The data in the model projection was used in this simulation. 100 iterations of simulation were run per each rotation crossed with corn weed management regime, with non-manipulated seed production.

# event sequence: seed dropped - chisel - overwinter - field cultivator - emerge - survive - new seed  
  
# create a function   
# vec: starting seed column  
# poh: post-harvest tillage  
# ow: over winter seed survival  
# prt: pre-planting-tillage  
# em: emergence  
# sv: seed survival rate and seedling to maturity success rate  
# seed: fecundity  
  
rot\_2year\_conv <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,  
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S){  
  
 # corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
# soybean phase dynamics  
  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn   
  
 after\_soy  
}  
  
rot\_2year\_low <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,  
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S){  
  
  
 # corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
# soybean phase dynamics  
  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn   
  
 after\_soy  
}

##### with corn under conventional weed management {-}  
t <- 100  
N\_2yr\_conv <- list() # blank data frame to save loop output   
N\_2yr\_conv[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_2yr\_conv[[i]] = rot\_2year\_conv(vec = N\_2yr\_conv[[i-1]],  
 poh\_C = fall\_tillage$C2\_conv,  
 ow\_C = overwinter$C2\_conv,  
 prt\_C = spring\_tillage$C2\_conv,  
 em\_C = emergence$C2\_conv,  
 sv\_C = summer\_survival$C2\_conv,  
 seed\_C = fecundity18$C2\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S2\_conv,  
 ow\_S = overwinter$S2\_conv,  
 prt\_S = spring\_tillage$S2\_conv,  
 em\_S = emergence$S2\_conv,  
 sv\_S = summer\_survival$S2\_conv,  
 seed\_S = fecundity18$S2\_conv)  
}  
  
N\_2yr\_conv\_df <- N\_2yr\_conv %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "2-year",  
 Corn\_weed\_management = "conventional") %>%  
 na.omit()

##### with corn under low herbicide weed management {-}  
N\_2yr\_low <- list() # blank dataframe to save loop output   
  
N\_2yr\_low[[1]] <- starting\_point   
for (i in 2:t) {   
 N\_2yr\_low[[i]] = rot\_2year\_low(vec = N\_2yr\_low[[i-1]],  
 poh\_C = fall\_tillage$C2\_low,  
 ow\_C = overwinter$C2\_low,  
 prt\_C = spring\_tillage$C2\_low,  
 em\_C = emergence$C2\_low,  
 sv\_C = summer\_survival$C2\_low,  
 seed\_C = fecundity18$C2\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S2\_low,  
 ow\_S = overwinter$S2\_low,  
 prt\_S = spring\_tillage$S2\_low,  
 em\_S = emergence$S2\_low,  
 sv\_S = summer\_survival$S2\_low,  
 seed\_S = fecundity18$S2\_low)  
}  
  
N\_2yr\_low\_df <- N\_2yr\_low %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = sqrt(lambda\_cycle),  
 Rotation = "2-year",  
 Corn\_weed\_management = "low") %>%  
 na.omit()

rot\_3year\_conv <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O){  
   
  
  
  
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
   
 after\_oat  
}  
  
### low herbicide weed management  
## Manipulation note: if cohorts 1 through 3 were reduced to rlnorm(1, 2.65, 0.89), alphas are around 0.5 --> super "safe", but hard  
## cohorts 1 through 3 at rlnorm(1, 5.2, 0.51): more realistic  
rot\_3year\_low <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O){  
   
  
  
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
   
 after\_oat  
}

##### with corn under conventional weed management {-}  
N\_3yr\_conv <- list() # blank dataframe to save loop output   
  
N\_3yr\_conv[[1]] <- starting\_point   
  
  
for (i in 2:t) {   
 N\_3yr\_conv[[i]] = rot\_3year\_conv(vec = N\_3yr\_conv[[i-1]],  
 poh\_C = fall\_tillage$C3\_conv,  
 ow\_C = overwinter$C3\_conv,  
 prt\_C = spring\_tillage$C3\_conv,  
 em\_C = emergence$C3\_conv,  
 sv\_C = summer\_survival$C3\_conv,  
 seed\_C = fecundity18$C3\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S3\_conv,  
 ow\_S = overwinter$S3\_conv,  
 prt\_S = spring\_tillage$S3\_conv,  
 em\_S = emergence$S3\_conv,  
 sv\_S = summer\_survival$S3\_conv,  
 seed\_S = fecundity18$S3\_conv,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O3\_conv,  
 ow\_O = overwinter$O3\_conv,  
 prt\_O = spring\_tillage$O3\_conv,  
 em\_O = emergence$O3\_conv,  
 sv\_O = summer\_survival$O3\_conv,  
 seed\_O = fecundity18$O3\_conv)  
}  
  
N\_3yr\_conv\_df <- N\_3yr\_conv %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,3),  
 Rotation = "3-year",  
 Corn\_weed\_management = "conventional") %>%  
 na.omit()

##### with corn under low herbicide weed management {-}   
N\_3yr\_low <- list() # blank dataframe to save loop output   
  
N\_3yr\_low[[1]] <- starting\_point   
  
  
for (i in 2:t) {   
 N\_3yr\_low[[i]] = rot\_3year\_low(vec = N\_3yr\_low[[i-1]],  
 poh\_C = fall\_tillage$C3\_conv,  
 ow\_C = overwinter$C3\_low,  
 prt\_C = spring\_tillage$C3\_low,  
 em\_C = emergence$C3\_low,  
 sv\_C = summer\_survival$C3\_low,  
 seed\_C = fecundity18$C3\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S3\_low,  
 ow\_S = overwinter$S3\_low,  
 prt\_S = spring\_tillage$S3\_low,  
 em\_S = emergence$S3\_low,  
 sv\_S = summer\_survival$S3\_low,  
 seed\_S = fecundity18$S3\_low,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O3\_low,  
 ow\_O = overwinter$O3\_low,  
 prt\_O = spring\_tillage$O3\_low,  
 em\_O = emergence$O3\_low,  
 sv\_O = summer\_survival$O3\_low,  
 seed\_O = fecundity18$O3\_low)  
}  
  
N\_3yr\_low\_df <- N\_3yr\_low %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,3),  
 Rotation = "3-year",  
 Corn\_weed\_management = "low") %>%  
 na.omit()

### conventional weed management  
rot\_4year\_conv <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O,  
 poh\_A, ow\_A, prt\_A, em\_A, sv\_A, seed\_A){  
   
  
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
# alfalfa phase dynamics  
after\_alfalfa <- ow\_A %\*% poh\_A %\*% seed\_A %\*% sv\_A %\*% em\_A %\*% prt\_A %\*% after\_oat   
   
 after\_alfalfa  
}  
  
### low herbicide weed management  
rot\_4year\_low <- function(vec, poh\_C, ow\_C, prt\_C, em\_C, sv\_C, seed\_C,   
 poh\_S, ow\_S, prt\_S, em\_S, sv\_S, seed\_S ,  
 poh\_O, ow\_O, prt\_O, em\_O, sv\_O, seed\_O,  
 poh\_A, ow\_A, prt\_A, em\_A, sv\_A, seed\_A){  
   
  
  
# corn phase dynamics   
 after\_corn <- ow\_C %\*% poh\_C %\*% seed\_C %\*% sv\_C %\*% em\_C %\*% prt\_C %\*% vec   
 # soybean phase dynamics  
 after\_soy <- ow\_S %\*% poh\_S %\*% seed\_S %\*% sv\_S %\*% em\_S %\*% prt\_S %\*% after\_corn  
# oat phase dynamics  
 after\_oat <- ow\_O %\*% poh\_O %\*% seed\_O %\*% sv\_O %\*% em\_O %\*% prt\_O %\*% after\_soy   
# alfalfa phase dynamics  
 after\_alfalfa <- ow\_A %\*% poh\_A %\*% seed\_A %\*% sv\_A %\*% em\_A %\*% prt\_A %\*% after\_oat   
   
 after\_alfalfa  
}

##### with corn under conventional weed management {-}  
N\_4yr\_conv <- list() # blank dataframe to save loop output   
  
N\_4yr\_conv[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_4yr\_conv[[i]] = rot\_4year\_conv(vec = N\_4yr\_conv[[i-1]],  
 poh\_C = fall\_tillage$C4\_conv,  
 ow\_C = overwinter$C4\_conv,  
 prt\_C = spring\_tillage$C4\_conv,  
 em\_C = emergence$C4\_conv,  
 sv\_C = summer\_survival$C4\_conv,  
 seed\_C = fecundity18$C4\_conv,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S4\_conv,  
 ow\_S = overwinter$S4\_conv,  
 prt\_S = spring\_tillage$S4\_conv,  
 em\_S = emergence$S4\_conv,  
 sv\_S = summer\_survival$S4\_conv,  
 seed\_S = fecundity18$S4\_conv,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O4\_conv,  
 ow\_O = overwinter$O4\_conv,  
 prt\_O = spring\_tillage$O4\_conv,  
 em\_O = emergence$O4\_conv,  
 sv\_O = summer\_survival$O4\_conv,  
 seed\_O = fecundity18$O4\_conv,  
   
 #alfalfa dynamics   
 poh\_A = fall\_tillage$A4\_conv,  
 ow\_A = overwinter$A4\_conv,  
 prt\_A = spring\_tillage$A4\_conv,  
 em\_A = emergence$A4\_conv,  
 sv\_A = summer\_survival$A4\_conv,  
 seed\_A = fecundity18$A4\_conv)  
}  
  
N\_4yr\_conv\_df <- N\_4yr\_conv %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,4),  
 Rotation = "4-year",  
 Corn\_weed\_management = "conventional") %>%  
 na.omit()

##### with corn under low herbicide weed management {-}   
N\_4yr\_low <- list() # blank dataframe to save loop output   
  
N\_4yr\_low[[1]] <- starting\_point   
  
for (i in 2:t) {   
 N\_4yr\_low[[i]] = rot\_4year\_low(vec = N\_4yr\_low[[i-1]],  
 poh\_C = fall\_tillage$C4\_low,  
 ow\_C = overwinter$C4\_low,  
 prt\_C = spring\_tillage$C4\_low,  
 em\_C = emergence$C4\_low,  
 sv\_C = summer\_survival$C4\_low,  
 seed\_C = fecundity18$C4\_low,  
   
 #soybean dynamics   
 poh\_S = fall\_tillage$S4\_low,  
 ow\_S = overwinter$S4\_low,  
 prt\_S = spring\_tillage$S4\_low,  
 em\_S = emergence$S4\_low,  
 sv\_S = summer\_survival$S4\_low,  
 seed\_S = fecundity18$S4\_low,  
   
 #oat dynamics   
 poh\_O = fall\_tillage$O4\_low,  
 ow\_O = overwinter$O4\_low,  
 prt\_O = spring\_tillage$O4\_low,  
 em\_O = emergence$O4\_low,  
 sv\_O = summer\_survival$O4\_low,  
 seed\_O = fecundity18$O4\_low,  
   
 #alfalfa dynamics   
 poh\_A = fall\_tillage$A4\_low,  
 ow\_A = overwinter$A4\_low,  
 prt\_A = spring\_tillage$A4\_low,  
 em\_A = emergence$A4\_low,  
 sv\_A = summer\_survival$A4\_low,  
 seed\_A = fecundity18$A4\_low)  
}  
  
N\_4yr\_low\_df <- N\_4yr\_low %>%   
 unlist(recursive = FALSE) %>%  
 data.frame() %>%  
 dplyr::rename(counts = ".") %>%  
 dplyr::mutate(category = rep(c("top", "bottom", "cohort\_1", "cohort\_2", "cohort\_3", "cohort\_4", "cohort\_5", "cohort\_6"),t)) %>%  
 filter(category %in% c("top", "bottom")) %>%  
 unnest(cols = everything() ) %>%  
 mutate(cycle\_no = rep(1:t, each = 2)) %>%  
 group\_by(category) %>%  
 mutate(lambda\_cycle = counts/lag(counts),  
 lambda\_annualized = nthroot(lambda\_cycle,4),  
 Rotation = "4-year",  
 Corn\_weed\_management = "low") %>%  
 na.omit()

## Warning: Removed 982 rows containing missing values (geom\_point).

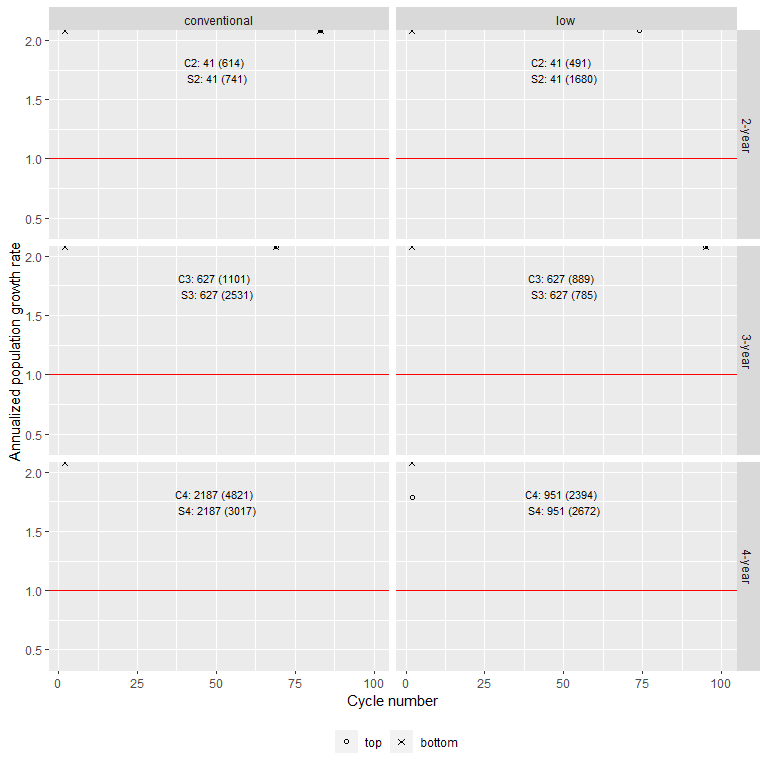


Figure 1: Population growth rates over 100 rotational cycles. All simulations started with a seed column of 10000 female seeds in the top 0 - 2 cm soil stratum and 0 female seed in the bottom 2 - 18 cm soil stratum. The simulation applied weed management on cohorts 1 through 3 in corn and soybean only. The relationships of aboveground mass and fecundity in Nguyen and Liebman (2022b) were used to estimate cohort-based fecundity. In corn and soybean, only the fecundity of cohorts 1 through 3 fecundity were manipulated to find the seed allowance in the corn and soybean environments, the fecundity of cohorts 4 and beyond were kept as they were measured from 2018. Each panel was annotated with the average fecundity allowance for the first three plant cohorts and the whole crop phase. The red horizontal line marks lambda = 1.

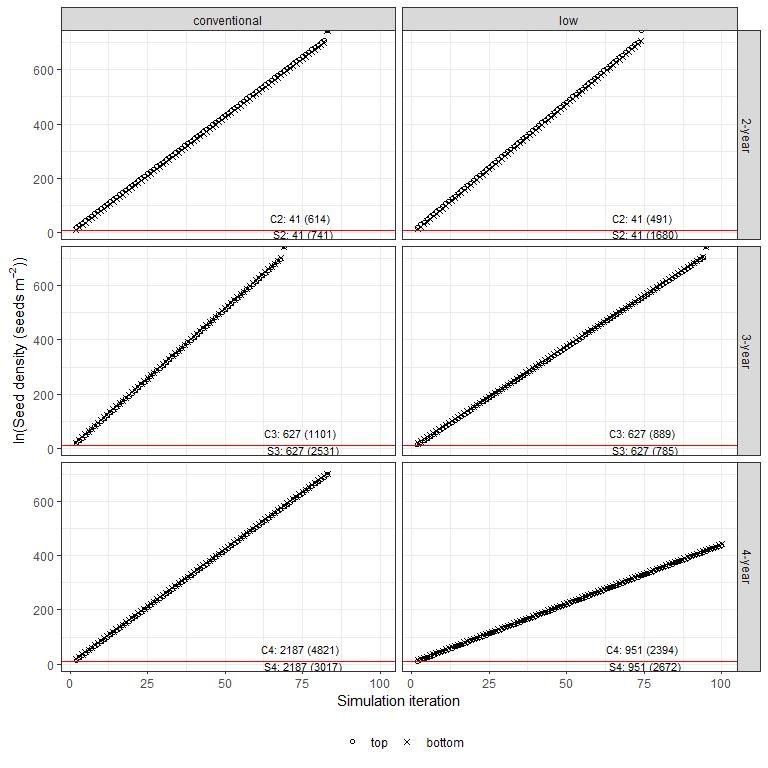


Figure 2: Population size at the end of a rotation cycle over 100 rotational cycles (the 2-year rotation ended at the soybean phase, the 3-year rotation ended at the oat phase, and the 4-year rotation ended at the alfalfa phase). All simulations started with a seed column of 10000 female seeds in the top 0 - 2 cm soil stratum and 0 female seed in the bottom 2 - 18 cm soil stratum. The simulation applied weed management on cohorts 1 through 3 in corn and soybean only. The relationships of aboveground mass and fecundity in Nguyen and Liebman (2022b) were used to estimate cohort-based fecundity. In corn and soybean, only the fecundity of cohorts 1 through 3 fecundity were manipulated to find the seed allowance in the corn and soybean environments, the fecundity of cohorts 4 and beyond were kept as they were measured from 2018. Each panel was annotated with the average fecundity thresholds for the first three waterhemp cohorts and the whole crop phase. The red horizontal line marks lambda = 1.