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Modeling for Predicting the Growth of *Salmonella* in Chicken Fillets Under Different Temperatures

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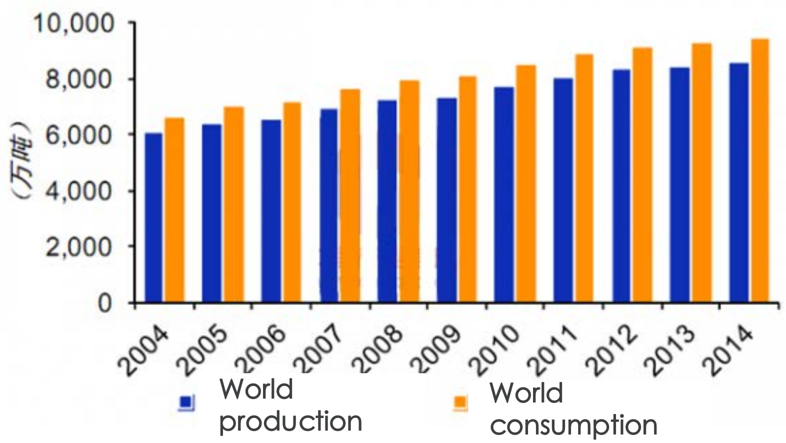
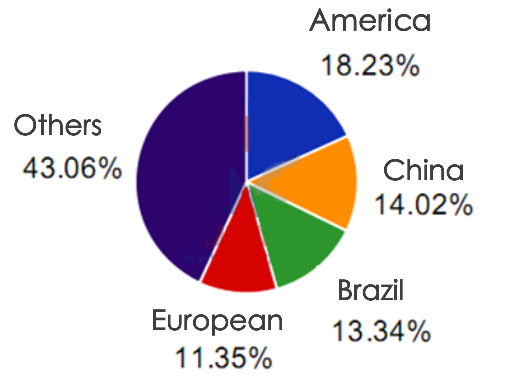
1 Introduction

Chicken





The world's major chicken consumption in 2014 accounted for the proportion of chicken consumption

- Over the past three decades, China's per capita poultry consumption has increased from barely **1 kg to over 9 kg per year**.
- On a macro level, by 2011 China was already **the second largest producer** of poultry meat and eggs in the world and the size of the poultry industry continues to expand.
- Today, the poultry industry in China is dominated by chicken production which comprises **70 to 80 percent of all poultry production**.
- In 2011, chicken meat was **the second largest protein sector** after pork. Within the meat protein sector, Chinese people are gradually substituting pork with poultry, which is perceived as healthier than pork.

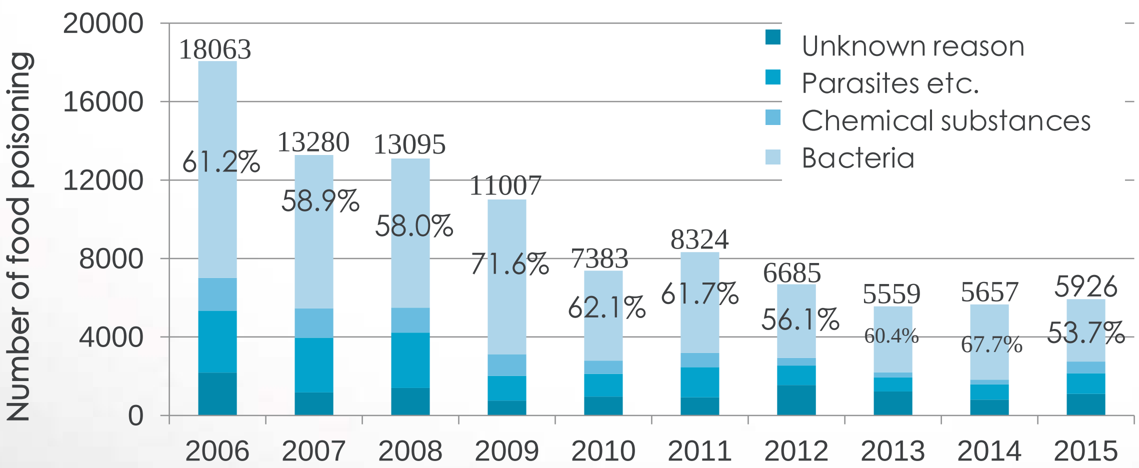
1 Introduction

Foodborne pathogens

http://www.who.int/mediacentre/factsheets/fs399/en/

WHO，2015-12

- About **600 million people** worldwide (10% of the world's population) suffer from food-borne diseases, of which 42 million people die.
- **Children** under 5 years of age account for **40%** of the total number of food borne diseases, about 125,000 deaths per year.
- Diarrhea is the most common food borne disease, with about 550 million patients and 230,000 deaths each year



http://www.nhfpc.gov.cn/

NHFPC，2006-2016

1 Introduction

Salmonella

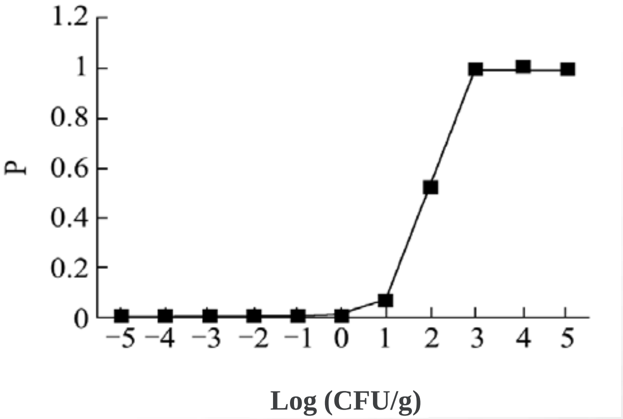
Salmonella

- Poultry supply chains including producers, processors, distributors and retailers face intense pressure from public health agencies and consumers concerning food safety.
- In China, approximately **70% of foodborne bacterial infections in humans were caused by *Salmonella***. It not only causes serious economic losses to the poultry industry in the country, but, poses a serious threat to human health.
- In nature, **chckein is the major host of *Salmonella*** and can provide for widespread transmission of the infection among poultry.

Bacteria	Clinical symptoms	distributed
Salmonella	Nausea, diarrhea, fever etc.	Eggs, poultry, meat

Bacteria	GB detection method	Limited standard
Salmonella	GB 4789.4-2010	n=5， c=0,m=0

N: the number of samples of a batch of products;
C: the number of samples in the batch of samples exceeds the limit of the number of samples (the results exceed the maximum number of qualified bacteria limit);
M: qualified bacteria limit



Exposure - dose model

2 Purpose

Walmart Foundation founded project:

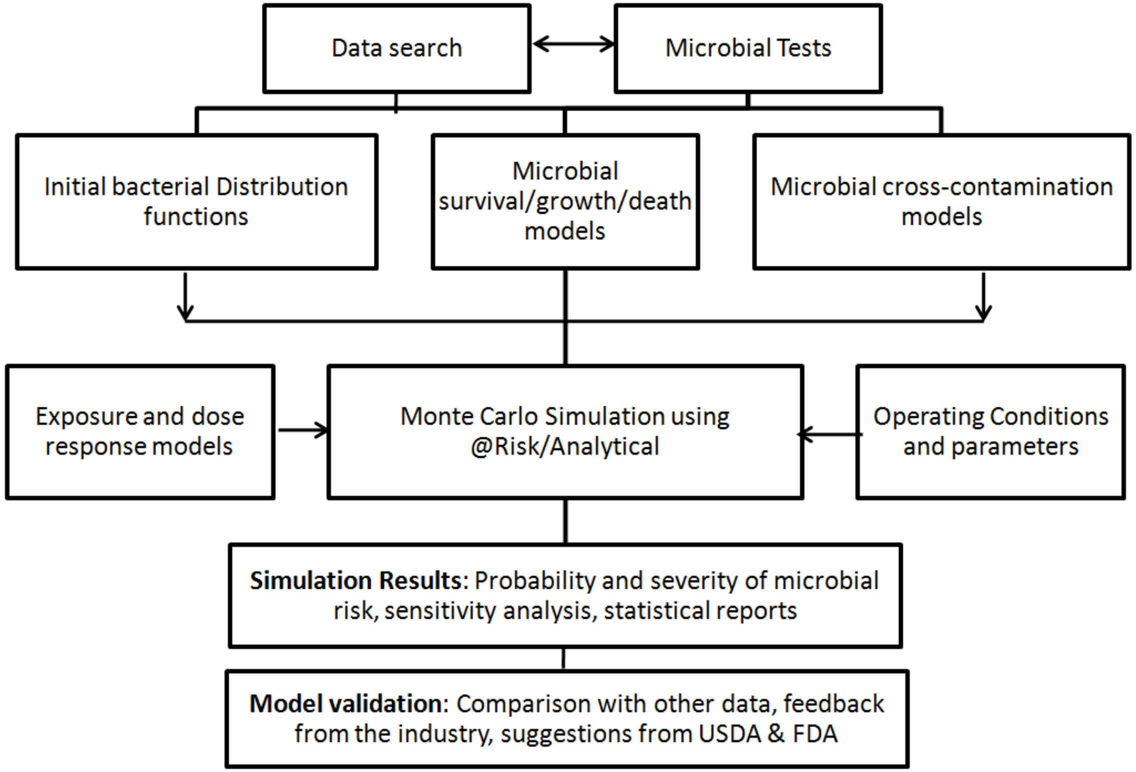
Poultry Excellence in China: Improving Food Safety in Poultry Supply Chains

3. Supply chain management integrated with risk assessment for food safety of poultry products:

- To construct a quantative risk assessment model for Salmonella in yellow broiler and white broiler from farm to table.
- To identify the critical control points where the bacteria prevalence and contamination level could be changed.
- To assess the effects of intervention measures aimed at reducing risk.

1 Introduction

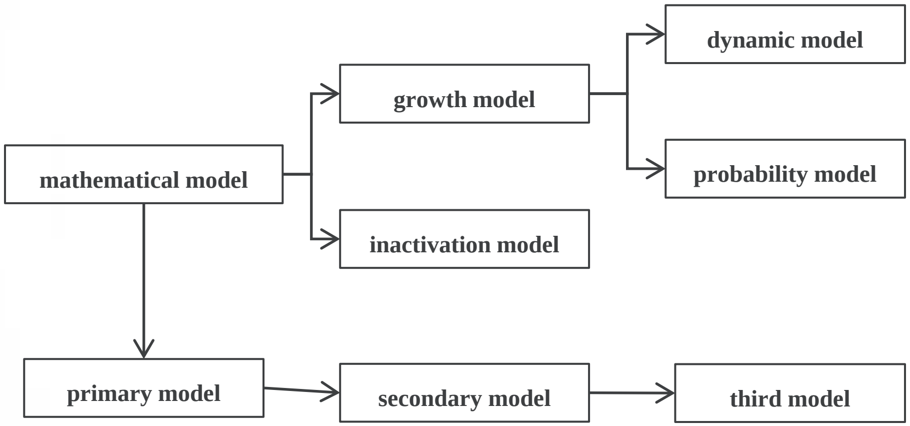
Microbiological Quantitative Risk Assessment

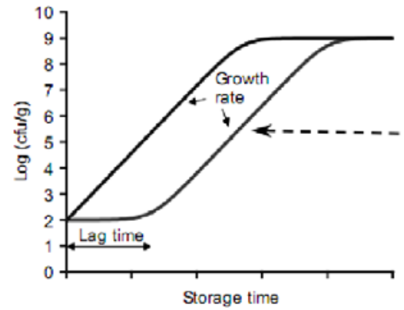


- A food from farm to table goes through the production, processing, distribution, sales and storage and many other links. In the process of exposure assessment, the main factors affecting the safety of food throughout the process should be considered and analyzed to find out, Breaking time lag and the result lagging behind of the traditional method and take effective measures to control risk.

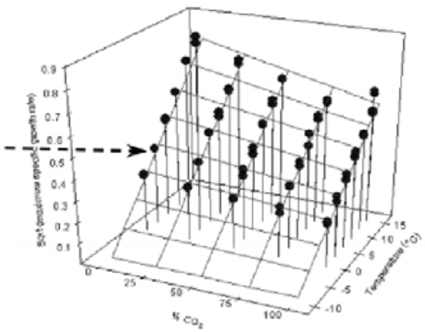
1 Introduction

Microbial prediction model classification





Primary model



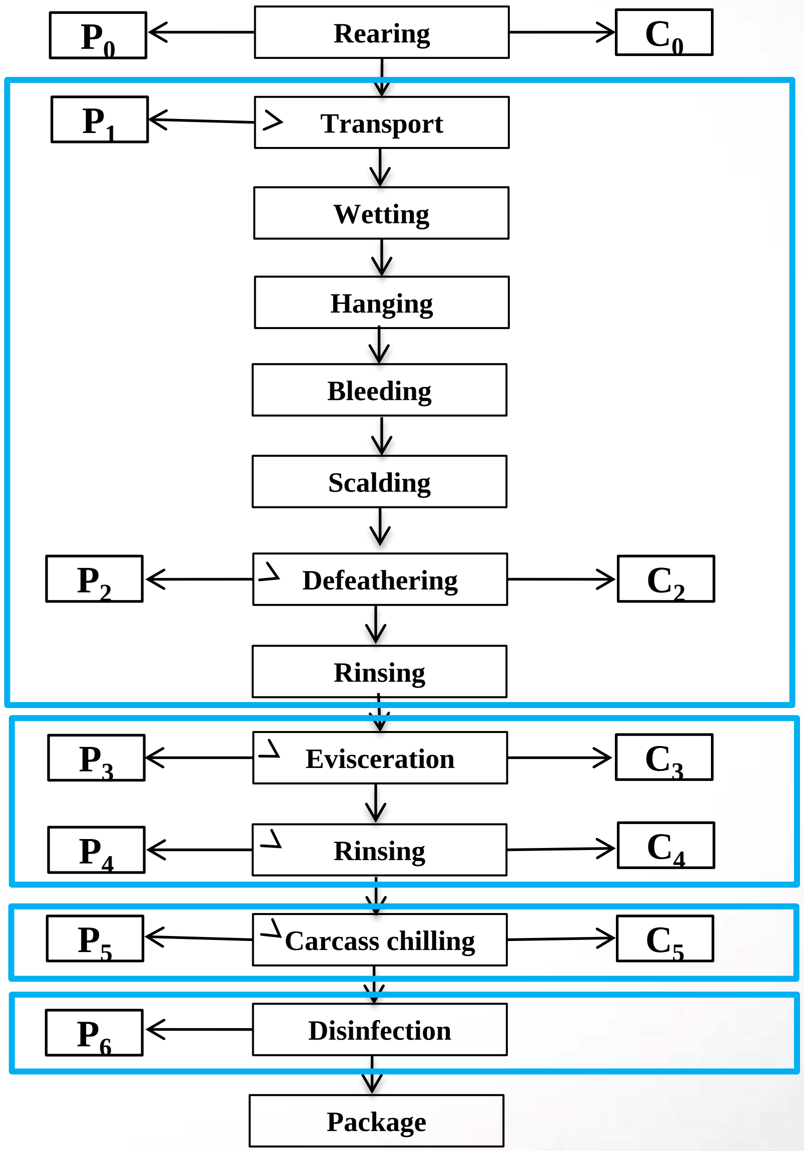
Secondary model

Primary models	Secondary models	Teriary models
Gompertz function	Square root models	Pathogen Modeling Programme
Logistic model	Arrhenius model	Growth Predictor
Baranyi model	Arrhenius model	Pseudomonas Predictor
Rosso model	Response surface models	ComBase
Monod model	γ-models	Sym' Previus
D value of inactivation	Z models	Seafood Spoilage and Safety Predictor

2 Purpose

Module	Factor
Module 1	The initial contamination prevalence, concentration, room temperature, time scald temperature, scald time.
Module 2	Bore out and Inside Washing cross contamination.
Module 3	Chilling temperature, time, cross contamination.
Module 4	Concentration of disinfection, temperature, time , cross contamination.

- The objective of this study was to compare the performance of empirical models for predicting the growth kinetics of *Salmonella* in chicken fillets under different temperatures.



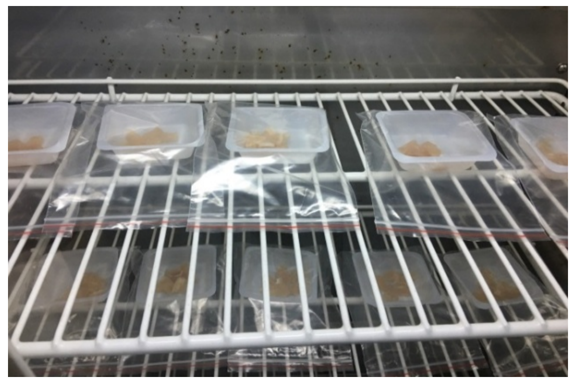
Schematic diagram of exposure assessment for *Salmonella* in yellow broiler slaughter house

3 Methods

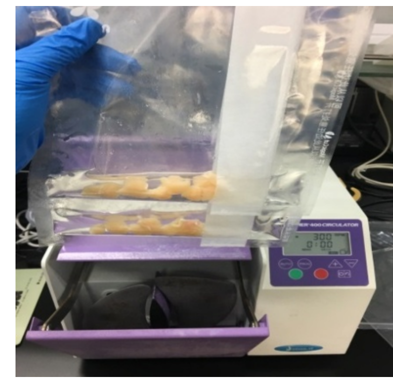
- Chicken fillets (size: 2cm×1cm×1cm; weight: 2±0.3g) were inoculated with three-strains of cocktail *Salmonella* (ATCC 14028, 50335, 51957) at the initial contamination level of 4~5 $\log_{10}$ CFU/g, and then stored at temperatures of 13, 16, 25, 33 and 37°C.

1、Inoculation

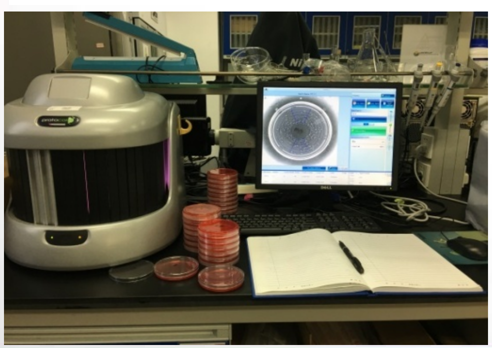
2、Incubate under different temperature



3、Stomacher



6、Colony Counter



5、Incubator, 37 ℃

4、Spiral plate

3 Methods

➢ Primary model

Huang model (Huang, 2008)

$$Y(t) = Y_0 + Y_{max} - ln\{e^{Y_0} + [e^{Y_{max}} - e^{Y_0}]\, e^{-\mu_{max} B(t)}\}$$

$$B(t) = t + \frac{1}{\alpha} ln \frac{1 + e^{-\alpha(t-\lambda)}}{1 + e^{\alpha\lambda}}$$

Baranyi model (Baranyi and Roberts, 1995)

$$Y(t) = Y_0 + \mu A(t) - ln\left\{1 + \frac{exp[\mu_{max} A(t)] - 1}{exp(Y_{max} - Y_0)}\right\}$$

$$A(t) = t + \frac{1}{\mu_{max}} ln[exp(-\mu_{max} t) + exp(-h_0) - exp(-\mu_{max} t - h_0)]$$

Reparamerized Gompertz model (Zwietering, Jongenburger, Rombouts, and van' t Riet, 1990)

$$Y(t) = Y_0 + (Y_{max} - Y_0) exp\left\{-exp\left[\frac{\mu_{max} e}{Y_{max} - Y_0}(\lambda - t) + 1\right]\right\}$$

Three-phase linear model (Buchanan, Whiting, and Damert, 1997)

$$y = y_0, if\ t < lag$$

$$y = y_0 + k(t - lag), if\ lag \leq t < t_{max}$$

$$y = y_{max}, if\ t \geq t_{max}$$

$$y = y_0, if\ t < lag$$

$$y = y_0 + k(t - lag), if\ t \geq lag$$

3 Methods

- Secondary model

Ratkowsky square-root model （Ratkowsky et al.，1983）

$$\sqrt{\mu} = a(T - T_0)$$

Huang square-root model（Huang，Hwang，and Phillips，2011a）

$$\sqrt{\mu} = a(T - T_{min})^{0.75}$$

Arrhenius-type model（Huang，Hwang，and Phillips，2011b）

$$\mu_{max} = a(T + 273.15)exp\left\{-\left[\frac{\Delta G'}{R(T + 273.15)}\right]^{n}\right\}$$

- Model evaluation

Statistical indices of R^2 and RMSE were used for model evaluation. Independent trials were conducted, and Bias factors (B_f) and Accuracy factors (A_f) were calculated for model validation.

$$\text{AIC} = n \times ln\left(\frac{SEE}{n}\right) + 2(p+1) + \frac{2(p+1)(p+2)}{df-2}$$

$$Af = 10^{(\Sigma(N_{pre} - N_{obs}))/n}$$

$$Bf = 10^{(\Sigma|N_{pre} - N_{obs}|)/n}$$

4 Results

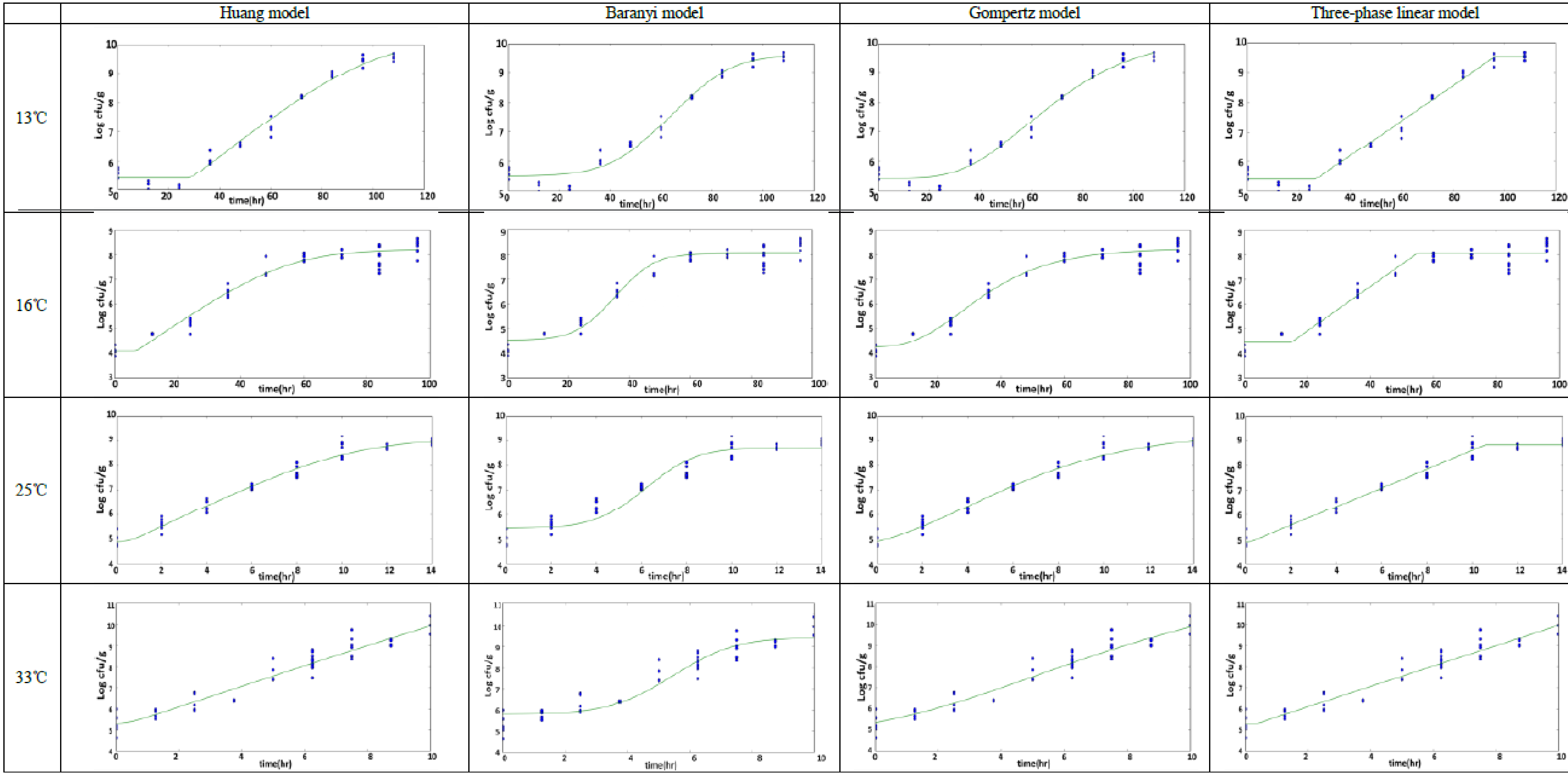


Fig.1 Primary model fitting results

The modified Gompertz model described growth data the best, followed by Huang model.

4 Results

Tab.1 Goodness-of-fit and comparison of primary model

		Huang model	Baranyi model	Gompertz model	Three-phase linear model
13℃	SSE	2.150	2.220	2.103	1.865
	MSE	0.065	0.065	0.064	0.057
	RMSE	0.255	0.256	0.252	0.238
	residual stdev	0.241	0.245	0.238	0.224
	AIC	-94.28	-95.10	-95.10	-99.55
	critical t-value	2.034	2.032	2.034	2.034
16℃	SSE	5.364	6.159	4.935	5.780
	MSE	0.114	0.128	0.105	0.123
	RMSE	0.338	0.358	0.324	0.351
	residual stdev	0.324	0.348	0.311	0.337
	AIC	-103.86	-99.81	-108.11	-100.05
	critical t-value	2.012	2.011	2.012	2.012
25℃	SSE	3.204	9.927	3.335	2.851
	MSE	0.056	0.171	0.059	0.050
	RMSE	0.237	0.414	0.242	0.224
	residual stdev	0.229	0.403	0.234	0.216
	AIC	-168.74	-102.76	-166.29	-175.85
	critical t-value	2.003	2.002	2.003	2.003
33℃	SSE	8.560	12.443	8.359	8.570
	MSE	0.171	0.244	0.167	0.168
	RMSE	0.414	0.494	0.409	0.410
	residual stdev	0.398	0.480	0.393	0.398
	AIC	-88.46	-71.26	-89.75	-91.40
	critical t-value	2.009	2.008	2.009	2.008

Tab.2 Fitting parameters of primary model

	Parameters	Huang model	Baranyi model	Gompertz model	Three-phase linear model
13℃	Y0	5.397	5.508	5.439	5.397
	Lag	28.41	-	33.41	26.61
	Ymax	10.11	9.587	10.24	9.536
	mumax	0.066	0.110	0.072	0.059
16℃	Y0	4.106	4.525	4.242	4.449
	Lag	7.084	-	12.13	15.03
	Ymax	8.207	8.043	8.241	8.063
	mumax	0.088	0.191	0.094	0.090
25℃	Y0	4.868	5.424	4.541	4.868
	Lag	0.540	-	-0.111	0.209
	Ymax	9.111	8.691	9.379	8.807
	mumax	0.444	1.073	0.433	0.379
33℃	Y0	5.318	5.811	4.865	5.315
	Lag	0.383	-	-0.023	0.380
	Ymax	12.40	9.419	12.26	-
	mumax	0.490	1.249	0.527	0.482

The average maximum growth rates of *Salmonella* in chicken fillets were 0.075, 0.090, 0.438, 0.508, 0.785 CFU/g per hour at 13, 16, 25, 33 and 37°C, respectively.

4 Results

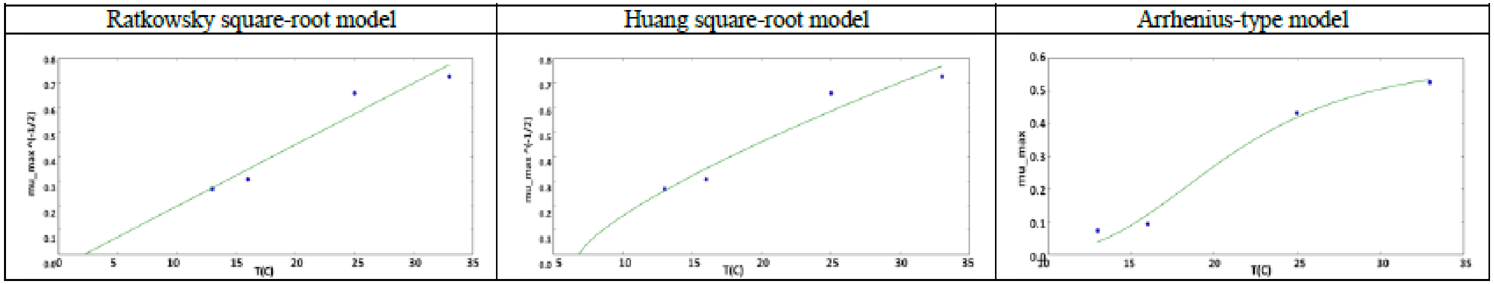


Fig.2 Secondary model fitting results

Tab.3 Goodness-of-fit and comparison of secondary model

	Ratkowsky square-root model	Huang square-root model	Arrhenius-type model
SSE	0.011	0.009	0.002
MSE	0.006	0.005	0.002
RMSE	0.075	0.068	0.046
residual stdev	0.053	0.048	0.023
critical t-value	4.303	4.303	12.71
R^2	0.932	0.942	0.988
Bf	1.01	1.01	1.01
Af	1.10	1.10	1.04

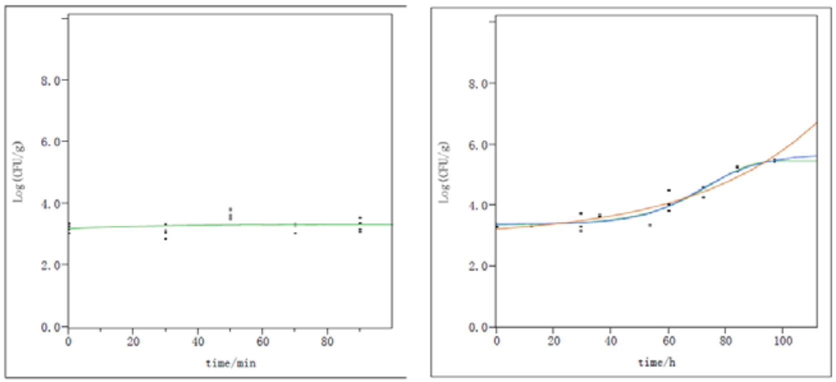
R^2 for Arkhenky model describing the maximum growth rate obtained from the modified Gompertz model was 0.99, which was the best among selected secondary models (RMSE=0.047, B_f=1.01, A_f=1.04).

4 Results

- Besides, another five-strain cocktail Salmonella were used to validate the models at 8C, 18C, 25C, 33C and the Af and Bf were within the acceptable range (using modified Gompertz model and Arkhenky model).

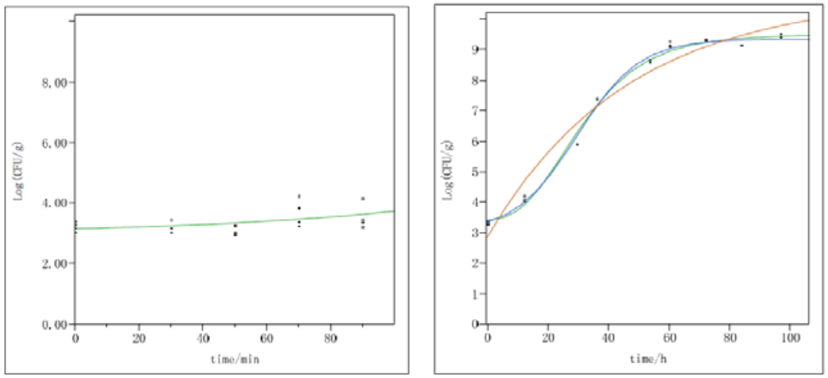
8C

30min~90min   0~100h



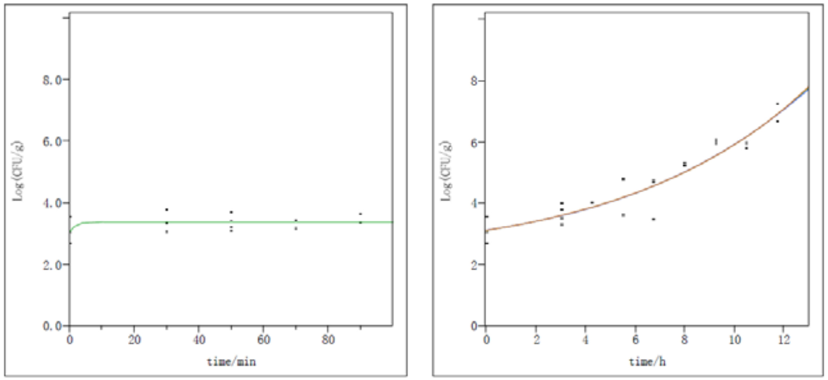
18C

30min~90min   0~100h



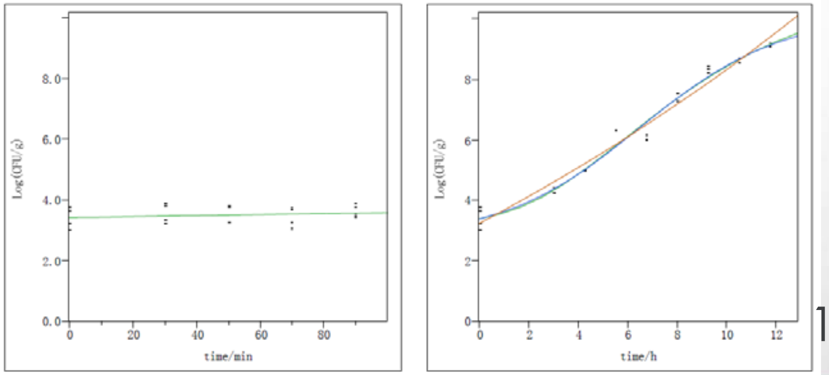
25C

30min~90min   0~12h



33C

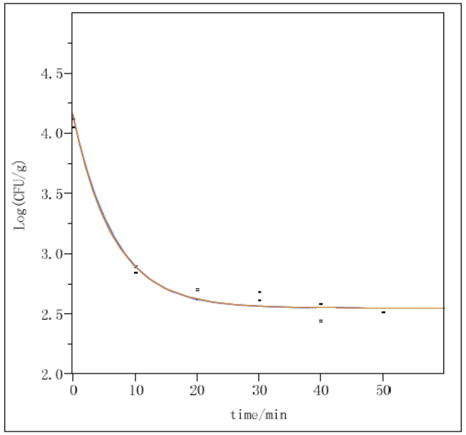
30min~90min   0~12h



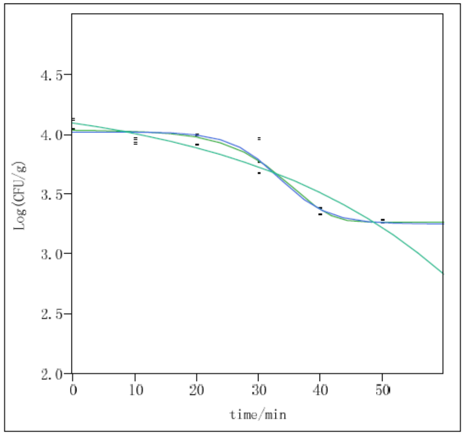
4 Results

- Other works: Carcass chilling & Disinfection
- Concentration of disinfection, temperature, time

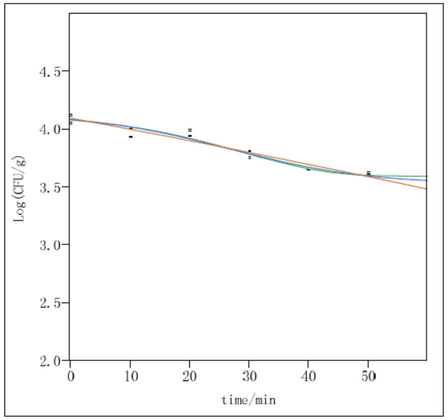
90ppm



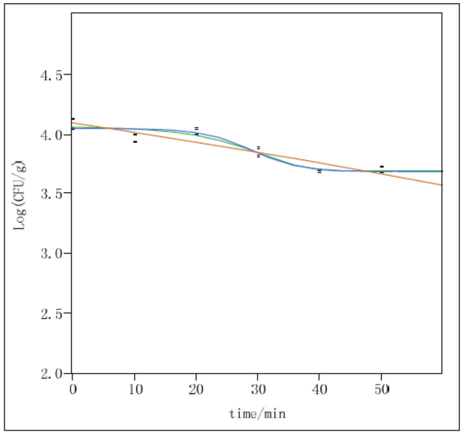
70ppm



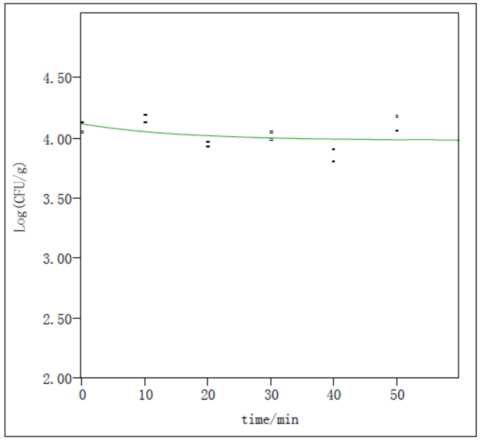
50 ppm



30 ppm



0 ppm



5 Significance

- The selected model is able to predict the growth of *Salmonella* in chicken fillets under different temperatures in processing and storage conditions, which will be used in microbial prediction models and quantitative risk assessment model for *Salmonella* in white and yellow broiler supply chains.

Thanks for your attention.