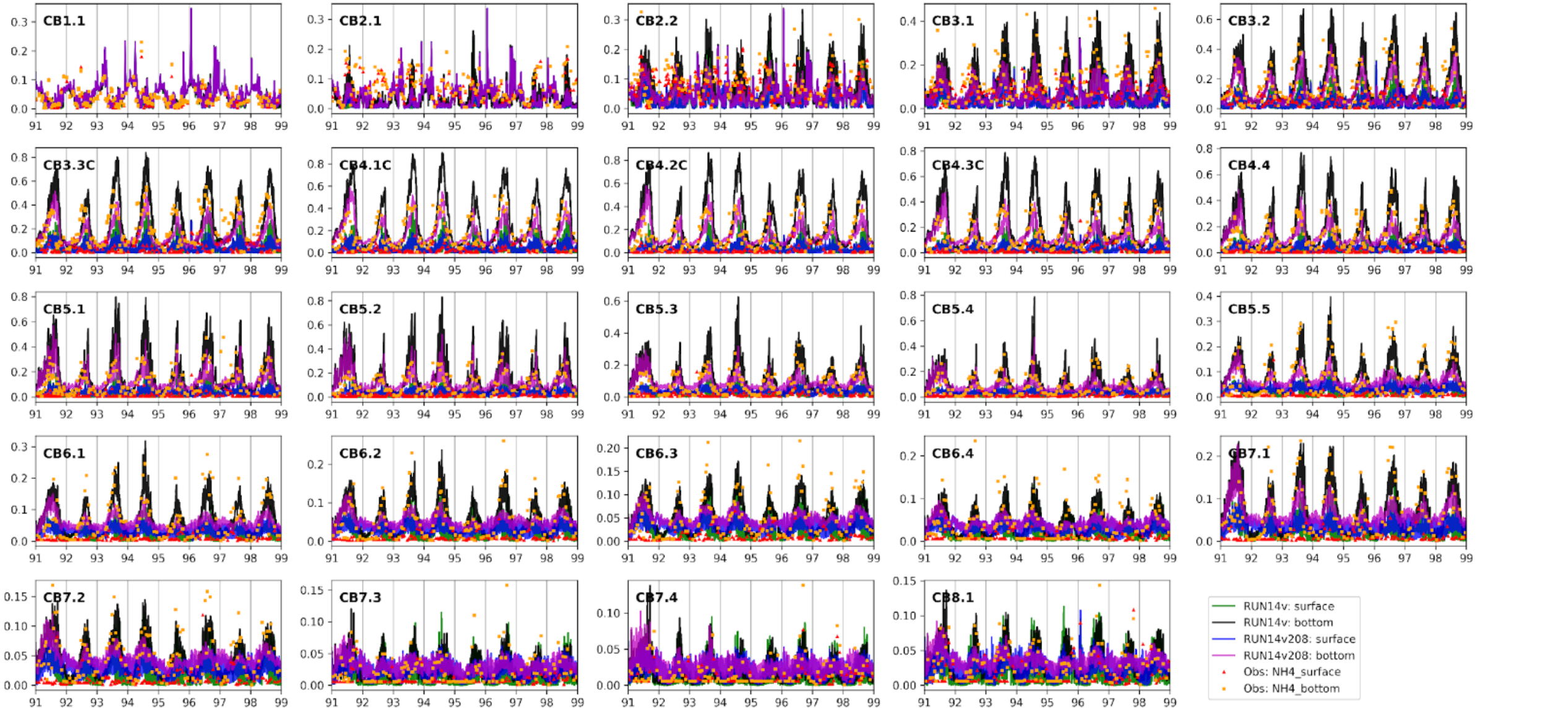


Improvement on NH4 along main-bay channel

- The NH4 in MBM baseline biases high. By adjusting the decay rate of DON, the simulated NH4 improved in middle bay. However, the NH4 in lower bay still needs improvement.

surface base new OBS

bottom base new OBS

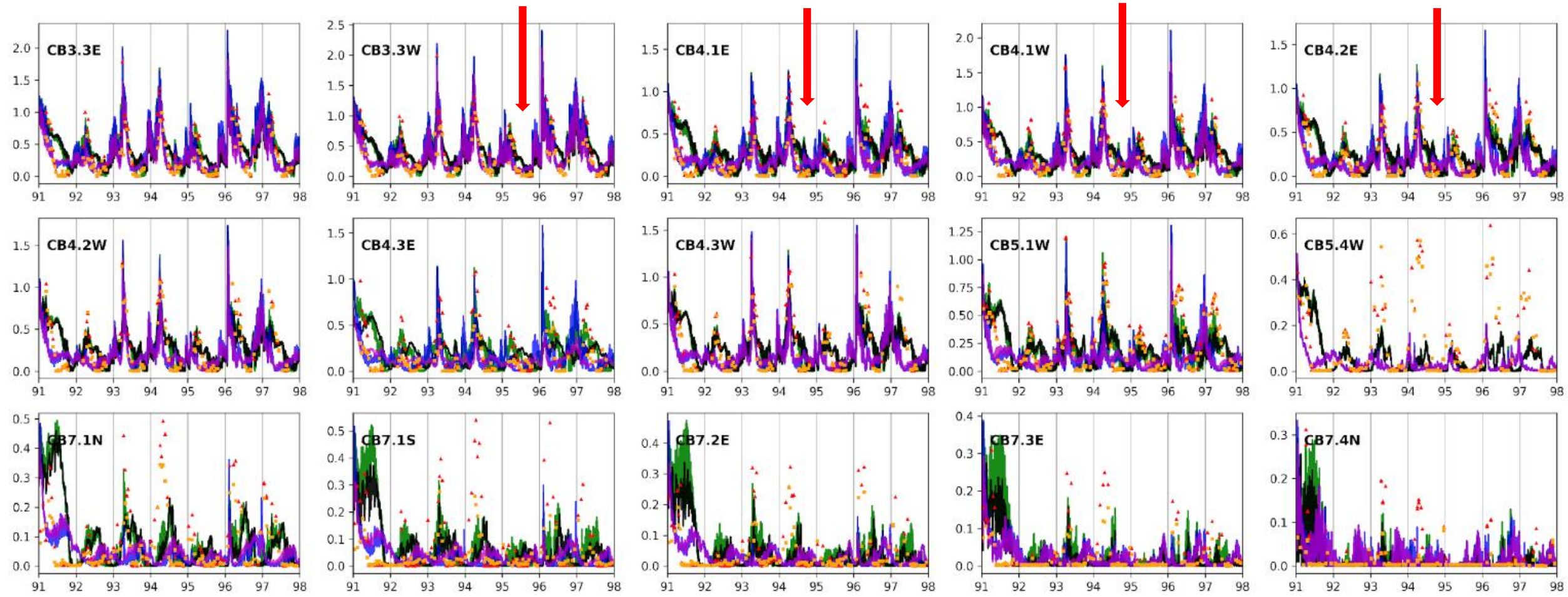


Improvement on NO3 simulation in summer

surface base new OBS

bottom base new OBS

- Baseline MBM tends to have high NO3 in the summer period. By adding the denitrification term, NO3 simulation is improved.
- NO3 simulation biases low in current simulation, which needs further improvement.



Summary and future work

- MBM now uses new, pure Phase-7 nutrient loadings. We established a baseline MBM calibration using P7 July 2025 beta.

- Baseline MBM results are satisfactory for most variables, and the results are generally comparable to CH3D.

- We are reviewing MBM, and received many useful comments/suggestions from Carl.

- Based on the review, we are fixing a few systematic biases in MBM simulation.
  - Partitioning from phytoplankton biomass to POM is important to keep its consistency with Chl-a.
  - Algal effect seems to play a role on the decay rate of DOM.

- Future work
  - MBM documentation.
  - Continue to improve MBM model skill (NO3/PO4; living resources).
  - Continue to work with WSM team to test new April 2026 beta version.