

Chapter 2 Production Module

Overview

The purpose of the Production Module is to simulate the number of cattle presented for slaughter that are *E. coli* O157:H7 -affected. It models the movement of cattle from the farm through livestock markets to slaughter plants. Both intestinal carriers and hide contaminated cattle are to be simulated.

Inputs to the Production module include national data on herd types (i.e., number of breeding [dairy and beef] and feeding herds), herd sizes, and number of cattle marketed by the types of herds. In addition, the number of cattle processed per type of slaughter plant is an input. Outputs from this module will be the number and percent of cattle that have *E. coli* O157:H7 in their intestinal tracts – or on their hides - just before slaughter. For affected cattle, an additional output is the density of organisms per gram (for intestinal carriers) or per square centimeter of surface area (for hide carriers). For the purposes of this document, cattle are defined as *E. coli* O157:H7 -affected if they have the organism either in their intestinal tract or on their hide.

Time units will be slaughter plant-days. For example, if slaughter plants are stratified into small and large plants, then each iteration of the model will simulate the processing of all cattle by plants in these strata. Using this approach, we can estimate the annual number of cattle processed, and the annual number of *E. coli* O157:H7 -positive cattle processed, in each plant size stratum.

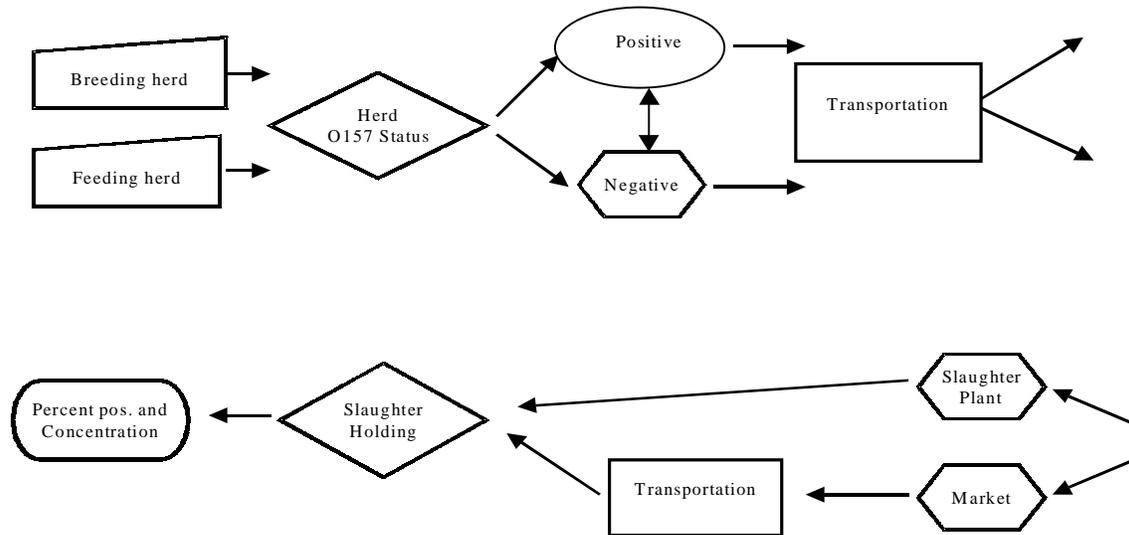
Module structure

During the movement of cattle from the farm to the slaughter plant, *E. coli* O157:H7 prevalence in marketed cattle is modified by the elapsed time in marketing channels. The three general stages of the Production Module are; on-farm, transport, and slaughter plant.

A simple flowchart of the Production Module (Figure 1) shows that cattle originating from breeding and feeding herds are separately modeled. For either herd type, the model predicts the *E. coli* O157:H7 status of the herd (i.e., affected or not), then predicts the within-herd prevalence of *E. coli* O157:H7 for affected herds. Cattle are modeled as either moving directly to slaughter or moving through one or more livestock markets before transport to slaughter. During movement from the farm to the slaughter plant, transmission of *E. coli* O157:H7 can occur between affected and unaffected cattle. Finally, cattle are penned and held at the slaughter plant before they are slaughtered. Again, transmission of *E. coli* O157:H7 from affected to unaffected cattle can occur during holding at the slaughter plant. The *E. coli* O157:H7 prevalence just prior to slaughter, and the density of *E. coli* O157:H7 organisms in, or on, affected cattle, represent the outputs from this module.

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Figure 1. *E. coli* O157 Production Module Flowchart



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3 Variable descriptions and evidence

4 Descriptions of variables needed to simulate the Production Module are presented below.
5 Evidence pertaining to each variable is listed below its description.

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7 ***Slaughter plant throughput per day.*** Presently, we plan to model different strata of
8 slaughter plants based on cattle throughput per day. For each size stratum, the number of
9 cattle slaughtered per day is a random variable which is dependent on whether the
10 slaughter plant processes cull breeding cattle or fed cattle.

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Evidence –

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- FSIS data shows the annual production per plant for cull breeding cattle (i.e., cows and bulls intended and/or used for breeding that are removed from production) and fed cattle (i.e., steers and heifers that are managed for beef production) slaughter plants. Using a cutoff of 200 animals slaughtered per year (an average of <1 animal per day) reduces the number of plants for consideration in the model by 43% in fed cattle slaughter facilities and by 66% in cull cattle slaughter facilities. Cattle processed in these plants account for <1% of cull or fed cattle annually slaughtered.

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Plant type	Annual number slaughtered	Number of plants in stratum (%)	Stratum percent of total production
Fed cattle	<200	336 (43)	0.1%
	200 to 100,000	397 (51)	3.6%
	100,001 to > 1million	39 (5)	96.3%
Cull cattle	<200	463 (66)	0.5%
	200 to 25,000	189 (27)	9.5%
	25,001 to >300,000	52 (7)	90.0%

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Source: USDA-FSIS

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- Demographic data concerning U.S. cattle herds is also available.

	Herd size (no. head per herd)	Number of herds (%)
Feeding cattle	1000-1999	875 (41.5)
	2000-3999	515 (24.4)
	4000-7999	304 (14.4)
	8000-15,999	187 (8.9)
	16,000-31,999	138 (6.5)
	32,000+	91 (4.3)
	Total	2,110
Breeding cattle		
Beef	1-49	718,500 (79.7)
	50-99	107,480 (11.9)
	100-499	69,160 (76.8)
	500+	5,540 (0.6)
	Total	900,680
Dairy	1-29	39,780 (31.4)
	30-49	28,410 (22.4)
	50-99	36,930 (29.1)
	100-199	14,750 (11.6)
	200+	6,930 (5.5)
	Total	126,800

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Source: USDA-NASS, 1996 (feedlot) and 1997 (beef and dairy).

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Truckloads accounting for daily throughput . The number of truckloads of cattle per day that are processed at slaughter plants is used to determine the origin of the cattle.

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Assuming that trucks either originate from a farm or a livestock market, the cattle on a

1 truck represent a cohort in which transmission of *E. coli* O157:H7 could occur. The
2 number of truckloads presented for slaughter is dependent on the size of plant and the
3 type of cattle.

4 **Evidence –**

- 6 • Generally, large capacity plants will receive cattle by the semi-load while small
7 capacity plants will receive cattle by smaller conveyances (e.g., gooseneck trailers,
8 horse trailer, pickup truck). Yet, some cattle are hauled to large plants in smaller
9 conveyances while others are hauled to small plants in semi-loads. Cattle hauled to
10 slaughter plants from livestock markets will usually be transported by the semi-load.
11 Cattle hauled directly from feedlots will usually move by the semi-load. Dairy and
12 beef cattle may move directly from farm to slaughter plant via the semi-load or via
13 smaller conveyances. This information is based on conversations within FSIS and
14 personal experience.

15
16 **Truck capacity.** The number of cattle shipped to slaughter plants per truck is also a
17 random variable in this module. The size of truck used to move cattle is dependent on the
18 herd type (breeding or feeding) and whether the cattle moved directly to slaughter or
19 through a livestock market.

20 **Evidence –**

- 21 • Generally, a semi-tractor trailer will carry 40-50 head of cattle, depending on the type
22 of cattle and distance of travel. Smaller conveyances may carry from one to typically
23 less than ten head. This information is based on conversations within FSIS and
24 personal experience.

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27 **Fraction of truckloads from livestock markets.** The percent of trucks comprising a
28 day's slaughter that originated from livestock markets (or buying stations) is dependent
29 on the type of slaughter plant. The complement of this variable is the fraction of
30 truckloads that moved direct from the farm to the slaughter plant.

31 **Evidence –**

- 32 • Approximately 40% of culled cows and bulls are marketed directly to slaughter
33 establishments. In contrast, approximately 95% of fed steers and heifers are marketed
34 directly to slaughter establishments. (USDA-APHIS-VS, 1994).

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37 **Duration of marketing from farm to market to slaughter plant.** Presently, we are
38 planning to model the total time elapsed between cattle leaving the farm and arriving at
39 the slaughter plant. This elapsed time will generally be longer for cattle moving through
40 livestock markets than for cattle moving directly from farm to slaughter. Time spent in
41 marketing channels is directly related to the risk of negative cattle becoming positive. We
42 plan to model the occurrence of new infections during livestock movement as a binomial
43 process where the number of newly positive cattle in a group of n cattle is a function of
44 the likelihood of becoming positive during holding and transportation. If y is the
45 calculated daily incidence of infection with *E. coli* O157:H7 and d is the duration (in
46 days) that a cohort is exposed to positive cattle, then $(1-y)^d$ is the probability that no

1 transmission occurs during d days. Consequently, $1-(1-y)^d$ is the probability that
 2 transmission will occur during d days.

3
 4 **Evidence –**

- 5 • Average time between sampling on farm of cull cows and slaughter was 2 days (range
 6 0-6 days). (Rice, 1997)
- 7 • Over 70% of cull cattle slaughter plants report receiving animals from distances >150
 8 miles. Less than 50% of fed cattle slaughter plants reported receiving cattle from
 9 distances >150 miles. . (USDA-APHIS-VS, 1994).

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 12 **Herd prevalence (fraction of herds with any *E. coli* O157:H7).** The fraction of
 13 herds that contain one or more *E. coli* O157:H7 -colonized cattle (i.e., herd prevalence)
 14 affects the likelihood that a given herd may contribute shedding animals to a cohort
 15 destined for slaughter. Depending on the available evidence, breeding and feeding herd
 16 prevalence at a national level may have different probability distributions. Evidence
 17 regarding herd prevalence will be adjusted to account for the likelihood that herds would
 18 be detected using sampling schemes that assay less than 100% of cattle in herds.
 19 Regional coverage, sampling methods, and culture methods in these studies will also be
 20 considered when depicting herd prevalence.

21
 22 **Evidence –**

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Study	Herd type	Animals sampled	Herds sampled	Herds <i>E. coli</i> O157-positive (%)	Sample size per herd
USDA-APHIS-VS, 1998	Dairy	Cows	91	22 (24%)	45-50
Hancock,1997a	Dairy	Post-weaned heifers	36	27 (75%)	60/month X 6 months = 360
Faith, 1996	Dairy	Heifers	70	5 (7.1%)	~8
Zhao, 1995	Dairy	Heifers and calves	50	11 (22%)	~13
USDA-APHIS-VS, 1994	Dairy	Calves	1068	19 (1.8%)	~6
Hancock, 1997b	Feedlot	All stages	100	63 (63%)	120
Hancock, 1998	Dairy	Heifers	6	6 (100%)	180
	Feedlot	All stages	6	6 (100%)	180
Hancock, 1994	Dairy	All ages	60	5 (8%)	60 +
	Beef	Cows	25	4 (16%)	~60
	Feedlot	All stages	4	2 (50%)	120

- The USDA-APHIS-VS, Hancock (1997b), and Zhao (1995), studies listed above were national in scope. In contrast, the remaining studies were conducted in the northwestern U.S. (Idaho, Oregon, and Washington) or Wisconsin. Furthermore, the USDA-APHIS-VS, Hancock (1997b), and Faith (1996) studies were based on randomly selected herds while the remaining studies were not. Nevertheless, there is no apparent bias in the results of these remaining studies.
- There is no available evidence to support the hypothesis that herd prevalence based on hide contamination is different from that based on fecal shedding.

Within-herd cattle prevalence of intestinal carriers. The fraction of cattle that are *E. coli* O157:H7 -colonized on any particular day (i.e., within-herd prevalence), given that the herd is *E. coli* O157:H7 -affected, influences the number of shedding cattle that an affected herd contributes to a cohort destined for slaughter. Absolute sensitivity of testing used to detect colonized animals may be used to adjust estimates from the reported evidence. Because we are interested in the prevalence at the time cattle leave the farm or feedlot, the ages of cattle sampled will also affect the contribution of each piece of evidence to this variable. For example, survey data on cull cow prevalence is more valuable than data on calf prevalence for characterizing this variable.

Evidence –

Study	Pos. Herd Type	Animals Sampled in Pos. Herds	Number of Animals Sampled In Pos. Herds	Animals <i>E. coli</i> O157 – positive (%)
Garber, 1998	Dairy	Cows	951	32 (3.4%)
		Culls	320	19 (6%)
Rice, 1997	Dairy	Cull cows	89	5 (5.6%)
Hancock, 1997a	Dairy	Heifers	9,720	179 (1.8%)
Besser, 1997	Dairy	Mostly cows	2,662	69 (2.6%)
Zhao, 1995	Dairy	Heifers	132	7 (5.3%)
Dargatz, 1997	Feedlot	All stages	11,881	209 (1.7%)
Hancock, 1998	Dairy	Heifers	1,097	25 (2.3%)
	Feedlot	All stages	1,046	38 (3.6%)
Hancock, 1994	Dairy	All ages	300	10 (3.3%)
	Beef	Cows	240	10 (4.2%)
	Feedlot	All stages	240	2 (0.8%)

- Broth enrichment of samples, plating of enriched samples onto sorbitol-McConkey (SMAC) media enriched with selective antibiotics, and plating at two dilutions were shown to be important components of protocols for detecting cattle shedding *E. coli* O157:H7 . Use of immunomagnetic beads during incubation was shown to be slightly more sensitive in detecting known positive samples than broth enrichment alone. Calculated relative sensitivity varied from 33% (when 0.1g samples were enriched and plated on SMAC with cefixime) to 79% (when 10g samples were enriched then plated on SMAC with cefixime and tellurite) for samples collected from naturally

- 1 colonized cattle. The minimum 50% detection threshold limit (CFU/g) in samples
2 from experimentally inoculated calves was 10^2 . This minimum threshold was
3 calculated for both routine enrichment and immunomagnetic bead separation.
4 (Sanderson, 1995)
- 5 • Of the studies listed above, most added antibiotics to the SMAC media. Size of
6 sample processed varied from 0.1 g (e.g., all Hancock et al. studies) to 1 g (e.g.,
7 Garber, 1998) to 10 g (e.g., Zhao, 1995). None of these survey results reflect use of
8 the immunomagnetic beads technique.
- 9

10 ***Duration that cattle remain E. coli O157:H7 -colonized.*** The length of time that
11 colonized cattle carry viable *E. coli* O157:H7 organisms in their intestinal tracts is used to
12 calculate the incidence of newly acquired intestinal infection during transport from farm
13 to slaughter. Incidence is the probability of becoming positive during a specified time.
14 Prevalence is the probability of being positive at any given time. For a given prevalence
15 of positive cattle in a cohort moving to slaughter, the incidence of new positives per day
16 can be calculated as Prevalence + Duration of days cattle remain positive.

17

18 Evidence –

- 19 • Thirty-five of 56 *E. coli* O157:H7-positive cattle were negative when retested 30 days
20 later, suggesting that duration of infection is typically <30 days for most cattle.
21 However, 1 of the 56 cattle maintained positive culture results four consecutive
22 months with the same PFGE type of *E. coli* O157:H7, suggesting that infection could
23 be maintained >120 days in some cattle. (Besser, 1997)
- 24

25 ***Within-herd cattle prevalence of hide contaminated cattle.*** The fraction of hide-
26 contaminated cattle in affected herds is assumed to correspond with the fraction of
27 intestinal carriers in these herds. The dynamics of hide contamination seem complex.
28 Cattle hides may be contaminated via direct fecal contamination, environmental
29 contamination (e.g., mud, dirt, or bedding), or skin to skin contact. Furthermore, the
30 extent to which a cattle hide is contaminated can be from an area less than 1 cm^2 to
31 something close to the entire surface area of the animal. Because there is inadequate
32 research on hide contamination, we will model the prevalence of hide contaminated cattle
33 from farm to slaughter as some function of the prevalence of intestinal carriers.

34

35 Evidence –

- 36 • In a study of adult cattle cohorts moving from farm to slaughter, fecal and hair
37 samples were cultured for *Salmonella typhimurium*. Prior to leaving the farm, the
38 prevalence of fecal- and hair-positive cattle was 4/80 (5%) and 6/80 (7.5%),
39 respectively. Following transport to the slaughter plant, the prevalence of fecal- and
40 hair-positive cattle was 7/80 (8.7%) and 20/80 (25%), respectively. Such findings
41 suggest that hair contamination increases substantially during transportation while
42 fecal carriage increases less during this same period. (Puyalto, 1997)
- 43

44 ***E. coli O157:H7 per gram of feces in, or per cm^2 of hide on, affected cattle.*** The
45 density of *E. coli* O157:H7 organisms shed in feces from colonized cattle – or present on

1 the hide of contaminated cattle - is used as a starting point for the transmission of
2 organisms from live cattle to carcasses during the slaughter process.

4 **Evidence –**

- 5 • Data show that 15 (48%) of 31 *E. coli* O157:H7-infected cattle had concentrations of
6 $<10^2$ CFU/g of feces. In this cohort, the concentration ranged up to 10^5 CFU/g.
7 (Cassin, 1998 adapted from Zhao, 1995)
- 8 • An *E. coli* O157:H7-positive bovine manure pile was culture positive at a
9 concentration of $<10^2$ CFU/g for 47 days. (Kudva, 1998)
- 10 • The distribution of *E. coli* (Biotype I) on raw beef carcasses showed that ~80% of
11 those carcasses found positive had concentrations $<10^2$ CFU/g. The maximum
12 concentration detected was $\leq 10^6$ CFU/g. (USDA-FSIS, 1994)
- 13 • There is no available evidence on the concentration of *E. coli* O157:H7 per surface
14 area of hide. Lacking this evidence, we might assume some equivalency in the
15 distributions of *E. coli* O157:H7 per gram of feces and per cm^2 of hide. This
16 assumption seems reasonable given the similarity - described above - between
17 concentrations found in feces and those found on carcasses. Because hide
18 contamination occurs as a result of organisms shed in the feces, we might expect
19 concentrations on hides to be no greater than what we see in feces. What is not
20 implied here is the extent to which hides are contaminated. The extent of hide
21 contamination (i.e., the proportion of total cattle surface area which is contaminated)
22 is not available from the literature.

23
24 **Other considerations.** Although there is evidence suggesting a seasonal pattern in
25 cattle prevalence for *E. coli* O157:H7, and this pattern is also evident in human infection
26 data, we are not planning to incorporate seasonal effects in the model at this time. It is
27 expected that season is a confounding variable with risk factors that are not yet clearly
28 defined in cattle. Season is also correlated with other variables in the model (e.g., number
29 and type of cattle slaughtered per day), and its incorporation would complicate the
30 development of a working model.

31
32 We are not planning to explicitly incorporate on-farm risk factors in the model. On-farm
33 research of *E. coli* O157:H7 has explored the role of many putative risk factors in the
34 maintenance and transmission of this agent in herds. This research is still inconclusive.
35 Yet, the incorporation of risk factor information into the model should be relatively
36 direct, once such associations are demonstrated through research.

37
38 Because risk factors will typically affect either the herd, or within-herd, prevalence of *E.*
39 *coli* O157:H7, their influence can be modeled simply by adjusting the prevalence
40 variables in this module relative to the baseline distributions, after accounting for the
41 frequency of the risk factor among the population of herds/cattle. For example, suppose a
42 study should find that of herds with a particular risk factor, 100% are *E. coli* O157:H7-
43 affected. The study also show that 50% of herds without that risk factor are *E. coli*
44 O157:H7-affected. In this case, the risk difference between herds with the factor and
45 those without the factor is 50% (100%-50%). If that risk factor occurs in 50% of herds,
46 then the risk attributable to that factor among the total population is 25% (Prevalence of

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1 risk factor X risk difference = 50% X [100%-50%]). We calculate in this example that the
2 overall prevalence of positive herds is 75% ([Prevalence of risk factor X Prevalence of *E.*
3 *coli* O157:H7 herds in risk factor group] + [Prevalence of no risk factor X Prevalence of
4 *E. coli* O157:H7 herds in non-risk factor group] = [50% X 100%]+[50% X 50%]).
5 Therefore, the fraction of herd prevalence explained by this risk factor is 33% (25% /
6 75%). Complete control of this risk factor should result in a 33% reduction in herd
7 prevalence and would be modeled as such (with attendant uncertainty).
8

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