

**POSTER SUMMARY****REVEALING THE EPIGENETIC DIVERSITY OF SOUTH AFRICAN SUGARCANE  
(*SACCHARUM* SPP.) GROWN IN DIFFERENT AGROCLIMATIC ZONES THROUGH  
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Modern sugarcane cultivars have complex polyploid genomes that impede genetic improvement by using conventional breeding methods. Epigenetic resources can be used as alternative tools to improve cultivars. We hypothesise that their epigenetic differences could account for this characteristic in the few cultivars that are considered to be adaptable to different agroclimatic zones. In order to evaluate the diversity and epigenetic structure of two widely-grown sugarcane cultivars, NCo376 and N41, across various regions and environments in KwaZulu-Natal [viz. Empangeni, Eston, Glenside, Mount Edgecombe, Umzimkhulu and Pongola], a total of 200 genomic DNA samples were analysed, using Methylation-Sensitive Amplified fragment length Polymorphism (MSAP). The results showed that the diversity within the cultivars was influenced by cytosine methylation (epigenetic loci), rather than non-methylation (genetic loci). The NCo376 populations across all five regions had a population differentiation index value ( $\phi_{st}$ ) of 61%, while 47% indicated a moderate differentiation for the N41 populations. The Shannon diversity indices were  $0.524 \pm 0.140$  and  $0.555 \pm 0.128$ , respectively, for the NCo376 and N41 populations. The results further revealed that the Eston region had more influence on the variability of cytosine methylation in NCo376 than the Mount Edgecombe, Empangeni, Pongola and Umzimkhulu regions. Taking into account the methylation status of each cultivar, better management of crosses can be achieved during breeding. The under-utilised epigenetic aspect of sugarcane can be used to reveal and study the regulation of novel biotic and abiotic resistance genes for both sugar and biofuel production. Given the likelihood that different environments induce heritable epigenetic adaptation, we propose that the current elite sugarcane genotypes could be 'prepared' for climate change by using epimutagenesis.

**Keywords:** Climate change, Cytosine methylation, Epigenome diversity, MSAP markers, Polymorphism, *Saccharum* spp.