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Two New Steroidal Saponins from *Diuranthera inarticulata*

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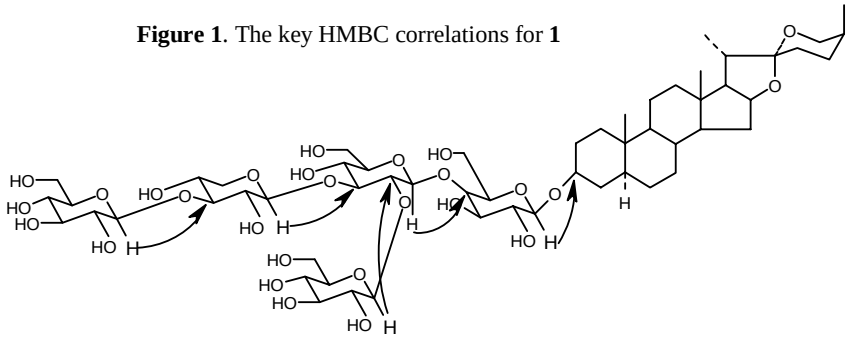
Abstract: Two new steroidal saponins, diuranthosides D and E, were isolated from the whole plant of *Diuranthera inarticulata* Wang *et* K. Y. Lang. By means of spectral and chemical analysis, the structure of the new compounds were established as neotigogenin-3-*O*-*β*-D-glucopyranosyl (1→3)-β-D-xylopyranosyl-(1→3)-[β-D-glucopyranosyl(1→2)]-β-D-glucopyranosyl(1→4)-β-D-galactopyranoside (**1**) and neotigogenin-3-*O*-β-D-glucopyranosyl(1→3)-β-D-glucopyranosyl (1→3)-β-D-xylopyranosyl(1→3)-[β-D-glucopyranosyl(1→2)]-*β*-D-glucopyranosyl(1→4)-β-D-galactopyranoside (**2**) respectively.

Keywords: *Diuranthera inarticulata*, Liliaceae, steroidal saponin, diuranthosides D and E.

There are only three species in the genus *Diuranthera* (Liliaceae), which is endemic in the southwest of China[1]. Four steroidal saponins, diuranthosides A-C and chloromalo-side A were isolated from the fresh roots of *D. major*. This paper deals with the structure elucidation of two new steroidal saponins, diuranthosides D and E, which were isolated from the methanolic extract of whole plant of *D. inarticulata* Wang *et* K. Y. Lang.

Figure 1. The key HMBC correlations for **1**

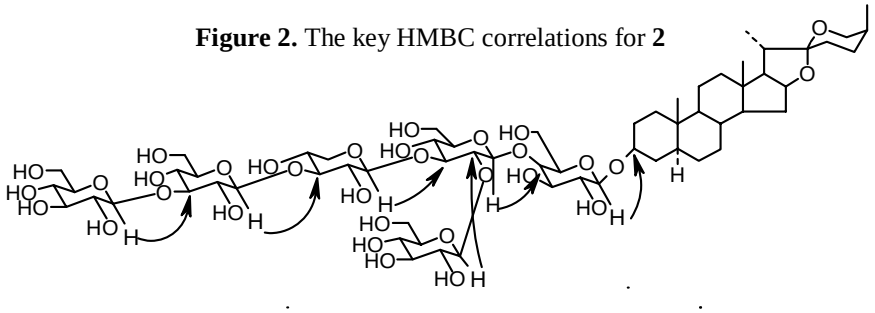


Diuranthoside D (**1**), $[\alpha]_D^{22}$ -38 (c 0.08, pyridine), afforded galactose, glucose and xylose as sugar components and neotigogenin as an aglycone on acid hydrolysis on TLC. Its molecular formula was assigned as $C_{56}H_{92}O_{27}$ by HRFABMS. The IR, ^1H and ^{13}C NMR spectra of **1** showed it was a neotigogenin 3-O-glycoside[2]. The anomeric proton signals of the sugar moiety at δ_H 4.86, 5.12, 5.15, 5.25, 5.50 (each 1H, d, J $\approx$ 7.5 Hz) suggested one galactose, one xylose and three glucose units are presented and all sugar linkages should be the β-configuration. The fragment ion peak at *m/z* 1033[M – glc]$^-$, 901[M – xyl-glc]$^-$ and 870[M – glc-glc]$^-$ indicated only presence of terminal glucose

units and the xylose should locate in an inner position in the sugar chain. On comparison of the whole ^{13}C-NMR spectrum of **1** with that of diuranthosides A[2], a set of additional signals, corresponding to a β-glucopyranosyl unit appeared, and the signals due to xylose moiety varied, while all the other signals remained almost unaffected. It was observed that the signal of C-3 of xylose was markedly displaced downfield at δ_C 86.4 and the remaining carbon signals were shifted upfield to various degrees. The ^{13}C-NMR signals of sugar chain of **1** are almost the same as the signals of diuranthosides B[2], which isolated from *D. major*[2]. So this branched pentasaccharide moiety is identical with the sugar moiety of diuranthosides B. Based on the above evidence, The structure of **1** was considered as **Figure 1**. ^{1}H-^{13}C long-range correlations were showed in **Figure 1**.

Diuranthoside E (**2**), $[\alpha]_D^{22}$ -23, gave neotigogenin as aglycone and galactose, glucose and xylose as sugar residues on acid hydrolysis on TLC. Its molecular formula was assigned as $C_{62}H_{102}O_{32}$ by HRFABMS. The IR, ^{1}H and ^{13}C NMR spectra of **2** showed it is also a neotigogenin 3-O-glycoside[2]. On comparison of ^{13}C NMR spectrum with **1** and **2** only showed a set of additional signals of a terminal β-glucopyranosyl unit which was deduced to be attached to the hydroxy group at C-3(δ 87.8) of a terminal glucose of **1**. In the FAB mass spectrum of **2**, the fragment ion peak at *m/z* 1195[M – glc]$^-$, 1033[M – 2×glc]$^-$, 901[M –xyl-glc-glc]$^-$ were present, but not 1063[M –xyl-glc]$^-$. This suggested that the additional glucose should be linked to the glucose which was attached to C-3 of xylose. Consequently, the structure of **2** was established as **Figure 2**. The structure is further confirmed by HMBC spectrum (**Figure 2**).

Figure 2. The key HMBC correlations for **2**



The biological test showed both **1** and **2** have against *Bacillus cereus.*

Acknowledgments

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References

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