Use of thermal parameters to reduce the number of sugarcane clones required for trash blanketing trials

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Abstract

Green cane harvesting and trash blanketing has been adopted by the sugar industry in northern regions to conserve soil, water, organic carbon and nutrients. New varieties which can ratoon under the wet and cool conditions of southern regions are required and the first step in this process is to ascertain whether genetic variability exists for this character. One problem when assessing agronomic practices across a range of sugarcane genotypes is that the number of clones/cultivars involved frequently imposes severe constraints on trial design due to the size and cost of trial required. We used thermal parameters for sugarcane development as a means of reducing the number of genotypes required for experiments without compromising the variability present in the population. Comparison of base temperatures and thermal time (degree days) for shoot emergence, stalk elongation and leaf appearance across 50 clones showed that this number could be reduced to 25 without any significant loss in variability for these parameters, or to 10 with only minor changes in variability.

Key words: Thermal time, base temperature, sugarcane, green cane harvesting, trash blanketing.

Green cane harvesting and trash blanketing (GCTB) was introduced to Australia in the 1970's (4) and has been widely adopted by the sugar industry, particularly in northern Queensland (3), as an environmental protection measure. The trash blanket conserves soil structure, moisture and nutrients and the lack of cane fires has reduced the smoke and ash nuisance for nearby communities. Unfortunately, adoption of GCTB in southern regions of Australian sugar industry has been severely restricted due to poor ratooning through a trash blanket when soil conditions are cool and wet (1). One solution to this problem is to seek new varieties which can ratoon successfully under these conditions.

Many current sugarcane varieties do not ratoon under these conditions because they have not been selected under the GCTB system and a program to screen genotypes from earlier in the breeding program has been initiated. Plant breeders (T. McRae, *pers comm*) have estimated that a minimum of 50 clones should be evaluated to provide a reliable estimate of the genetic variation for a parameter present in a breeding population. However, inclusion of 50 clones can not be accommodated in a replicated agronomic trial involving several GCTB conditions because of size, resource and cost constraints. Hence, a reliable method to reduce this number of clones to a manageable number without restricting the extent of variation present was required.

Previous experiments (2) have shown that the base temperature and thermal periods (degree days) for shoot emergence, stalk elongation and leaf appearance vary between genotypes. Accordingly, this paper reports on the use of these thermal parameters as a means to assess the variability present and of selecting a representative number of genotypes for trash blanketing trials without loosing this variability.

Material and methods

Experiments were conducted on a Euchrozem soil at the Bureau of Sugar Experiment Stations, Bundaberg, Queensland. Forty unselected clones from stage III of the selection program and 10 commercial cultivars were used as a source of genotypes. Shoot emergence was evaluated across 5 planting dates between October 1996 and June 1997. Three replicates were planted as single row plots in a randomised block design. Plots were 5 m long and separated by a 2 m gap. Shoot emergence was observed 2 to 3 times a week and achievement of one shoot per linear metre was defined as completion of the emergence stage.

Stalk elongation and leaf appearance were measured for 6 randomly chosen stalks per clone in 2 row by 50 m propagation plots. Measurements of stalk elongation and leaf appearance were made between 19 February 1997 and 1 August 1997 at fortnight intervals. Plots were irrigated regularly to maintain non-stressed conditions. Daily maximum and minimum air temperatures were recorded by an automatic weather station. Thermal parameters for the three processes (shoot emergence, stalk elongation and leaf appearance) were determined by the method of Liu *et al*. (2). Shoot emergence is the most important character for assessing ratooning ability in the GCTB system. Thus, the selection of representative clones was firstly based on shoot emergence. The base temperatures for shoot emergence for the 50 clones/ cultivars were sorted into classes differing by 0.5^{o}C. Then thermal times were sorted within each class. After the selection of each clone/cultivar, the thermal para-meters for stalk elongation and leaf appearance were checked to ensure that the extent of variation was retained

Results and discussions

A major constraint to the adoption of the GCTB system is the failure of shoot emergence of ratoons under cold conditions. Base temperature determines the lower temperature limit for emergence, while thermal time measures the degree days required for completion of emergence. Estimating these parameters and incorporating them into a measure of the similarity among clones can help to reduce the number of clones required for a trial and minimise the prospect of losing genotypic variability for these parameters.

Genotypic variation in base temperatures and thermal times for shoot emergence, stalk elongation and leaf appearance are shown in Fig. 1a, 1b and 1c, respectively. The thermal parameters (base temperature and thermal time) for stalk elongation and leaf appearance were highly correlated, but unrelated for shoot emergence. These data show that 25 clones/cultivars can be selected to cover the full range of base temperature and thermal time without reducing this variability, and that selection of 10 clones/cultivars may sufficiently cover the range of thermal parameters if resources for the trials are seriously limited.

This study demonstrates the effectiveness of using thermal parameters to reduce the number of sugarcane clones/cultivars required to assess genotype by agronomic treatment interactions for clone evaluation.

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