

Table S8. The Kempthorne and Nordskog Restrictive Linear Phenotypic Selection Index (RLPSI) code in R to compute the different selection parameters.

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#Economic weights per trait: Stripe rust, leaf rust, leaf spot, and common bunt (-1, -3, -5, -7, and -9 for
each); grain yield (1, 3, 5, 7, and 9)

#Restricted (constrained trait): expected genetic gain for grain yield = 0

# The economic weights for the example below are as follows: stripe rust = -7, leaf rust = -9, leaf spot = -9,
common bunt = -9, grain yield =1

# Restrictions: 0= no restriction; 1 = expected genetic gain restricted (fixed) to zero

# RLPSI analysis was done by restricting the expected genetic gain for grain yield to zero

# This code below is an example for just one of the 3,125 economic weights used in our study.

rm(list=ls())

setwd("C:/R-packages/RLPSI/Data")

P<- as.matrix(read.csv("POP1-P-matrix.csv", header = TRUE, nrow =5))

G <- as.matrix(read.csv("POP1-G-Matrix.csv", header = TRUE, nrow =5))

Y<- as.matrix(read.csv("POP1_Data_Non-centered.csv", header = TRUE, nrow =196))

GID<- as.matrix(read.csv("POP1_GID.csv", header = TRUE, nrow =196))

IP=solve(P);IP          # P inverse matrix

w=c(-7,-9,-9,-9,1); w   # Economic weights for stripe rust, leaf rust, leaf spot, common bunt, and grain
yield, respectively.

b=IP%*%G%*%w; b         # LPSI vector of coefficients

CC1 <- c(0,0,0,0,1)      # Matrix of restrictions for stripe rust, leaf rust, leaf spot, common bunt, and
grain yield, respectively.

Ut=rbind(CC1); Ut

At=Ut%*%G; At
```

```

II=diag(c(1,1,1,1,1)); II
IQ=solve(At%*%IP%*%t(At)); IQ
Q=IP%*%t(At)%*%IQ%*%At; Q
KK=II-Q; KK
bs=KK%*%b; bs          # RLPSI vector of coefficients

ks=1.755                # Selecion intensity

Vp=t(bs)%*%P%*%bs; Vp ; SD=sqrt(Vp); SD      # Variance and standard deviation of the RLPSI
Es=(ks*(G%*%bs))/as.vector(SD) ; Es          # Estimated Expected genetic gain per trait
Rs=ks*SD;Rs             # Estimated LRPSI Selection response

VH=t(w)%*%G%*%w; SH=sqrt(VH); VH; SH         # Variance and standard deviation of the net
genetic merit H
corHI=SD/SH; corHI      # Estimated correlation between the RLPSI and H

LSI=Y%*%bs              # Estimated RLPSI values

datos <-data.frame(GID=GID, Y=Y,LSI=LSI)

datos <- datos[with(datos, order(-LSI)), ]     # Orden inverso

write.table(datos, "C:/R-packages/RLPSI/Results-RLPSI-Weight_1-all.txt", sep="\t")

X5=datos[1:20,1:7]

write.table(X5, "C:/R-packages/RLPSI/Results-RLPSI-Weight_1-selected.txt", sep="\t")

```