**Appendix A.** Expected value and variance of germination count range.

Let random variables, independent and identically distributed with the function . In this paper we have assumed . The distribution function of the order statistics and are

,

.

So that the probability mass functions are

.

And,

.

Now, the expected value of *X* can be calculated using the Riemann-Stieltjes integration:

.

In the discrete case and for *X* non-negative,

.

Thus,

.

.

**Appendix B.** R code for the probability mass function and the cumulative distribution function of the range.

# Input arguments:

# r, the germination count range

# size, the number of seed samples

# N, the seed lot size

# K, the number of germinating seeds in the seed lot

# n, the number of seeds per sample

dRangeHyper <- function(r, size, N, K, n)

{

 sapply(r, function(r) {

 if(r < 0) {

 prob <- 0

 } else if(r == 0) {

 prob <- sum(dhyper(0:n, K, N-K, n)^size)

 } else {

 prob <- 0

 for(x in 0:n) {

 prob <- prob +

 (phyper(x+r, K, N-K, n) - phyper(x-1, K, N-K, n))^size -

 (phyper(x+r, K, N-K, n) - phyper(x, K, N-K, n))^size -

 (phyper(x+r-1, K, N-K, n) - phyper(x-1, K, N-K, n))^size +

 (phyper(x+r-1, K, N-K, n) - phyper(x, K, N-K, n))^size

 }

 }

 return(prob)

 })

}

pRangeHyper <- function(r, size, N, K, n)

{

 sapply(r, function(r) {

 sum(dRangeHyper(0:r, size, N, K, n))

 })

}