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Implementing withincross genomic prediction to reduce oat breeding costs

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SUPPLEMENTAL MATERIALS

Supplementary Table S1. Phenotypic traits assessed in the ‘Buffalo x Tardis’ population in this study including trait name and method used for assessment.

Trait	Method of assessment
Internode 1 length	Length (cm) from the panicle basal node to the next node below (node 1)
Kernel content	Determined by passing 25 g of whole grain through a Laboratory Oat Huller (Codema Model LH5095; Maple Grove, Minneapolis, USA) set at 100 bar for 60 seconds and then separating the output into groats and whole grain. Kernel Content (%) calculated as (Groat weight (g) / (Initial weight (g) – Whole grain weight (g)) x 100
Maturity	Days from 1 st April to GS92 (Zadoks <i>et al.</i> , 1974)
Mildew	Scored in early spring on a 1-9 scale with 9 representing no damage (AHDB, 2012)
Panicle extrusion	Length (cm) from the flag leaf ligule to the panicle basal node
Winter hardiness	Scored in early spring on a 1-9 scale with 9 representing no damage (AHDB, 2012)
Grain yield	Grain harvested using a small plot combine and grain yields were adjusted to 15% moisture content
Ear emergence	Days from 1 st April to 50% of ears emerged in each plot (GS55; Zadoks <i>et al.</i> , 1974)
Height	Scored immediately prior to harvest (5 measurements per plot in cm from ground level to the tip of the panicle)
Grain length	Determined using a MARVIN grain analyser (GTA Sensorik GmbH, Germany)
Grain width	Determined using a MARVIN grain analyser (GTA Sensorik GmbH, Germany)
Hullability	Determined from kernel content determination as $100 - (100 \times \text{Whole grain weight (g)} / \text{Initial weight (g)})$
Panicle length	Distance in cm from the basal panicle node to the tip of the panicle (5 plants per plot)
β-glucan	Determined on a subsample of ground groat using the McCleary method Megazyme™ kit K-BGLU (Megazyme International Ireland Ltd., Wicklow, Ireland).
Grain area	Determined using a MARVIN grain analyser (GTA Sensorik GmbH, Germany)

References

AHDB (2012) Recommended list protocol. Available from: <https://ahdb.org.uk/knowledge-library/recommended-lists-protocols>
 Zadoks JC, Chang TT, Konzak CF (1974) Decimal code for growth stages of cereals. *Weed Research* 14, 415-421.

Supplementary Figure S1. Theoretical programme design to increase selection pressure within a cross using genomic prediction based on development of a predictive model from F₂ genotypes and F₄ phenotypes applied to estimate between lineage performance in recombinant inbred lines (RILs). We propose that this scheme would permit stronger selection within cross without a loss of accuracy.

