

SMART Freeze Drying of Highly Concentrated Amorphous Systems: Comparison of MTM-Based vs. TDLAS-Based Methods

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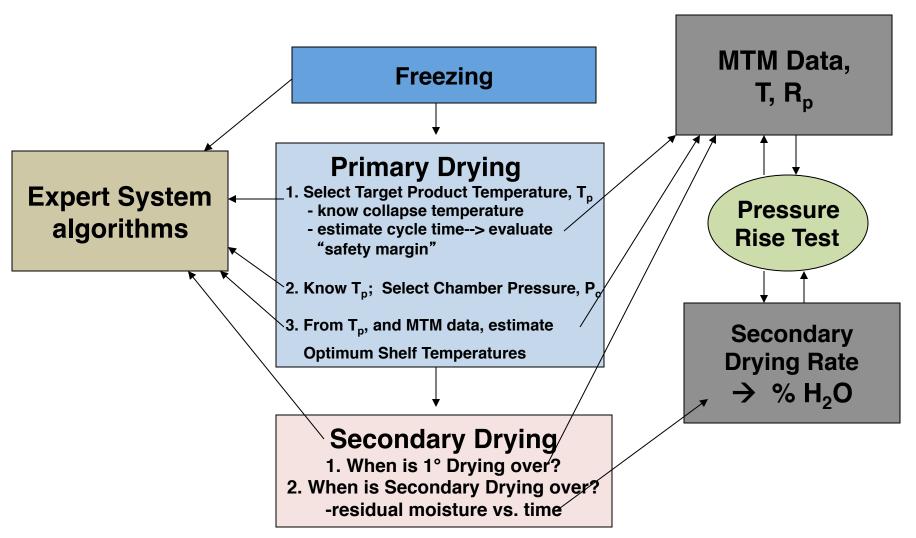


TDLAS-Based "Smart Freeze Dryer"

- Smart Freeze Dryer Concept
 - Develop "optimum" process in one laboratory experiment
 - Data from process plus Expert System algorithms
 - Current Smart Freeze Dryer operates on MTM
 - Evaluate mass flow and product T
 - Works well in most cases,
 - but not with high concentration of amorphous solid
 - TDLAS method uses mass flow monitor for mass flow and product T
 - Should give good results in <u>all</u> cases



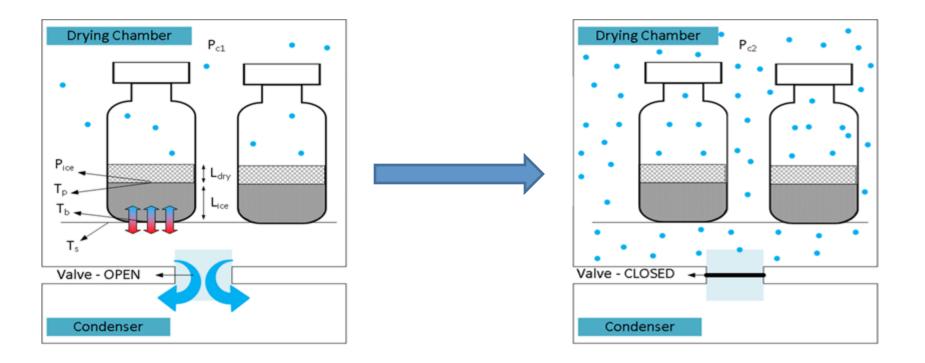
Operation of the Smart Freeze Dryer





Manometric Temperature Measurement (MTM)

❖ MTM analysis involves quickly isolating the freeze chamber from the condenser (~25 sec) and analyzing the resultant pressure rise in drying chamber





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$$P(t) = P_{ice} - (P_{ice} - P_0) \cdot \exp \left[-\left(\frac{3.461 \cdot N \cdot A \cdot T_v}{V \cdot (\hat{R}_p + \hat{R}_s)} \right) \cdot t \right]$$

$$+ 0.465 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + Ex \cdot t = 0.25 \cdot P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{0.114}{L_{ice}} \cdot t \right) \right] + P_{ice} \cdot \Delta T \cdot \left[1 - 0.811 \cdot \exp \left(-\frac{$$

- Pressure at the sublimation interface (P_{ice})
- ♦ Mass transfer resistance (R_D)
- **❖**Temperature at the sublimation interface (T_{sub})
- ❖Temperature at vial bottom (T_b)
- ❖Vial heat transfer coefficient (K_v)
- *Heat transfer into the product (dQ/dt)
- *Sublimation rate (dm/dt)

MTM is meant to evaluate "representative" product temperature during freeze drying, without placing thermocouples into product vials



Manometric Temperature Measurement (MTM)

Advantages

- **❖** MTM technique gives product temperature of the batch as a whole and does not require insertion of temperature sensors into the vials
 - **❖** Works well for many typical formulations
 - Crystalline solutes
 - **❖** 5% sucrose, ...
- Assessment of critical process attributes
 - Mass transfer resistance (Rp)
 - Vial heat transfer coefficient (Kv)
 - Sublimation rate (dm/dt)

Disadvantages

- **Requires the periodic disruption of the drying process**
- Not easily installed in manufacturing
- MTM may fail in cases of high levels of amorphous solids after creation of a significant dry layer
 - due to water re-absorption, MTM temperature is too low after a few hours of primary drying



Temperature and Resistance Comparison Between MTM and Thermocouples

For Crystalline and <u>high concentration</u> Amorphous

Temp Compare Resistance Compare

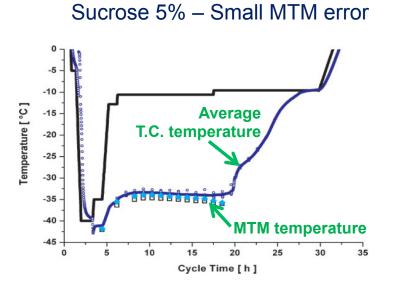
| Materials | Ts | P ₀ | T _{MTM} | T _{TC} | R _{MTM} | Rgravimetric |
|--------------|-----|----------------|------------------|-----------------|------------------|--------------|
| Glycine | -20 | 80 | -33.6 | -32.7 | 3.1 | 3.4 |
| Glycine | +37 | 120 | -23.6 | -24 | 2.7 | 2.6 |
| Mannitol | +40 | 300 | -8.8 | -9.1 | 8.0 | 8.4 |
| Amorphous I | +31 | 143 | -22.2 | -17 | 8.3 | 8.4 |
| Amorphous II | +16 | 85 | -33.0 | -26 | 2.8 | 3.3 |

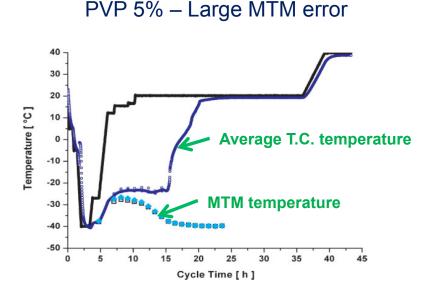
 Good agreement for crystalline solids, poor for high concentration amorphous- due to water re-sorption!



Manometric Temperature Measurement (MTM)

❖ For amorphous solutes - MTM under-predicts the product temperature, especially at high amorphous concentration





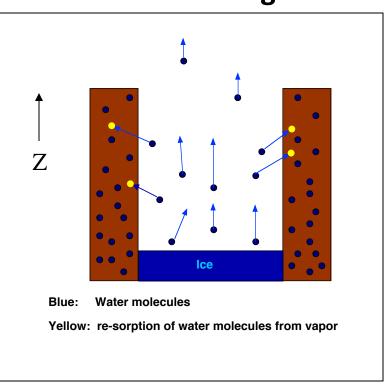
Due to water resorption by amorphous solutes partially dried layer

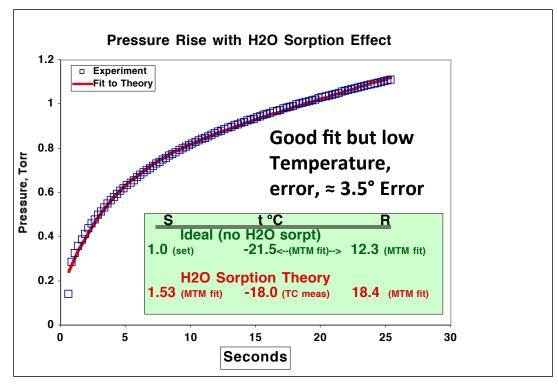


Re-Sorption of H₂O:

Not all water sublimed reaches the chamber

High Concentration Amorphous solid

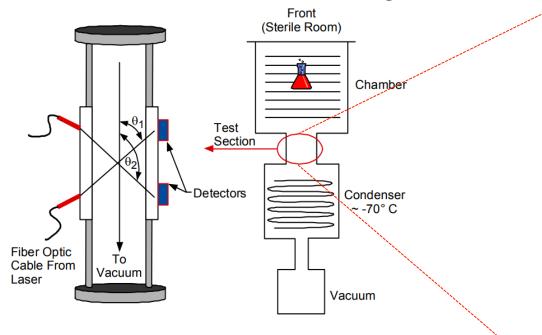


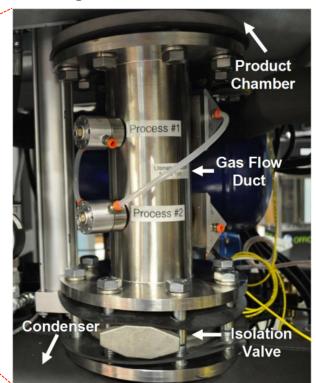




Tunable Diode Laser absorption spectroscopy (TDLAS)

Tunable Diode Laser Absorption Spectroscopy (TDLAS) is an optical method for detecting trace concentrations of one or more selected gases mixed with other gases.





- Advantages:
- Does not require any probes to be inserted in the dryer equipment
- Can be implemented on laboratory, pilot and production scale freeze-dryers
- Continuous, real-time, nonintrusive

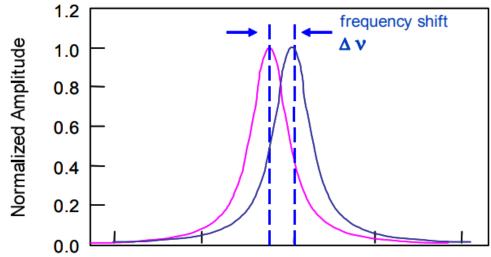


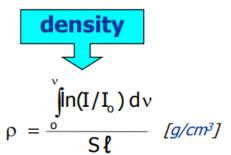
Gas Mass Flow and Velocity

Laser

Detector vapor flow

Doppler shifted absorption lineshape measurement





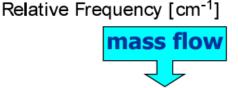
Laser

Determined using absoption linestrength, pathlength, integrated Area and the laser frequency increment



$$u = \frac{\Delta v c}{v_o (\cos \theta_1 - \cos \theta_2)} [cm/s]$$

Determined using Doppler shift, speed of light, measurement angle and transition frequency



$$dm/dt = u \cdot \rho \cdot A [g/s]$$

Determined using velocity, density and duct cross-sectional area



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TDLAS Measure of Product Temperature

Steady State Heat and Mass Transfer Model

$$\begin{cases}
dQ / dt = A_V \cdot K_V \cdot (T_S - T_b) \\
dQ / dt = \Delta H_S \cdot dm / dt
\end{cases}$$

dQ/dt : heat flow (cal/s) dm/dt : sublimation rate

 ΔH_s : water heat of sublimation

A_v : cross sectional area of vials

K_v: vial heat transfer coefficient

T_s : shelf temperature

T_b : product temperature at vial bottom

$$T_b = T_S - \left[\frac{\left(\Delta H_S \cdot \left(\frac{dm}{dt} \right) \right)}{A_V \cdot K_V} \right]$$

$$K_v = \Delta H_s \left(\frac{dm}{dt} \right) / \left(A_v \cdot (T_s - T_p) \right)$$

- > Through the combination of TDLAS measurements and a well-established heat and mass transfer model describing freeze drying, Tb or Kv can be acquired interchangeably.
- Input Kv accounts for <u>all</u> sources of heat & is weighted average of edge and center vials.
- Accurate, non-intrusive determination of batch average product temperature.



TDLAS Measured Temperature is not quite the "Average Temperature"

- TDLAS determines temperature by input of sublimation rate (via TDLAS) and vial heat transfer coefficient, but,
 - Edge vials contribute more to the sublimation rate than their numbers would suggest, since they sublime faster

$$T_p^{TDLAS} = r \cdot T_p^E + (1 - r) \cdot T_p^c,$$

$$r = \frac{f_E \cdot K_v^E}{\left(f_c \cdot K_v^c + f_E \cdot K_v^E\right)}$$



The Difference between Number Average Product Temperature and TDLAS average is small

| Formulation | Mean Tb (TC) | Tb TDLAS | TDLAS Bias |
|-----------------|-----------------|----------|------------|
| Sucrose-Protein | -26.75 | -26.65 | 0.11 |
| Sucrose | -31.25 | -31.08 | 0.17 |
| Mannitol | -13.91 | -13.83 | 0.08 |

 Fortunately, the difference (bias) is expected to normally be quite small, less than the actual experimental error due to errors in sublimation rate and Kv



Experimental Error in TDLAS T_b

$$\sigma T_p = \left(T_s - T_p\right) \sqrt{\left(\frac{\sigma K_v}{K_v}\right)^2 + \left(\frac{\sigma \dot{Q}}{\dot{Q}}\right)^2}$$

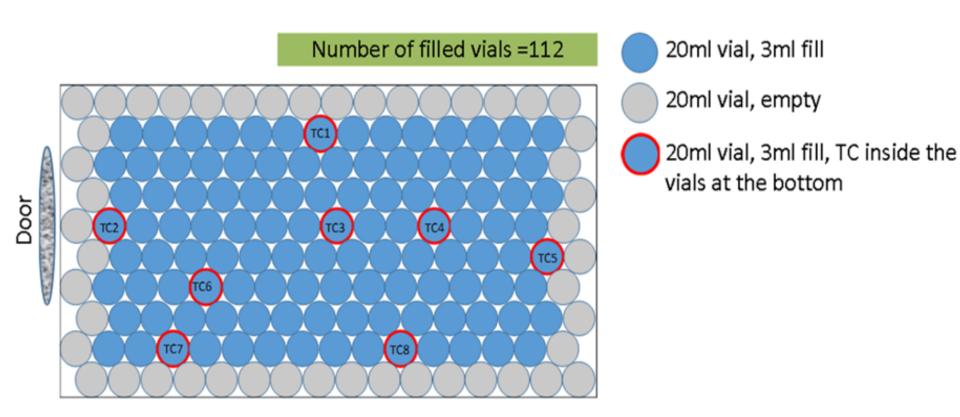
Estimate ≈ 3% Error in both Kv and Q

| Formulation | Error TDLAS T _b | | |
|-----------------------|----------------------------|--|--|
| Sucrose protein (1:1) | 0.71 | | |
| Sucrose | 0.39 | | |
| Mannitol | 1.01 | | |

- Expected errors modest
 - but need to be considered when comparing temperature data



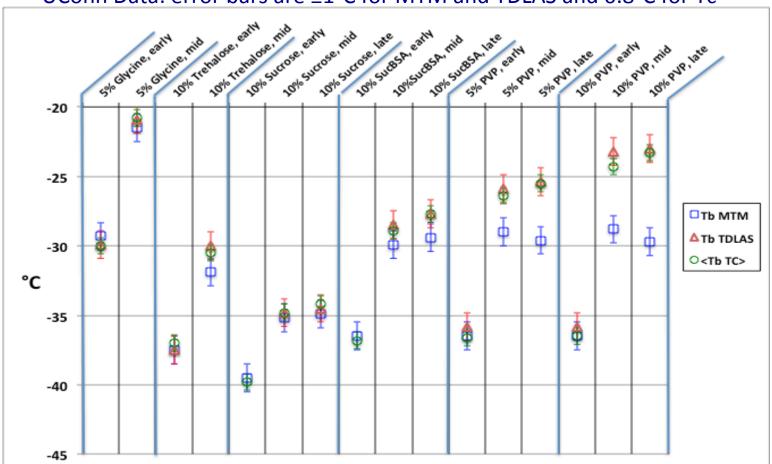
Experimental Setup





Comparison of T_b: MTM, TDLAS, TC avg

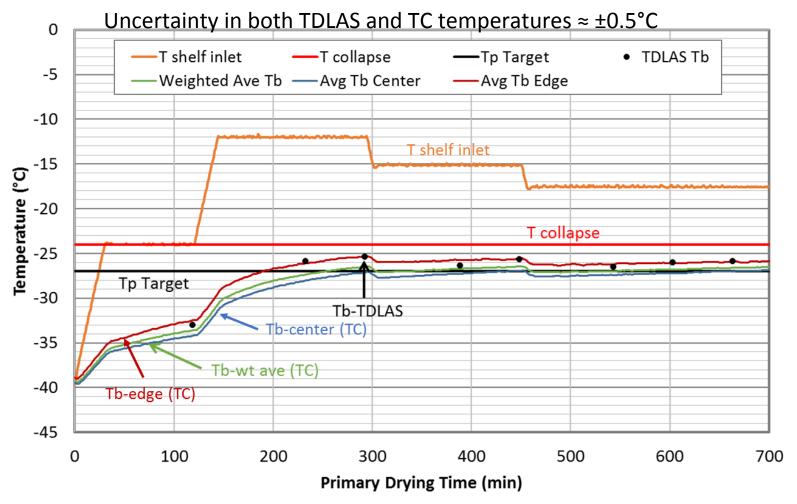
UConn Data: error bars are ±1°C for MTM and TDLAS and 0.8°C for Tc



- Excellent agreement between TDLAS and Tc in all cases
- Good agreement between MTM and Tc for Glycine, acceptable for 10% sucrose, Trehalose, fair for BSA-Sucrose, but poor for PVP except for early data.



Example of TDLAS SMART FD Run on 10% PVP

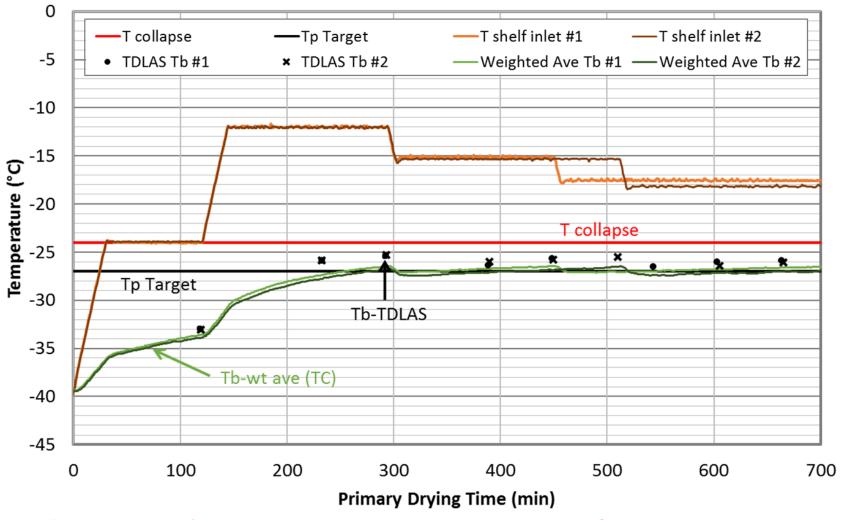


- Good agreement between TDLAS and TC temperatures
- Sensible cycle output from SMART: objective is Tb-TDLAS within ±1°C of Target once in control at ≈ 200 min



TDLAS SMART FD Run Repeatability: 10% PVP

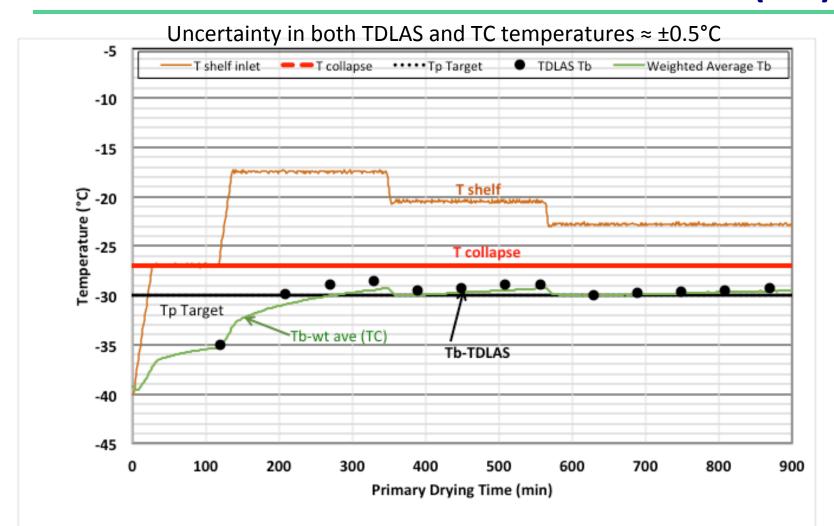
Uncertainty in both TDLAS and TC temperatures ≈ ±0.5°C



Good agreement between two TDLAS SMART FD runs for 10% PVP



TDLAS SMART FD Run on 10% Sucrose:BSA (1:1)



- Good agreement between TDLAS and TC temperatures
- Sensible cycle output from SMART: objective is Tb-TDLAS within ±1°C of Target once in control at ≈ 200 min



Summary & Conclusions

- Tunable Diode Laser Absorption Spectroscopy (TDLAS) is a noninvasive method to continuously measure the water vapor concentration and the vapor flow velocity and with a given value of vial heat transfer coefficient, can accurately measure product temperature over the full range of product drying.
- ❖ Product temperatures measured by TDLAS are accurate and in agreement with thermocouple data even when MTM fails badly due to the water-resorption phenomena.
- ❖ TDLAS sublimation rates and the calculated product temperatures can be combined with heat and mass transfer models of freeze drying to provide a SMART Freeze Drying procedure unencumbered by the inaccuracies of the MTM method.
- TDLAS is applicable to laboratory, pilot and production scale freeze dryers (process scaleup and process control), thus enabling a SMART freeze drying procedure in manufacturing.



Thank you!