Read.me file

Hi,

Thanks for your interest in this data. If you have any questions please get in touch. Also, if you find errors or ambiguities, please let us know.

Finally, please get in contact if you actually use this data. I would love to hear if/where it ends up.

Regards

Tom

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Datasheet : Field\_all

Exp: factor (2 levels) wild = natural populations, tp = experimental populations

Env: environment, factor (3 levels) H = headland, D = Dune, I = island

Block: Experimental block nested in environment. 4 levels.

Row, col: seeds were layed out in a grid (see methods). Row = grid row, col = grid column

Leaf: leaf number, nested in individual plant. Leaf 1-5 for most plants.

Leaf shape traits (see methods, or contact authors for more information)

(area,perimeter,compactness,circularity,width,length,numindent,indentdens,dissection)

Datasheet : GH\_leaf

Pop: source population, factor (3levels), ) H = headland, D = Dune, I = island

Fam: seed family, nested within pop.

Leaf shape traits (see methods, or contact authors for more information):

leaf

area

perimeter

compactness

circularity

width

length

numindents

indentdens

dissection

Datasheet : tp\_layout

Identifying data for individual plants in field experiment

Env: environment, factor (3 levels) H = headland, D = Dune, I = island

Block: Experimental block nested in environment. 4 levels.

Row, col: seeds were layed out in a grid (see methods). Row = grid row, col = grid colum

Rep: experimental family

POPULATION: crosstype with parental details (see methods for more info)

w.b: factor (2 levels) within: crosses within wild population, between: cross between population(hybrids)

crosstype: factor (5 levels). Backcross, F1, F1 (hybrid crosstypes), parentals/ancestors (non hybrid crosstypes)

X.local: expected proportion of genes local to the environment in which the individual was planted.