Development of a setting and qualification method for a Biological TTI to ensure temperature control during the cold chain

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1. Introduction

2. Biological TTIs: Development of a setting model

3. Model Validation

4. Evaluation of (eO)\(^{®}\) performances

5. Conclusions and perspectives
Introduction

• Food poisoning = major concern in Europe
  – 6,860 outbreaks in 2004 (EFSA, 2007)

• Systems like the HACCP system have improved the food quality and limited the bacterial concentration \( (N_0) \) of the produced goods.

• Still, poor temperature control is observed in the distribution network.

• New regulations engage the food business processors responsibility.

→ Traceability tools are required
Introduction
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**Biological TTIs: Development of a setting model**

- Growth models
  - $N_f \mu_{max} t$
- Lactic Acid production model
  - $[\text{Lactic Acid}] (t)$
- Anderson Hasselbach Relation
- Buffer effect model

**Model**

- Simulated response time = $\Sigma \delta_i$

- New [AH]t
- New pH(t)
Biological TTIs: Development of a setting model

The primary model: Rosso (1995)

\[ \ln N = \begin{cases} 
\ln N_0, & t \leq \text{lag} \\
\ln N_{\text{max}} - \ln \left[ 1 + \left( \frac{N_{\text{max}}}{N_0} - 1 \right)^{-\mu_{\text{max}}(t-\text{lag})} \right], & t > \text{lag} 
\end{cases} \]

\( \mu_{\text{max}} \cdot \text{lag} = k \)

\( k \): physiological state constant

\[ \mu_{\text{max}} = \mu_{\text{opt}} \cdot \gamma_2(T) \cdot \gamma_1(pH) \cdot \gamma_1(Aw) \cdot \gamma(AH) \]

\( \mu_{\text{opt}} \): optimal growth rate

\[ \gamma(X) = \begin{cases} 
0, & X \leq X_{\text{min}} \\
\frac{(X - X_{\text{opt}})(X - X_{\text{max}})^{n-1}}{(X_{\text{opt}} - X_{\text{min}})(X - X_{\text{opt}})(X_{\text{opt}} - X_{\text{max}})(X_{\text{opt}} + X_{\text{min}} - nX)}, & X_{\text{min}} < X < X_{\text{max}} \\
0, & X \geq X_{\text{max}} 
\end{cases} \]

\( X \): pH, aw or T

\( X_{\text{min}} \): X value below which no growth is observed

\( X_{\text{max}} \): X value above which no growth is observed

\( X_{\text{opt}} \): X value for which \( \mu_{\text{max}} = \mu_{\text{opt}} \)

\( n \): Shape parameter. For T \( n = 2 \) for pH and Aw \( n = 1 \)

\[ \gamma(AH) = 1 - \left( \frac{[AH]}{\text{MIC}} \right)^s \]

[AH]: Undissociated lactic acid concentration

MIC: Minimal Inhibitory Concentration of Lactic acid

s: shape parameter. For Lactic acid = 0.48.
Lactate produced by *C. piscicola*

*(Vereecken and Van Impe, 2002)*

\[
\frac{dLac}{dt} = Y_p \frac{dN}{dt}
\]

- $Lac$ : lactic acid concentration
- $N$ : number of cells at $t$ time
- $\mu_{max}$ : maximum growth rate
- $Y_p$ : acid production rate

Simulated response time=$\sum \delta_i$
Biological TTIs: Development of a setting model

Relating the lactic acid concentration to pH

Logistic model Whiting (1993)

\[
pH(Lac) = pH_0 \left[ f \frac{1 + e^{-k_1 \lambda}}{1 + e^{-k_1 (Lac - \lambda)}} + (1 - f) \frac{1 + e^{-k_2 \lambda}}{1 + e^{-k_2 (Lac - \lambda)}} \right]
\]

\(pH_0\): initial pH of the medium
\(\lambda\): required acid concentration for the acidification reaction
\(k_1\): acidification rate of the first part of the curve
\(k_2\): acidification rate of the second part of the curve
\(f\): pH proportion for the acidification rate \(k_1\)

\[F = \log_{10} \left( \frac{f}{1 - f} \right)\]

\(F\) estimates the relative importance of the two acidification processes

\[F = a \cdot pH_0 + b\] 
a and \(b\) are regression parameters.

Undissociated lactic acid concentration

(Anderson Hasselbach relation)

\[
pH = pKa + \log \left( \frac{Lac}{[AH]} \right)
\]

\(Lac\): lactic acid concentration
\(pH\): pH of the medium
\(pKa\): Lactic acid pKa
\([AH]\): Undissociated lactic acid
Biological TTIs: Development of a setting model

The model parameters

<table>
<thead>
<tr>
<th>Parameters</th>
<th>Estimate</th>
<th>CL 95%</th>
</tr>
</thead>
<tbody>
<tr>
<td>$\mu_{opt}$</td>
<td>0.8992</td>
<td>[0.8570, 0.9601]</td>
</tr>
<tr>
<td>$k$</td>
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<td>$\log(N_{max})$</td>
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<td>$\lambda$</td>
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<tr>
<td>$a$</td>
<td>-0.0667</td>
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<td>$b$</td>
<td>0.7896</td>
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Cardinal Values

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<td>$X_{min}$</td>
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<tr>
<td>$X_{max}$</td>
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<td>10.24 [9.74 ; 10.73]</td>
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Biological TTIs: Development of a setting model

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Model Validation

Model

Storage temperature

Shelf life

Observed response time

Storage temperature

N₀
Aw
N₀
pH
Aw
pH

(eO)°
freshness at a glance

good not good
Model Validation

- **Shelf life**:
  - TTIs number (shelf life = 11.5 days)
  - Observed time of response (days)

- **Observed response time**:
  - TTIs Number (shelf life = 4 days)
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Evaluation of (eO)® performances

\[ \Delta E = \sqrt{(L - L_0)^2 + (a - a_0)^2 + (b - b_0)^2} \]
Evaluation of (eO)® performances

\[ \Delta E = \Delta E_{\text{min}} + \frac{\Delta E_{\text{max}} - \Delta E_{\text{min}}}{1 + \exp[-\mu_{\Delta E}(t - t_i)]} \]

- \( \Delta E_{\text{min}} \): initial \( \Delta E \) value,
- \( \Delta E_{\text{max}} \): maximum \( \Delta E \) (estimated)
- \( \mu_{\Delta E} \): maximum rate for \( \Delta E \) evolution
- \( t \): time (h)
- \( t_i \): the time (h) when \( \Delta E = \Delta E_{\text{max}}/2 \)

\[ \Delta E = \Delta E_{\text{min}} \quad \Delta E = 9.31 \]

\( \Rightarrow \) Deduce the response time \( t \)

\[ \ln N = \begin{cases} \ln N_0, & t \leq \text{lag} \\ \ln N_{\text{max}} - \ln \left[ 1 + \left( \frac{N_{\text{max}}}{N_0} - 1 \right) \mu_{\text{max}}(t-\text{lag}) \right], & t > \text{lag} \end{cases} \]

- \( N \): number of cells at time \( t \)
- \( N_0 \): initial cell density
- \( N_{\text{max}} \): maximum cell density
- \( \mu_{\text{max}} \): maximum growth rate
- \( \text{lag} \): lag time

\( \Rightarrow \) Deduce the \( \mu_{\text{max}} \)
Evaluation of (eO)\textsuperscript{®} performances

\[ \ln(Y) = \ln(Y_{\text{ref}}) - \frac{E_a}{R} \left( \frac{1}{T} - \frac{1}{T_{\text{ref}}} \right) \]

- \( T \) the absolute temperature (°K),
- \( T_{\text{ref}} \) the reference temperature (°K)
- \( t \) the time of response (h)
- \( t_{\text{ref}} \) the time of response at \( T_{\text{ref}} \) (h)
- \( E_a \) the activation energy (kJ/mol)
- \( R \) the universal gas constant

\[ Y = \frac{1}{t} \]

\( \Rightarrow E_{a_t} \text{ of (eO)}\textsuperscript{®} \text{ is 80 kJ/mol.} \)

\[ Y = \mu_{\text{max}} \]

\( \Rightarrow E_{a_{\mu_{\text{max}}}} \text{ of (eO)}\textsuperscript{®} \text{ is 86 kJ/mol.} \)
Evaluation of (eO)® performances

$\rightarrow E_a (eO)® = 80 \text{ kJ/mol}.$

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<tr>
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<th>60 kJ/mol</th>
<th>100 kJ/mol</th>
</tr>
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<tr>
<td>76 kJ/mol</td>
<td>82 kJ/mol</td>
<td>83 kJ/mol</td>
</tr>
<tr>
<td>Pseudomonas in poultry</td>
<td>Pseudomonas in fish</td>
<td>Shewanella putrefaciens in fish</td>
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Conclusion & perspectives

• The model:
  – successfully predicts the response times of (eO)®
  – provides a range of possible settings to manufacture several TTIs suitable to different refrigerated goods.

• (eO)® is able to mimic the behaviour of several spoilage bacteria in different food.

→ (eO)® is a useful device for monitoring the quality of refrigerated food throughout the cold chain.

• New ranges of settings are now being developed to meet our clients requirements.
Acknowledgements

Project partners:
Thank you for your attention

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