Prediction of Heterosis in Hybrid Crops

Transcriptome analysis to predict the performance of hybrids

Proof of concept achieved in Maize and Arabidopsis

Evaluation and Licensing Opportunities

For further information on this technology and evaluation/ licensing opportunities please contact:

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Patent Literature

Patent applications pending

Prof Ian Bancroft and colleagues at the John Innes Centre, UK have developed a revolutionary new method to predict heterosis. The method can be used to accurately predict hybrid vigour for a range of important crop performance traits, including yield.

The technology arose from microarray studies of the transcriptome designed to observe the genome-wide reprogramming, or “remodelling”, of gene expression that occurs in hybrids when compared to their corresponding parents. Many of the changes in transcript abundance are completely unrelated to the level of performance of a given trait in the hybrid. HOWEVER, using linear regression algorithms, the JIC team has discovered that it is possible to identify subsets of genes whose transcript abundance is correlated with the magnitude of heterosis in hybrids. Using these subsets, it is now possible to **accurately predict the level of heterosis in novel hybrid combinations**.

The allelic combinations present in inbred lines result in transcriptome features that can be used as markers for the prediction of heterosis in hybrids formed by the lines. This approach was initially shown to work in *Arabidopsis thaliana* and has now also been extended to and **demonstrated in maize**. In maize the method has been used successfully to predict the performance of hybrids for yield and other traits, based solely on the transcriptome characteristics of parental inbred lines.

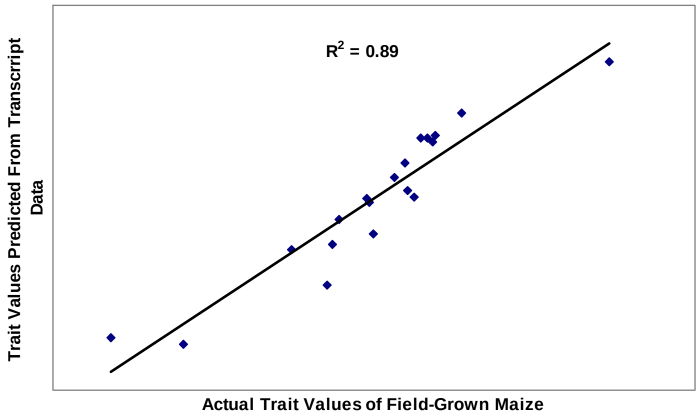

Figure 1. Yield values of 19 field grown maize hybrids plotted against greenhouse grown parental inbred transcriptome derived predictions. Predictions were made using a 45 gene-marker subset.

This successful fusion of transcriptomic technology and mathematical modelling has proven so successful, in both monocot and dicotyledonous species, that it is likely to prove an **invaluable technology for a huge range of commercial and research plant breeding programmes.**

The technology was developed by the John Innes Centre with support from PBL, and is the subject of patent applications filed by PBL.

PBL is currently offering the technology for evaluation by the seeds and plant breeding industry. The technology is available for in-house evaluation under licence from PBL, and PBL is also able to arrange bespoke demonstration and evaluation projects to be performed on behalf of interested parties, at the John Innes Centre.

Applications:

Prediction of heterosis in hybrid crop breeding - Save time and money

- Aid early decision making on line/hybrid advancement
- Choice of best tester line for early performance testing
- Selection of hybrids for advancing to yield trialling
- Predict yield plus other traits of interest

Identification of genes controlling or related to heterosis for particular traits

- Gene cloning
- Molecular markers

References: Not yet published in scientific literature.