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Discrimination of the Geographical Origin of *Sclerocarya birrea* by ^{1}HNMR and LC-MS Based Metabolite Profiling

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Abstract

Sclerocarya birrea (*S. birrea*) is an African tree used traditionally to treat various human ailments. The origin of *S. birrea* can be determined by its biochemical composition. This study identifies the biochemical composition of *S. birrea* leaf extracts from 5 provinces within South Africa namely Limpopo, KwaZulu-Natal, North-West, Gauteng and Mpumalanga by both ^{1}H Nuclear Magnetic Resonance (NMR) and Liquid Chromatography Mass Spectroscopy (LC-MS), followed by multivariate data analysis. The Orthogonal Partial Least Squares Discriminant Analysis (OPLS-DA) and Partial Least Squares Discriminant Analysis (PLS-DA) from ^{1}HNMR and LC-MS respectively, clearly discriminated between extracts from five provinces. Putatively annotated metabolites including kaempferol, quercetin, gallic acid, sucrose and glutamate contributed to discriminating the geographical origin of *S. birrea* extracts. These results established biochemical profiles of *S. birrea* extracts and indicate that the two techniques; NMR and LC-MS can be used in the discrimination of the geographical origin of *S. birrea*.

Keywords: Geographical origin; *Sclerocarya birrea*; Multivariate data analysis; ^{1}HNMR; LC-MS

Introduction

Sclerocarya birrea is distributed from Senegal to Ethiopia and South Africa and is also found in Madagascar [1]. The stem bark, roots and leaves of *S. birrea* has been used for decades as a traditional medicine as anti-bacterial [2], anti-proliferative [3] and anti-diabetes [4]. The geographical origin of *S. birrea* trees can be determined by its biochemical composition. Therefore, it is possible to measure the metabolite content of a plant in order to determine how it differs with others from different origins. Metabolic profiles have become important in several plant science areas; in particular, metabolomics combined with a multivariate statistical approach has proven valuable in many chemical analyses of plant studies [5].

Liquid Chromatography-Mass Spectroscopy (LC-MS) and Nuclear Magnetic Resonance (NMR) are frequently used as a technological platform for metabolomics applications [6]. These analytical methods provide information about the chemical composition of biological samples. In plant metabolomics these two technologies are commonly used as independent approaches for profiling plant systems [7-10]. The two techniques are distinct concerning their detection ability and sensitivity [10]. Liquid Chromatography Mass Spectroscopy is highly sensitive and enables extensive detection of metabolites within a sample. Although a reference database search is essential for the structural assignment processes of untargeted LC-MS data [11], the results allows the comprehensive metabolite annotation without dependence of standard compounds or even isolation of individual metabolites [8]. On the other hand NMR is a highly selective technique distinguishing molecular structures but has the lowest sensitivity compared to MS [12].

The statistical combination of the data from NMR and LC-MS offers an opportunity to relate spectrometric and spectroscopic properties for a single metabolite [10]. Although both NMR and LC-MS have been used previously to profile metabolites from plants [10,13-15], these two techniques have also been used to identify metabolites present in the leaves of wild and cultivated *S. birrea* trees [16]. In the present study both NMR and LC-MS were used to construct the metabolite profile of metabolites from five geographical origins of *S. birrea*.

While NMR based metabolomics approach has been used in many plant studies [17], no metabolomics profiles related to the geographical origin of *S. birrea* have been reported. Among possible analytical techniques, ^{1}HNMR and LC-MS are well suited to metabolite profiling, because they allows simultaneous detection of a diverse group of secondary metabolites in addition to abundant primary metabolites [18]. Moreover, NMR based metabolomic analysis are reproducible and do not require complex sample preparation procedures [19]. In this study, a metabolomics approach based on ^{1}HNMR and LC-MS was used to determine the differences in chemical composition in *S. birrea* growing in Limpopo, Gauteng, North West, Mpumalanga and KwaZulu-Natal provinces of South Africa. The study aimed at identifying the different chemical compositions of *S. birrea* extracts depending on geographical origin using ^{1}HNMR, LC-MS as well as multivariate analysis.

Materials and Methods

Study sites and sample collection

Leaf samples from 12 *Sclerocarya birrea* trees were collected in October 2013, from each of the five sampling areas Limpopo, Gauteng, North West, Mpumalanga and KwaZulu-Natal. From each province, two regions were identified for collection, and in each region, samples were collected from three different trees with two samples per tree. The two samples from each tree were collected randomly, and from the trees of almost the same height (9.5 m).

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Extraction of *Sclerocarya birrea* samples for NMR and LC-MS

Methanol (d4) (400 µl) was added to 15 mg of the dried leaf material, and this was vortexed for 1 min and sonicated for 20 min. The mixture was centrifuged at 10,000 rpm for 10 min and the supernatant (200 µl) was transferred into 3-mm NMR tubes. After the NMR analysis, the methanol-d4 *S. birrea* extracts were diluted to 25% (v/v) ultrapure water. The diluted extracts were sonicated, centrifuged and filtrated before LC-MS analysis.

NMR analysis

[1]HNMR spectra were acquired on a bruker 600 MHz spectrometer (Wageningen University, Netherlands) operating at a proton NMR frequency of 600.13 MHz. A PRESAT pulse sequence was applied to suppress the water signal. For each sample, 64 K data points for the FID and 64 data points after Fourier transformation were used, 128 scans were acquired with 60 degrees pulses at an acquisition time of 1.817 s. The spectral width was 18028 Hz with a relaxation delay of 4 s, and 0.2 Hz line broadening was used before Fourier transformation.

Data analysis

All NMR spectra were phase- and baseline corrected using MestReNova 10.01 (Mestrelab Research). Normalization was also done with MestReNova to ensure that all the spectra have the uniform norm. The regions containing the water and methanol peaks (4.60-5.00 ppm and 3.28-3.36 ppm) were excluded and the remaining spectral regions were divided into 0.04-ppm bins, converted to ASCII format, and imported to Microsoft Excel 2010.

Multivariate statistical analysis for NMR

The resulting Microsoft Excel file was imported to SIMCA version 13.0 (Umetrics) for multivariate data analysis. All imported data were pareto-scaled for multivariate data analysis. Pareto scaling, in which each variable is divided by the square root of the standard deviation, gives greater weight to NMR data variables with higher intensities but is not as extreme as the use of no scaling [20]. Principal Component Analysis (PCA) was initially performed to determine the basic variation, the presence of extreme outliers and to obtain an overview of variation among the groups. The quality of the model was described by R2 and Q2 values. R2 is defined as the proportion of variance in the data explained by the model, and indicates the goodness of and Q2 is defined as the proportion of variance in the data predictable by the model and indicates predictability [21].

Untargeted metabolite profiling

Quantification of metabolites was achieved by 600 MHz library of Chenomx NMR suite version 8.2 which uses the concentrations of the known reference signals to determine the concentrations of individual compounds. The library contains 338 metabolites. Other metabolites were identified using published literature on compounds isolated from the leaves of *S. birrea*.

LC-MS analysis

The extracts were analysed by reverse phase LC-MS for their metabolite contents. The LC-QTOF MS analysis was carried out in Electronspray (ESI) negative mode. The mass rate and scan rate were set to record m/z 100-1500/s.

Multivariate statistical analysis for LC-MS

Quantification of *S. birrea* metabolite profiles of LC-MS analyses was performed using XCMS online data analysis software, which can be accessed freely from the Scripps Centre for Metabolomics (https://xcmsonline.scripps.edu). This software approach employs peak alignment, matching, and comparison. The raw LC-MS files were first converted to MZxmL files using MS convert. Peaks were subsequently extracted using XCMS. The final statistical analysis where performed by employing MetaboAnalyst 3.0-a comprehensive tool suite for metabolomic data analysis, which also can be accessed freely from http://www.metaboanalyst.ca/MetaboAnalyst. This software employs data normalization, multivariate analysis methods (PCA and PLS-DA), clustering analysis and many more analysis approaches. All the samples were auto scaled prior to the analysis.

Results

[1]H NMR analysis

Figure 1 shows representative one-dimension [1]H NMR spectra of *Sclerocarya birrea* from Limpopo, Gauteng, North West, KwaZulu-Natal and Mpumalanga. No clear visual differences were observed in the overall spectroscopic fingerprint among *S. birrea* samples from five provinces. However, close inspection of the spectra revealed that the chemical compositions of metabolites between *S. birrea* samples obtained from five provinces were distinctly different. Visual inspection of the five spectra also revealed more intense sugar relative to aliphatic and aromatic compounds. Very few metabolites were annotated putatively using 600 MHz library from Chenomx NMR Suite version 8.2 which contains 338 metabolites, together with published literature [16,22] on compounds isolated from plant leaves. Intense signals in the sugar region from Gauteng (Figure 1) were however, clearly observed, indicating the presence of glycosylated metabolites and free sugars.

Metabolomic analysis of *Sclerocarya birrea* extracts from different provinces

To provide comparative interpretation and visualization of the fundamental variations and metabolite differences in the samples from different origins, Principal Component Analysis (PCA) and Orthogonal Partial Least square-Discriminant Analysis (OPLS-DA) were applied to the 1H NMR spectrum dataset. The PCA model for distinguishing *S. birrea* samples obtained from five provinces revealed R2X and Q2 values of 0.85 and 0.78 respectively (Figure 2a). The PCA scores were used to determine whether metabolic fingerprints of *S. birrea* extracts were sufficiently different to distinguish geographical origin and to identify specific markers of each origin. To improve the clustering and to identify the metabolites responsible for the differences between the provinces, OPLS-DA model was constructed (Figure 2b), and revealed RY2 and Q2 values of 0.73 and 0.62 respectively. The samples from five provinces were clearly separated in the OPLS-DA score plot (Figure 2b), which means that the non-correlated variation in X metabolites to Y metabolites was removed, resulting in maximum separation [23]. This maximum separation also indicates that the levels of *S. birrea* metabolites were strongly influenced by the various growing conditions in each region [24].

To further understand, the underlying variables contributing to the differentiation, the contribution plots were constructed. Figures 3a-3e shows the metabolites responsible for the separation observed in the OPLS-DA. All provinces showed a unique pattern of compounds important in their composition. KwaZulu-Natal samples were characterized by the higher levels of phenolics; quercetin 3-0-β-D glucopyranoside (bin at 4.19, 4.23, 5.41, 6.17, 6.36, 6.71, 7.42 and 7.57 ppm), gallic acid (bin at 7.04 ppm), quercetin

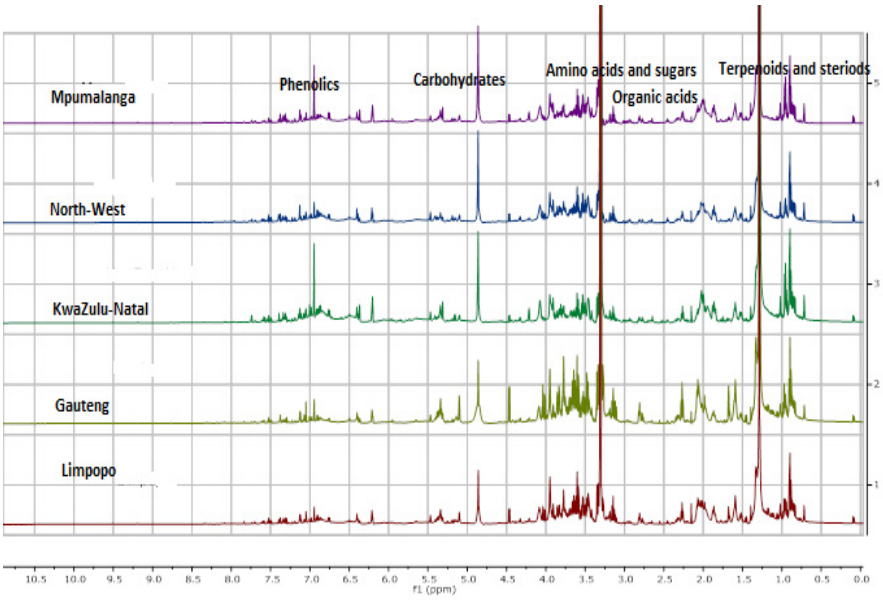

Figure 1: Average NMR spectra of *Sclerocarya birrea* from five provinces.

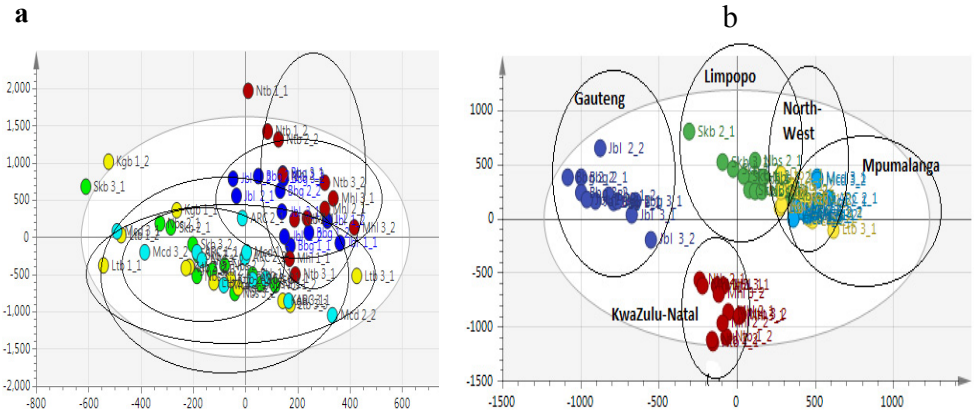

Figure 2: Representative PCA (a) and OPLS-DA (b) scores from ^{1}H NMR Spectra of *Sclerocarya birrea* from five provinces.

3-0-β-Dgalactopyranoside (bin at 4.04, 4.08, 5.36, 6.18, 6.39, 6.81, 7.51 and 7.65 ppm), quercetin 3-0-α-L-rhamnopyranoside (bin at 5.24, 6.19, 6,38, 6.85, 7.24 and 7.28 ppm) and threonine (bin at 1.32 ppm) compared to other provinces. Gauteng samples showed no phenolic compounds as metabolites that contributed to it being different to the other provinces, however the sugar; sucrose (bin at 3.44, 3.54, 3.68, 3, 76, 3.78-3.90, 4.04, 4.17 and 5.39 ppm), unknown sugars (bins at 5.12, 5.32 and 5.4 ppm), lactate (bin at 1.32 and 4.04 ppm) and an unknown amino acid (bin at 0.92) appeared to be the important metabolites in this province. In addition to the profile observed in the samples from Gauteng, Limpopo also showed sucrose (bin at 3.44, 3.54, 3.68, 3.76, 3.78-3.90, 4.04, 4.17 and 5.39 ppm) as an important metabolite, fatty acid (bin at 0.88 ppm) was also observed in the samples from this province. Mpumalanga showed a combination of sugars, amino acids, and phenolics as the important metabolites. Higher levels of leucine (bin at 0.96 ppm), unknown sugars (bins at 4.24, 4.88 and 5.32 ppm), gallic acid (bin at 7.04 ppm), quercetin 3-0-β-D glucopyranoside (bin at 4.19, 4.23, 5.41,6.17, 6.36, 6.71, 7.42 and 7.57 ppm), quercetin 3-0-β-D galactopyranoside (bin at 4.04, 4.08, 5.36, 6.18, 6.39, 6.81, 7.51 and 7.65 ppm), kaempferol-3-0-α-L-rhamnopyranoside (bin at 5.43,6.20, 6.38 ppm) and (-)-epigallocatechin 3-0-galloyl ester (bin at 2.92, 3.04, 5.65, 6.03 and 6.06 ppm), where observed as important metabolites in Mpumalanga samples. The profile observed in North West province is almost identical as the one from Mpumalanga. The samples from North-west presented quercetin 3-0-β-D glucopyranoside (bin at 4.19, 4.23, 5.41,6.17, 6.36, 6.71, 7.42 and 7.57 ppm), quercetin 3-0-α-L-rhamnopyranoside (bin at 5.24, 6.19,6,38, 6.85,7.24 and 7.28 ppm), kaempferol-3-0-α-L-rhamnopyranoside (bin at 5.43,6.20, 6.38) and quercetin 3-0-β-D galactopyranoside (bin at 4.04, 4.08, 5.36, 6.18, 6.39, 6.81 7.51 and 7.65 ppm) as important metabolites.

The analysis of *S. birrea* leaf extracts from five provinces by ^{1}H NMR allowed the detection of essentially primary (polar) metabolites such as sugars, amino acids and organic acids and few secondary

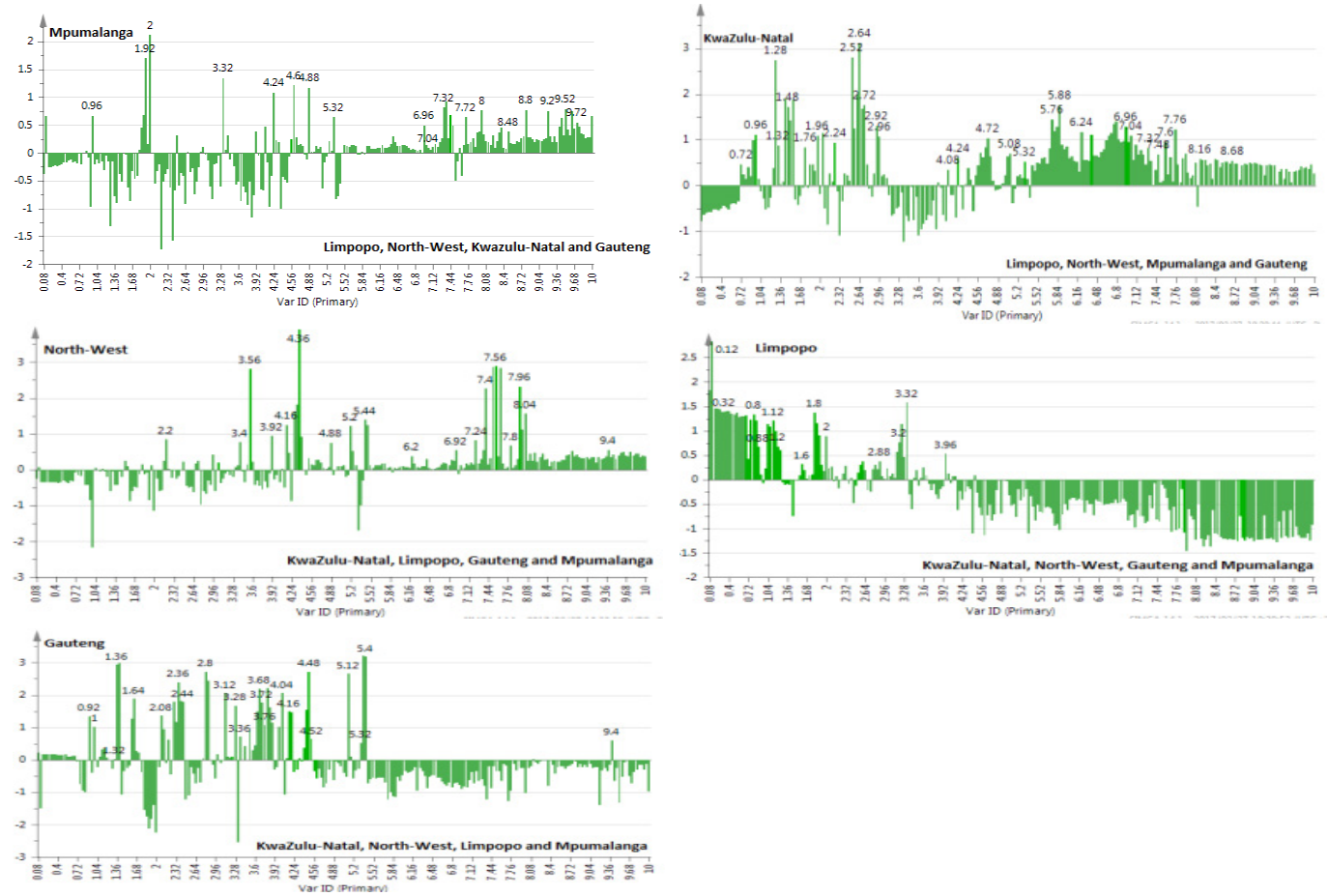

Figure 3: Contribution plots from OPLS-DA. **(a)** Mpumalanga vs. other four provinces; **(b)** KwaZulu-Natal vs. the other four provinces; **(c)** North-West vs. other four provinces; **(d)** Limpopo vs. other four provinces; and **(e)** Gauteng vs. other for provinces.

metabolites. The abundance of the corresponding resonances indicated the higher natural concentrations of these metabolites in the leaves. The relatively low abundance of secondary metabolites and the large amount of resonance of primary metabolites in the spectrum made the detection of secondary metabolites, such as phenolic and flavonoids more difficult as compared to the detection of the primary metabolites. Liquid Chromatography Mass Spectroscopy was applied to further investigate the abundance of secondary metabolites. When Patial Least Square (PLS) was performed on the methanol extracts from LC-MS, the samples appeared to be grouped according to their places of origin (Figure 4). The samples from Mpumalanga showed some similarities to those from, North-West and KwaZulu-Natal. The VIP scores where generated and the assignment of the metabolites in the VIP scores were based on previously published literature (Figure 5).

The VIP scores (Table 1) confirms the NMR profile that indeed the samples from Limpopo and those from Gauteng contained low to no secondary metabolites as important in differentiating them to the other provinces, this is shown by green and light green colors in the annotated metabolites of the VIP scores. The VIP scores also showed that the metabolite levels of Quercetin 3-0-β-D-(6"-galloyl)-galactopyranoside were high in the samples from North-West followed by the ones from KwaZulu-Natal and Mpumalanga (red, orange, and yellow respectively). The annotated metabolites in Table 1, confirmed the highest levels of the metabolites Quercetin 3-0-β-D-(6"-galloyl)-galactopyranoside, Kaempferol-3-0-α-L-rhamnopyranoside and (-)-Epigallocatechin3-0-galloyl ester in the samples from North-West, Mpumalanga and KwaZulu-Natal.

Sampling place	Latitude	Longitude
Limpopo province;		
-Mookgophong	24.5037°S	28.7140°E
-Ga-Sekgoboko	24.0894°S	28.9299°E
Gauteng province;		
-Jubilee	25.4057°S	28.2691°E
-Babelegi	25.3554°S	28.2790°E
North-West Province;		
-Letlhabile	25.4903°S	27.8415°E
-Kgabaatsane	25.5361°S	27.9571°E
Mpumalanga;		
-Machanodorp	25.6673°S	30.2455°E
-ARC-Nelspruit	25.4518°S	30.9697°E
KwaZulu-Natal;		
-Ntibane bushveld hideaway	27.7062°S	31.49032°S
-Mahlalela game range	27.7627°S	29.9344°S

Table 1: Leaf samples collected from different study sites.

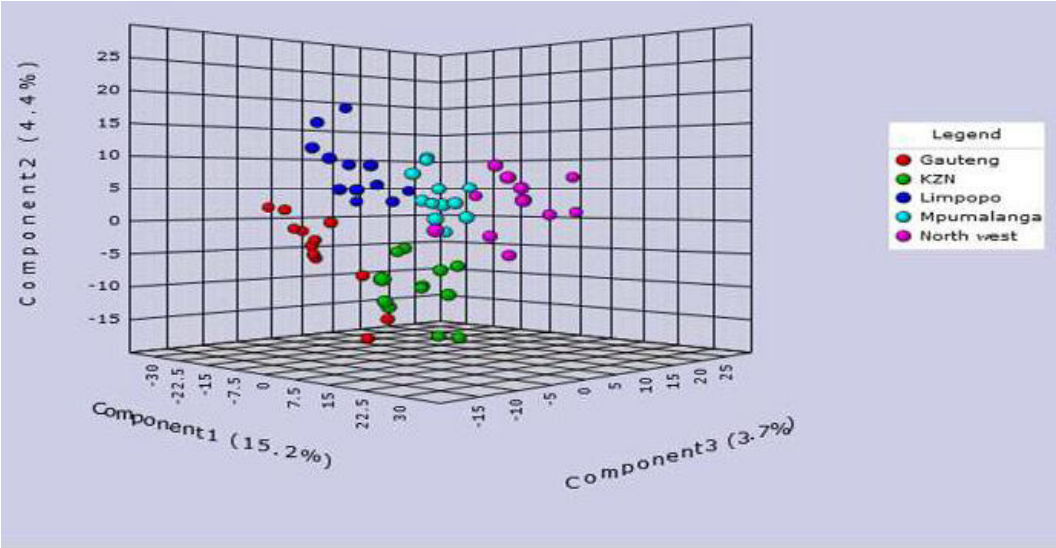

Figure 4: PLS scores of *Sclerocarya birrea* LC-MS from five provinces.

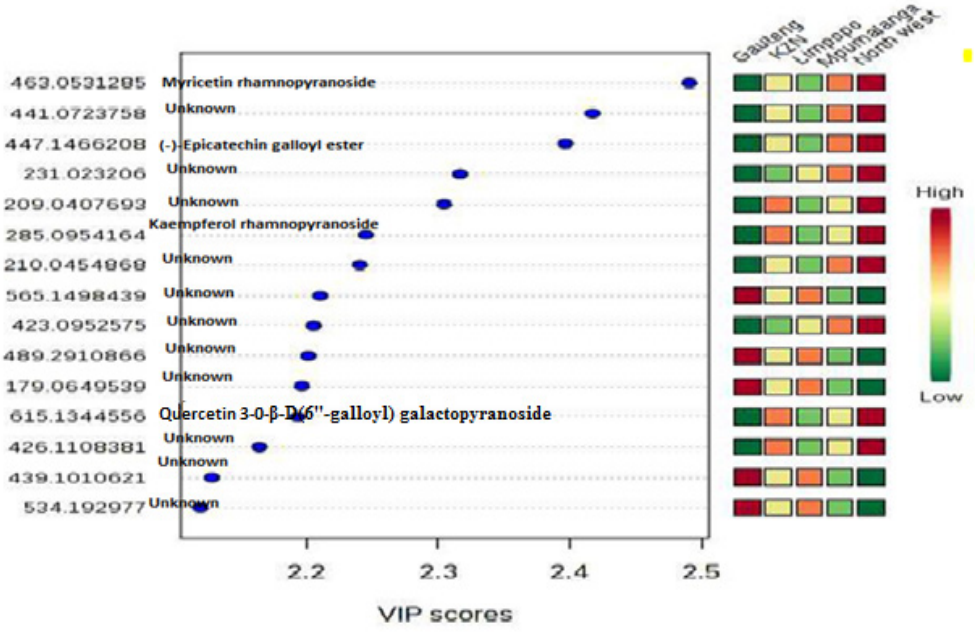

Figure 5: VIP scores from PLS scores of *Sclerocarya birrea* from five provinces.

Discussion

Virtual inspection of the [1]H NMR spectra showed no clear differences between samples from different provinces, this indicated the similarities within the species. Upon multivariate data analysis, five groups were observed according to the provinces, indicating the geographical influence on the chemical composition. The samples from Gauteng and KwaZulu-Natal was however clustered closer together and more separated from the other provinces. When the contribution plots were constructed on the samples from Gauteng, it was clear that no secondary metabolites contributed to the differences between Gauteng and other provinces. The putative annotation presented in Table 2 was based on previously published metabolites isolated from the leaves of *S. birrea* [16]. The samples from Gauteng presented sugars, and some amino acids as the metabolites of importance. On the other side, the samples from KwaZulu-Natal showed very few sugars, few aliphatic and more aromatics to be important in the clustering of the samples from this province (Figure 3b). Visual inspection of the contribution plots from both KwaZulu-Natal and Gauteng confirms that the samples from Gauteng are rich with sugars while those from KwaZulu-Natal are rich in aromatic metabolites. It can therefore be concluded based on [1]HNMR data analysis that the separation of samples from Gauteng to those from KwaZulu-Natal, Limpopo, Mpumalanga and North West is influenced by the combination of sugars and some

Province	Metabolite	Chemical shift
KwaZulu-Natal	1. Quercetin *3-0-β-D-* (6"-galloyl) glucopyranoside	4.19 (dd) 4.23 (dd) 5.41 (dd) 6.17 (d) 6.36 (d) 6.71 (d)
		7.42 (d) 7.57 (dd)
	2. Quercetin *3-0--β-D-* (6"-galloyl) galactopyranoside.	4.04 (dd) 4.08 (dd) 5.36 (d) 6.18 (d) 6.39 (d) 6.81 (d)
		7.51 (d) 7.65 (dd)
	3. Quercetin 3-0-α-L- rhamnopyranoside	5.24 (d) 6.19 (d) 6.38 (d) 6.85 (d) 7.24 (dd) 7.28 (d)
	4. Gallic acid	7.04 (s)
	5. Threonine	1.32 (d)
Mpumalanga	1.Quercetin *3-0-β-D-* (6"-galloyl) glucopyranoside	4.19 (dd) 4.23 (dd) 5.41 (dd) 6.17 (d) 6.36 (d) 6.71 (d) 7.42 (d) 7.57 (dd)
	2. Quercetin *3-0-β-D-* (6"-galloyl) galactopyranoside.	4.04 (dd) 4.08 (dd) 5.36 (d) 6.18 (d) 6.39 (d) 6.81 (d)7.51 (d) 7.65 (dd)
	3. Kaempferol-3-0-α-L- rhamnopyranoside	5.43 (d) 6.20 (d) 6.38 (d)
	4. Gallic acid	7.04 (s)
	5. (-)-Epigallocatechin3-0-galloyl ester	2.92 (dd) 3.04 (dd) 5.65 (s) 6.03 (d) 6.06 (d) 7.04 (s) 2.92 (dd) 3.04 (dd) 5.65 (s) 6.03 (d) 6.06 (d)
	6. Leucine	0.96 (d) 1.70 (m) 3.73 (m)
Gauteng	1.Sucrose	3.44 (t) 3.54 (dd) 3.68 (s) 3.76 (t) 3.78-3.90 (m) 4.04 (t) 4.17 (d) 5.39 (d)
	3. Lactate	1.32 (d) 4.03 (q)
North-West	1. Quercetin *3-0-β-D-* (6"-galloyl) Glucopyranoside	4.19 (dd) 4.23 (dd) 5.41 (dd) 6.17 (d) 6.36 (d) 6.71 (d)7.42 (d) 7.57 (dd)
	2. Quercetin 3-0-α-L- rhamnopyranoside	5.24 (d) 6.19 (d) 6.38 (d) 6.85 (d) 7.24 (dd) 7.28 (d)
	3. Kaempferol-3-0-α-L-	5.43 (d) 6.20 (d) 6.38 (d)
	4. Quercetin 3-0-b-D- (6"-galloyl) galactopyranoside.	4.04 (dd) 4.08 (dd) 5.36 (d) 6.18 (d) 6.39 (d) 6.81 (d)7.51 (d) 7.65 (dd)
	5.(-)-Epigallocatechin3-0-galloyl ester	2.92 (dd) 3.04 (dd) 5.65 (s) 6.03 (d) 6.06 (d)
Limpopo	1.Sucrose	3.44 (t) 3.54 (dd) 6.68 (s) 3.76 (t) 3.78-3.90 (m) 4.04 (t) 4.17 (d) 5.39 (d)
	2. Fatty acids	0.88 (t)

Table 2: Putative assignment of *S. birrea* metabolites from NMR buckets [CD_3OD].

amino acids, while the separation of samples from KwaZulu-Natal to those from the other four provinces is mostly influenced by aromatic compounds. Complementarily to NMR data, the use of C18 reversed phase LC-MS detected metabolites such as flavonoids with the PLS that is analogous to the one obtained in the OPLS-DA from NMR. Liquid Chromatography Mass Spectroscopy detected mostly the secondary metabolites, similar to those partially detected by NMR (Table 2).

Very few flavonoids annotated from *Sclerocarya birrea* from different provinces supports previously published literature that concluded the use of *S. birrea* to treat various human ailments. The anticancer potential of this plant is evidenced by the presence of the flavonoids; quercetin and kaempferol. These two metabolites are believed to act synergistically in the reduction of cell proliferation of cancer cells; this was concluded in an *in-vivo* study [25]. Moreover, in the study conducted by Alkhalidy et al. [26], the metabolite kaempferol showed potential in the treatment of diabetes. Alkhalidy et al. [26] concluded that kaempferol treatment reversed the high fat diet impaired glucose transport-4 and AMP-dependent protein kinase expression in both muscles and adipose tissues from obese mice. This study provided the baseline information on the healing effect of *S. birrea*, by providing the snapshot of the metabolites found in each province. This study will attract researchers to use samples from different geographical origins when screening for activity since the geographical origin affects the abundance of the metabolites.

Conclusion

In this study, *Sclerocarya birrea* leaf extracts from different provinces were compared and characterized based on multivariate statistical analysis of [1]H NMR and LC-MS based metabolomics data. Both the primary metabolites and secondary metabolites were annotated. *S. birrea* from different provinces exhibited significant differences in their metabolite profiles confirming that several metabolites can be used as markers for origin. The samples also showed some close similarities, in that some metabolites, Quercetin 3-0-β-D-(6"-galloyl) galactopyranoside, Kaempferol-3-0-α-L-rhamnopyranoside, (-)-Epigallocatechin-3-0-galloyl ester and gallic acid where common between samples from North-West, Mpumalanga and Kwazulu-Natal. The most significant difference was with regard to the sugars in the samples from Gauteng and Limpopo regions (Table 2) influenced by glycosylation. In this study, we demonstrated for the first time that [1]H NMR and LC-MS based profiling provides a fast and efficient method to fingerprint metabolic differences between same species of *S. birrea* grown in different regions.

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