**Table headings for sensitivity analyses simulations, including parameter estimates and model outputs**

Parameters included in all simulations

Temp: Constant temperature used in simulations (20°C, 24°C, 25°C, 30°C)

Parameters included in global sensitivity analysis

ddt: maximum distance proximity to transfer STEC directly from an infectious individual to an susceptible individual

pgrazeinfect: Probability of contact with CFU's of STEC in a contaminated grass patch

recovertime: Time in days until recovery after initial infection

plnmean: mean of the Lognormal-Poisson distribution sampled to determine CFU’s transmitted from an infectious individual to a susceptible individual.

plnsd: standard deviation of the Lognormal-Poisson distribution sampled to determine CFU’s transmitted from an infectious individual to a susceptible individual.

C: Concentration of STEC in feces (CFU/g)

K: Dose where 50 % of primary susceptible individuals get infected

SImult: Multiplier for K to increase resistance to secondary Infections

Parameters included in global sensitivity analysis of environmental structure

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NumTree: The number of trees included in the model

Meantree: the mean distance between trees

GtWratio: Grass (edible) to weed (non-edible) ratio in pasture

Lakesize: Size of lake in pasture

Shaderadius: Radius of shade cast by trees

X: X coordinate of lake creation point

Y: Y coordinate of lake creation point

Pos: characterization of lake position; Corner = originating in corner of pasture; Semi=Semi-circular along edges of pasture; Circle=circular pond in center of pasture (Note, this did not code for a parameter and was only for descriptive purposes).

Expanse: factor used to adjust the specified size from the default semi-circular along edge position

Parameters included in local sensitivity analysis

Basegrowth: Growth rate for grass (units per hour)

Latencyphase: number of days after colonization until shedding begins

Prob\_nearest\_patch: the proability: Probability of selecting the nearest water patch versus a random water patch

prob\_stay\_and\_drink: Probability of dominant cow staying in the current water patch to drink

prob\_move\_to\_dominant: Probability subordinate cow moves towards dominant cow during drinking

prob\_move\_new\_patch: The probability of staying and grazing versus moving to a new patch

prob\_move\_while\_rest\_dom: Probability of dominant cow moving while resting

prob\_move\_while\_rest\_sub: Probability of subordinate cow moving while resting

**Model outputs**

R0: The total number of secondary colonizations derived from the initially infected individual during the course of its infectious period, derived either from direct or environmental (Graze, Water) pathways.

Manure: Total average manure (Fecal pats) per day

TotalInf: Total incident cases occurring over the course of the model simulation from all pathways.

Prev: Prevalence over model simulation period, calculated as TotalInf/24 (since all simulations started with 1 incident case).

PDInf: Total primary incident cases (first time colonizations) from a direct pathway

PWInf: Total primary incident cases (first time colonizations) from the water pathway

PGInf: Total primary incident cases (first time colonizations) from the grazing pathway

SDInf: Total secondary (re-colonizations) from a direct pathway

SWInf: Total secondary incident cases (re-colonizations) from the water pathway

SGInf: Total secondary incident cases (re-colonizations) from the grazing pathway

DI: Total incident cases from a direct pathway

WI: Total incident cases from a water-based pathway

GI: Total incident cases from a grazing-based pathway