Kiwifruit maturity screening by NIR; dealing with genotype variation

V.A. McGlone,[a,*] R. Seelye,[a] E. Popowski,[b] R. Lowe[b] and L. Gea[b]
[a]*Plant and Food Research, Ruakura Research Centre, Hamilton 3240, New Zealand. E-mail: andrew.mcglone@plantandfood.co.nz*
[b]*Plant and Food Research, Te Puke Research Centre, Te Puke 3182, New Zealand*

Introduction

Large breeding and genomic discovery programmes are creating strong demand for smarter fruit screening methods. Dense plantings and young vines, necessary for the economic efficiency of large scale trials, often mean low fruit numbers per vine, creating problems in providing adequate data. The numbers could be lower than 30 fruit per genotype seedling, making robust quality testing (storage and/or sensory) difficult, notwithstanding any fruit losses due to maturity screening.

Non-destructive and field portable NIR technology has been suggested for the task of maturity screening, a task currently accomplished by destructive SSC measurement (refractometry) of juice samples. NIR is well known for accurate and non-destructive SSC prediction on fruit.[1]

The objective of this study was to evaluate whether NIR might be capable of dealing with the potentially large spectral diversity presented by the kiwifruit germplasm, and simultaneously produce useful indications of relative SSC levels.

Materials and methods

Thirteen established vines, each corresponding to a different genotype, were selected with the intent of spanning an appreciable range of the breeding population diversity. From each vine 25 fruit were removed, on up to 6 occasions over a 2 month pre-harvest period.

Spectra were collected with a Zespri NIR unit (Zespri, New Zealand); a bench-top laboratory system specifically designed for fast and simple fruit interactance measurements over the 300–1100 nm range. The basic instrumentation and measurement method is identical to that described by McGlone et al.[2] Two separate spectral measurements were made on each kiwifruit, on opposing sides of the transverse equator of the fruit, and were averaged prior to analysis.

The SSC readings, used as reference data, were measured using a digital refractometer (Atago; Japan) using juice expressed from 10 mm caps removed from the stem and distal ends of the fruit. Readings from each end cap were averaged.

Model training was accomplished using a PLS algorithm and 4-way cross-validation (PLS_Toolbox, Eigenvector Research, USA). Spectral pre-processing involved normalisation of the absorbance spectra in the range 800–1000 nm, with a 2nd derivative transformation formed using

the 2nd order Satvisky-Golay algorithm (~21 nm window range). The number of latent variables in the PLS model, up to a maximum of ten, was determined using 10-way cross-validation.

To examine the potential extent of genotype specific problems, different data set groupings in terms of genotype, and/or harvest date, were variously held-out of the calibration modeling process. The models were then applied to the held-out sets and predictive performance examined.

Results and discussion

Predictive models for SSC were good, the SSC prediction error across the whole data set being estimated at ±1.2% (Figure 1).

Predictive performance on separate held-out genotype groups was characterized by significant bias, the average absolute bias being ~0.8%. Bias persisted when examining smaller held-out groups, for example for single genotypes on individual harvest dates (Figure 2).

Bias thus appears to be a stubborn feature, dominated by variation due to fruit genotype, but perhaps including other unidentified factors, such as NIR instrument drift.

Bias did not reduce on averaging, imposing a finite limit on the accuracy in estimating a vine average, no matter how many fruit are measured by NIR.

Nonetheless, if many fruit can be measured by the NIR method then it may compare well with the accuracy of current destructive methodology, particularly for the critical lower SSC fruit below 10% (Figure 2). With the current 3 fruit destructive sampling regime used in the industry, the average SSC for a vine will have an uncertainty >±0.8%, since individual vines typically have

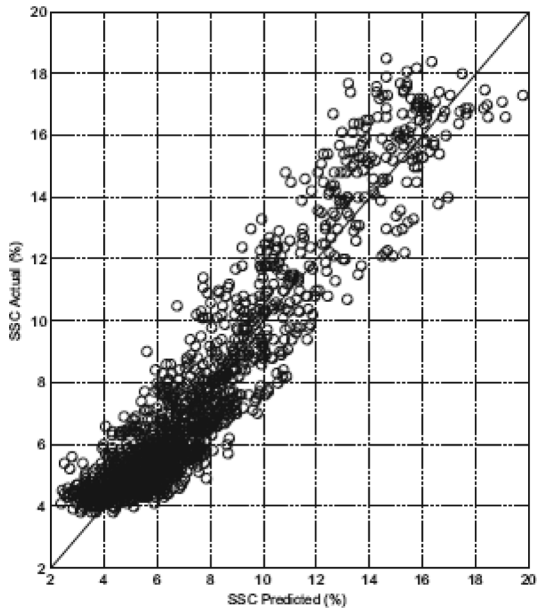

Figure 1. Actual SSC against SSC predicted by NIR on full data set ($N = 1641$). Calibration statistics (4-way cross-validation) of $R^2 = 0.90$, $RMSECV = 1.2\,\%$.

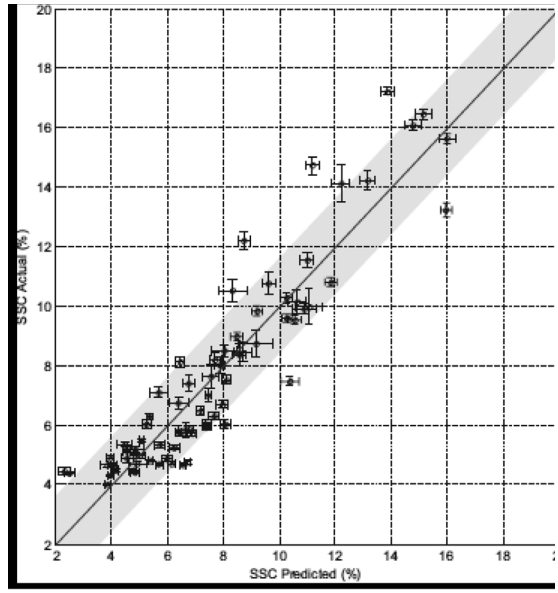

Figure 2. Average SSC measured against average NIR prediction of SSC for different held-out genotypes on different dates (*N*~25 per group). Error bars are standard errors. Grey strip is 95% C.I. for standard destructive sampling on vine with SSC standard deviation of 1.4%.

fruit SSC distributions with standard deviations >1.4%. The NIR method will deliver a comparable uncertainty, approaching the Bias limited value of ±0.8%, if 10 or more fruit on a vine can be measured (i.e., 10 fruit averaging at *RMSEP* = 1.2% and Bias = 0.8 gives a vine uncertainty of ±0.88%).

Research into the origin and elimination of the bias continues, currently in exploring modelling algorithms other than PLS. Future research is planned to conduct time series analysis, to follow individual fruit on vines as they mature, as a way to reduce bias effects directly (e.g., time series averaging) and/or develop alternative maturity screening metrics (e.g., rate of signal change).

Conclusion

Compared with current methods, the NIR method is possibly accurate enough for the maturity screening task. If the results reported here can be duplicated on a field portable NIR system then such NIR technology offers an attractive option for use in the breeding and/or genomic discovery programmes.

Acknowledgement

We acknowledge funding from the Kiwifruit Royalty Investment Programme (KRIP) of Plant&Food Research.

References

1. B.M. Nicolaï, K. Beullens, E. Bobelyn, A. Peirs, W. Saeys, K.I. Theron and J. Lammertyn, *Postharv. Biol. Technol*. **46,** 99 (2007).
2. V.A. McGlone, R.B. Jordan and C.J. Clark , *Postharv. Biol. and Technol*. **46,** 1 (2008).