PROFILES OF COMPOUNDS IN ROOT EXUDATES OF RICE, CYMBOPOGON, DESMODIUM, MUCUNA AND MAIZE

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Abstract: Roots of crop species produce exudates with biologically active chemicals which are known to affect the growth of crops and weed species. An experiment was conducted at the Uganda National Crop Resources Research Institute, Namulonge during 2016 to identify compounds released in root exudates of potted Cymbopogon nardus, Desmodium uncinatum, upland rice (NERICA 1), Mucuna pruriens and Zea mays (LONGE 6H) at forty-five days after planting. This marked near the average stationary phase for test crop growth when secondary metabolite levels were high. Organic compounds in soils were extracted using solid-phase micro-extraction (SPME) and by solvent extraction. Samples were subjected to analysis using a 7890A Gas Chromatography system. Data files were transferred into a distinct folder and data was uploaded onto the XCMS online platform for pairwise comparison and other related statistical analyses in the National Institute of Science and Technology Library. The blank soil produced 15 terpenoids, two alcohols and one each of trihalomethanes, ethers, phenols, ketones, furans, alkanes and aldehydes. Cymbopogon exuded five terpenoids, one phenol and an alkane. Desmodium plant roots released three terpenoids, one alkane and a phenol. The rice crop produced eight terpenoids, two alkanes and a furan. Five terpenoids, one phenol and an alkane were released by the mucuna crop, while six terpenoids were found in maize soil. The profiled compounds from cymbopogon, desmodium, rice, mucuna and maize could be responsible for allelopathic properties expressed by the study crops in natural and agricultural ecosystems and could be used in synthesis and development of herbicides.

Key words: alkanes, cymbopogon, desmodium, exudates, phenols, rice, terpenoids.

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Introduction

A wide range of biochemicals are synthesized during the shikimate pathway or, in the case of essential oils, from the isoprenoid pathway and are not required for the metabolism of the allelopathic organisms (Hussain et al., 2011). Allelochemicals are a subset of secondary metabolites released from plant parts by leaching, root exudation, volatilization and residue decomposition in both natural and agricultural systems. Li et al. (2010) reported that allelochemicals can be classified into 10 categories according to their different structures and properties, namely: (i) water soluble organic acids, straight-chain alcohols, aliphatic aldehydes and ketones; (ii) simple lactones; (iii) long-chain fatty acids and polyacetylenes; (iv) quinines (benzoquinones, anthraquinones and complex quinines); (v) phenolics, flavonoids and tannins; (vi) cinnamic acid and its derivatives; (vii) coumarins; (viii) steroids and terpenoids; (sesquiterpene, lactones, diterpenes and triterpenoids). The compounds with negative allelopathic effects are important in plant defence against herbivory (Rice, 1984). Root exudates affect soil-borne pests, pathogens, microorganisms, soil nutrients, microbial ecology and allelopathic activities of other plant species (Inderjit, 2003).

Flores et al. (1999) have indicated that 5–21% of plant photosynthates are released via root exudation over time in the rhizosphere depending on the size of the root system, plant responses to biotic and abiotic factors. Root exudation can often be modified by abiotic and biotic factors as well as physical and biological soil factors. Chuihua et al. (2004) and Kong et al. (2006) reported that the allelopathic rice varieties P1312777 and Huagan-1 released momilactone B, 3-isopropyl-5-acetoxycycloexane-2-one-1 and 5,7,4’-trihydroxy-3’,5’-dimethoxyflavone into the soil. Kato-Noguchi (2011) identified two main inhibitory substances in rice exudates by spectral data as 3-hydroxy-β-ionone and 9-hydroxy-4-megastigm-3-one. Kong et al. (2007) reported one aglycone, namely 5,7,4’-trihydroxy-3’,5’-dimethoxyflavone, in the soil planted with allelopathic rice. Hooper (2010) reported C-glycosylflavones as the major compounds in the root exudates of Desmodium uncinatum. L DOPA allelochemical was reported to be exudated from the roots of M. pruriens (Soares et al., 2014; Vadivel and Pugalenthi, 2008). Kato-Noguchi (2010) identified three allelochemicals in the acetone extract from the mesocotyls and coleoptiles of maize seedlings as 5-chloro-6-methoxy-2-benzoaxazolinone; 6-methoxy-2-benzoaxazolinone and 2,4-dihydroxy-1,4-benzoaxazin-3-one.

Upland rice-based ecosystems are characterised by mixed cropping and some plants are emerging key intercrops that provide alternative sources of revenue given the high demand for their products. In order to appraise the productivity of the rice ecosystems, it must be considered that allelopathic effects are produced by upland rice and some intercrops. Allelochemicals have been associated with weed
control (Tesio and Ferrero, 2010), growth of component crops (Soares et al., 2014), nutrient uptake (Cheng and Cheng, 2015) and, thus, they affect crop productivity. The bio-compounds in C. nardus, D. uncinatum, upland (NERICA 1), M. pruriens and Z. mays (LONGE 6H) that cause the allelopathic effects are, however, not well documented and there is little literature on the bio-compounds. The study aimed at identifying the organic compounds exudated via roots by the crops.

Materials and Methods

Profiling of the bioactive compounds

Potting in the screen house

A screen house study was conducted in 2016 based at the Uganda National Crops Resources Research Institute, Namulonge, Uganda. Five 4-day-old pre-germinated seeds each for rice, desmodium, mucuna and maize and five suckers of cymbopogon were potted separately. One pot without any plant was maintained as a control and about 120 ml of tap water was applied to each pot every two days for 45 days. One plant was uprooted and 100 g of soil collected from the middle to the bottom of each pot as representative samples at 50 days after planting. This time marked near the average stationary phase for test crop growth when secondary metabolites were presumed to be higher. The samples were oven-dried at 80 °C for 12 hours to constant weight for compound analysis.

Extraction and analysis of potential organic compounds from soil and plants

Organic compounds in soils were extracted using solid-phase micro-extraction (SPME) and by solvent extraction. Prior to the extraction, the SPME fibre was preconditioned for one hour at 250 °C under a stream of helium inside the gas chromatograph (GC) injection port liner. The SPME fibre used was gauge 24, 1 cm long, coated with divinyl benzene/ polydimethylsiloxane and with the film thickness of 65 µM. In a single manual injection, one gram of each soil sample was accurately weighed into a 10 ml airtight glass vial. The sample and blank extractions were placed into a thermostat heated block at 60 °C for 1 hour with the fibre exposed to the headspace for the entire duration. The fibre was retracted and introduced into the injection port of the GC in splitless mode. One gram of soil sample was accurately weighed into a 50 ml extraction tube and extracted with 10 ml of hexane by shaking at 250 revolutions per minute (rpm) in an orbital shaker for one hour. The two-milliliter extract was aliquoted into an Eppendorf tube and centrifuged at 5000 rpm for 10 minutes and 1 ml extract was aliquoted into a GC vial for injection. One hundred milligrams of freeze-dried samples were accurately weighed and each put into a 2 ml Eppendorf tube. 1800 µL of hexane and two mini
steel balls were also added to each of the Eppendorf tubes. The samples were vigorously ground in a genogrinder for 10 minutes. The extract was centrifuged at 5000 rpm for 5 minutes and 200 µL of the extract was diluted with 800 µL of hexane in a GC vial for injection.

Gas chromatography and mass spectrometry instrumental analysis conditions

Samples were subjected to analysis using a 7890A (Gas Chromatography) GC system (Agilent Technologies, USA) coupled to a 240 ion trap mass spectrometer (MS) detector (Agilent Technologies) using the Agilent 7693A automatic liquid sampler for solvent extracted samples. A VF5-MS (5% phenyl methylpolysiloxane), 30 m × 0.25 mm id, 0.25 µm film capillary column was used with the injector port set at 280 °C. Helium was used as carrier gas at a flow rate of 1 ml/min. The oven temperature was programmed to rise from 50 °C to 180 °C at 4 °C/min followed by an increase to 250 °C at 3 °C/min. The ion trap mass spectrometer parameters were as follows: scan range 50–540 (m/z), ionization mode EI and transfer line temperature, manifold temperature and trap temperature of 250 °C, 100 °C and 150 °C, respectively. Chromatograms and spectra representing individual samples were analysed using the automated mass spectral deconvolution and identification system software (AMDIS, US). The identification of the individual compounds was performed by comparing each of the mass spectra with the database of the National Institute of Science and Technology (NIST) 11 (Gaithersburg, MD, USA) and Wiley 7N (John Wiley, NY, USA) and also by comparing the calculated Kovats linear retention indices using retention times of n-alkane series against the values obtained in the NIST web book for the same capillary column stationary phase.

Chemometric analysis of GC-MS raw data using XC-MS online platform

Chemometric analysis of GC-MS raw data using XC-MS online platform

Data files in the common data formats corresponding to chromatograms from the various solvent extracted soil and SPME extracted volatiles in soil samples were obtained and transferred into a distinct folder. Data was uploaded onto the XCMS online platform for pair-wise comparison and other related statistical analyses. The analysis was performed using the default parameters under the GC/single quad (centwave) method as it matched the instrument operating conditions. The results obtained included: retention time corrected, total ion chromatograms, principal component analysis (PCA) plots and an annotated report. The generated report was used to identify the log-fold changes for various compounds earlier identified using AMDIS. Compounds with the log-fold changes > 0.30 were considered generated from the test samples.
Results and Discussion

Total ion chromatograms for compounds in test soils overlaid on control

Graphical images of the total ion chromatograms (TIC) generated from the solid-phase micro-extraction (SPME) data files for compounds in soil treatment samples potted with C. Nardus (S1), D. Uncinatum (S2), upland NERICA 1 (S3), M. pruriens (S4) and Z. mays (S5) overlaid against the blank soil sample (S0) as control are presented (Figure 1). The TIC spectra were similar with minor variations in the signal intensities of the TIC overlaid. The observation may be attributed to the availability of similar compounds in the control (S0) and treatment soils (S1, S2, S3, S4 and S5).

Analysis using XCMS online

The PCA showed no clustering of the sample spectra. The generated PCA plot for the blank soil (S0) was laid in quadrant 1. The PCA plots for D. uncinatum (S2) and upland rice, NERICA 1 (S3), were in the second quadrant (Figure 2). The PCA for C. nardus (S1) was positioned in quadrant 3 and the PCA plots for M. pruriens (S4) and Z. mays (S5) were both located in the fourth quadrant. The PCA plots that clustered closer signified similarity of the metabolites in the test samples and vice versa. Plant samples with similar classes of compounds clustered in the same quadrant.

Total ion chromatograms

![Figure 1](image_url)

Figure 1. Generated total ion chromatograms (TICs) for organic compounds from cymbopogon (S1), desmodium (S2), NERICA 1 rice (S3), mucuna (S4) maize (S5) and control (S0) overlaid. CDF = Compatible document format.
Bioactive compounds identified in the control and soil potted with test plants

Data on capillary column stationary phase retention time, relative match factors and the compounds identified in the control soil and soil potted with *C. nardus*, *D. uncinatum* and upland rice (NERICA 1) *M. pruriens* and *Z. mays* (LONGE 6H) are indicated in Tables 1–6. Twenty-four compounds were identified as the most probable compounds in the control (blank) soil (Table 1). This was dominated by fifteen terpenoids, namely: ethylbenzene, p-dimethylbenzene, vinyl benzene, o-methyl styrene, m-ethyl toluene, p-ethyl toluene, 1,3,5-trimethylbenzene, isopropyl benzene, 1,2,3-trimethylbenzene, o-dichlorobenzene, 1,2,4-trimethylbenzene, 1-isopropyl-2-methylbenzene, L-limonene, 3-phenylpropene and 1-3-diethylbenzene. Nine other compounds in the soil included
Profiles of compounds in root exudates of rice, *Cymbopogon*, *Desmodium*, *Mucuna* and maize

One trihalomethane called trichloromethane, n-butyl ether, oxime-methoxy-phenyl phenol, acetophenone ketone, 2-n-pentylfuran, 3,5-dimethyloctane alkane, n-octanal aldehyde and two alcohols identified as ethylhexanol and benzyl alcohol.

Table 1. Retention time, relative match factors and identified compounds in the blank soil.

| Retention time (min) | Relative match factor | Identified compound               |
|----------------------|-----------------------|-----------------------------------|
| 2.08                 | 875                   | Trichloromethane                  |
| 6.38                 | 820                   | Ethylbenzene                      |
| 6.73                 | 861                   | p-dimethylbenzene                 |
| 7.14                 | 867                   | n-butyl ether                     |
| 7.59                 | 873                   | Vinyl benzene                     |
| 8.19                 | 810                   | Oxime-, methoxy-phenyl            |
| 9.98                 | 795                   | o-methyl styrene                  |
| 10.34                | 814                   | Acetophenone                      |
| 10.72                | 915                   | m-ethyl toluene                   |
| 10.84                | 854                   | p-ethyl toluene                   |
| 11.13                | 897                   | 1,3,5-trimethylbenzene            |
| 11.50                | 887                   | Isopropyl benzene                 |
| 12.07                | 840                   | 2-n-pentylfuran                   |
| 12.22                | 883                   | 1,2,3-trimethyl benzene           |
| 12.47                | 866                   | 3,5-dimethyloctane                |
| 12.68                | 854                   | n-octanal                         |
| 13.13                | 919                   | o-dichlorobenzene                 |
| 13.36                | 866                   | 1,2,4-trimethylbenzene            |
| 13.52                | 888                   | 1-Isopropyl-2-methylbenzene       |
| 13.69                | 868                   | L-limonene                        |
| 13.80                | 822                   | 2-ethylhexanol                    |
| 13.90                | 789                   | 3-phenylpropene                   |
| 14.09                | 807                   | Benzyl alcohol                    |
| 14.42                | 822                   | 1,3-diethylbenzene                |

The twenty-four compounds identified in the control had the PCA plots (S0) clustered solely in the first quadrant. This signified that the compounds differed from sample treatments (S1-S5). The observation is supported by the result that only five compounds profiled from the 5 test crops were also found in the control. It is presumed that the bio-compounds identified in S0 had possibly been either released via root exudates by similar or different crops previously grown on the soil or were deposited from the decomposing plant materials. Rice (1984) and Uren (2000) have reported that root exudates contain different classes of primary and secondary compounds.

Seven compounds were profiled in the soil potted with *C. nardus*. One compound named 2-Ethylhexanol phenol, identified in the blank, was the only
major compound exudated with positive log-fold changes when overlaid with the control (Table 2). Three terpenoids named tert-Amylbenzene, pentamethylbenzene, 1,2-Di-tert-butylbenzene and 2,3-dimethylundecane alkane were released with high positive log-fold changes (≥0.3), while naphthalene and 1-Sec-butyl-4-methylbenzene terpenoids were exudated with lower log-fold changes. The PCA plot for cymbopogon (S1) solely lied in the third quadrant and far from S0 in Figure 2, due to the lower similarity between the metabolites in cymbopogon and the control (S0). There are no similar reported compounds in the available literature to the compounds profiled in root exudates of C. nardus.

Table 2. Retention time, relative match factors and log-fold changes for compounds in Cymbopogon nardus.

| Retention time | Relative match factor | Positive log-fold change | Identified compound                      |
|---------------|-----------------------|--------------------------|-----------------------------------------|
| 13.80         | 859                   | 0.70                     | 2-Ethylhexanol                          |
| 18.48         | 896                   | 0.37                     | tert-Amylbenzene                        |
| 18.98         | 892                   | 0.26                     | 1-Sec-butyl-4-methylbenzene             |
| 19.41         | 860                   | 0.17                     | Naphthalene                             |
| 19.70         | 876                   | 0.53                     | Pentamethylbenzene                      |
| 21.29         | 921                   | 1.80                     | 1,2-Di-tert-butylbenzene                |
| 18.83         | 867                   | 0.39                     | 2,3-Dimethylundecane                    |

D. uncinatum produced five dominant organic compounds with positive log-fold changes (≥ 0.3) that included one furan named 2-n-Pentylfuran which had been identified in the control (Table 3). Three terpenoids released via roots included tert-Amylbenzene; p-Ethyltoluene and 1-Sec-butyl-4-methylbenzene. An alkane named 2,3-Dimethylundecane was also exudated by D. uncinatum into the soil.

Table 3. Retention time, relative match factors and log-fold changes for compounds in Desmodium uncinatum.

| Retention time (Min) | Relative match factor | Positive log-fold changes | Identified compound                  |
|----------------------|-----------------------|---------------------------|-------------------------------------|
| 10.84                | 876                   | 0.36                      | p-Ethyltoluene                       |
| 12.07                | 874                   | 0.87                      | 2-n-Pentylfuran                      |
| 18.48                | 882                   | 0.74                      | tert-Amylbenzene                     |
| 18.83                | 867                   | 0.42                      | 2,3-Dimethylundecane                 |
| 18.98                | 901                   | 0.65                      | 1-Sec-butyl-4-methylbenzene          |

Eleven compounds were released by upland rice (NERICA 1) in the root exudates that included one furan named 2-n-pentylfuran that had been isolated from the control treatment (Table 4). One alkane named 2,3-dimethylundecane and six terpenoids identified as 1,2-dimethyl-3-ethyl benzene, 1-methyl-2-(2-
propenyl)benzene, 1,3-di-tert-butylbenzene, 1-Sec-butyl-4methylbenzene, tert-amylbenzene and pentamethylbenzine were exudated dominantly. Three compounds released with lower log-fold changes included 2-ethyl-p-xylene and 1-methyl-3-propylbenzene terpenoids and an alkane identified as 2,3-dimethyloctane.

Table 4. Retention time, relative match factors and log-fold changes for compounds in upland NERICA 1.

| Retention time | Relative match factor | Positive log-fold change | Identified compound               |
|----------------|-----------------------|--------------------------|----------------------------------|
| 12.07          | 894                   | 0.54                     | 2-n-pentylfuran                  |
| 12.47          | 883                   | 0.23                     | 3,5-dimethylcdecane              |
| 14.56          | 856                   | 0.11                     | 1-methyl-3-propylbenzene         |
| 14.84          | 856                   | 0.08                     | 2-ethyl-p-xylene                 |
| 15.53          | 876                   | 0.90                     | 2,3-dimethyldecane               |
| 15.87          | 843                   | 0.37                     | 1,2-dimethyl-3-ethyl benzene     |
| 18.14          | 857                   | 0.78                     | 1-methyl-2-(2-propenyl)benzene   |
| 18.48          | 877                   | 0.76                     | Tert-amylbenzene                 |
| 18.98          | 871                   | 1.30                     | 1-sec-butyl-4-methylbenzene      |
| 19.70          | 867                   | 0.83                     | Pentamethylbenzine               |
| 21.29          | 869                   | 0.34                     | 1,3-di-tert-butylbenzene         |

The five and eleven compounds profiled in the root exudates of desmodium and rice respectively were characteristically represented by the closely positioned PCA plots for both crops in the second quadrant, signifying a common association between their secondary metabolites (Figure 2). Two similar terpenoids, namely 1-Sec-butyl-4methylbenzene and Tert-Amylbenzene, one furan named 2-n-Pentylfuran and 2,3-Dimethylundecane alkane were commonly produced by the two crops. Hooper (2010) reported C-glycosylflavones as the major compounds in the root exudates of *D. uncinatum*. Several researchers have reported different compounds released by various cultivars of rice. Kong et al. (2007) reported momilactone B, 5,4-dihydroxy-3,5-dimethoxy-7-O-b-glucopyranosylflavone, 3-isopropyl-5-acetoxycyclohexene-2-one-1 and flavone, O-glycoside as released by rice roots. Kato-Noguchi et al. (2008) reported that rice secreted momilactones A and B into its rhizosphere. Kato-Noguchi (2011) identified 3-hydroxy-β-ionone and 9-hydroxy-4-megastigmen-3-one metabolites in rice root exudate. The profiled secondary metabolites were different from available literature and this may be attributed to differing genetic crop influences. Kim and Shin (1996) have reported that allelochemicals are influenced more by genetics than by the environment.

*Mucuna pruriens* released six organic compounds with high log-fold changes in its root exudates which included five terpenoids, namely: naphthalene, 1,2-dimethyl-1-ethylbenzene, 1,3-ditertiarybutylbenzene, 1-ethyl-3-methyl-benzene and 1,3-dichloro-benzene (Table 5). An alkane identified as n-Tetradecane was also profiled. Six compounds were exudated by *Z. mays*. A furan 2-n-pentylfuran
and three terpenoids, namely: m-ethyltoluene, 1,2,4 Trimethylbenzene and 2-ethyl-p-xylene which had been identified in the control soil (Table 6) were also profiled in the soil potted with *M. pruriens*. Two terpenoids, namely: 1-methyl-2-(2-propenyl) benzene and o-dichlorobenzene, were profiled with lower log-fold changes from the mucuna soil. The two terpenoids, namely: m-ethyltoluene and 2-ethyl-p-xylene, were dominant ($\geq$ 0.3) in the soil potted with LONGE 6H maize.

The PCA plots for mucuna (S4) and maize (S5) were both in the fourth quarter and closely clustered. This may be attributed to the dominance of a high number (5 and 6) of terpenoids released by mucuna and maize crops respectively via root exudates. The mucuna crop, however, clustered distantly from the control treatment relative to the maize crop. This was possible because mucuna and the control produced no similar compounds, while maize exudated four common compounds with the control.

Table 5. Retention time, relative match factors and log-fold changes for compounds in *Mucuna pruriens*.

| Retention time | Relative match factor | Positive log-fold change | Identified compound                  |
|----------------|-----------------------|--------------------------|-------------------------------------|
| 8.00           | 895                   | 0.38                     | Naphthalene                         |
| 12.45          | 899                   | 0.52                     | 1,2-Dimethyl-4-ethyl benzene        |
| 15.06          | 875                   | 0.46                     | n-Tetradecane                       |
| 16.71          | 872                   | 0.31                     | 1,3-Dtertiarybutylibenzene          |
| 8.27           | 869                   | 0.43                     | 1-ethyl-3-methyl-benzene            |
| 8.97           | 877                   | 0.48                     | 1,3-dichloro-benzene                |

Table 6. Retention time, relative match factors and log-fold changes for compounds in *Zea mays* (LONGE 6H).

| Retention time | Relative match factor | Positive log-fold change | Identified compound                  |
|----------------|-----------------------|--------------------------|-------------------------------------|
| 10.72          | 866                   | 0.30                     | m-Ethyltoluene                      |
| 12.07          | 894                   | 0.17                     | 2-n-Pentylfuran                     |
| 18.14          | 891                   | 0.07                     | 1-Methyl-2-(2-propenyl)benzene      |
| 13.13          | 897                   | 0.11                     | o-Dichlorobenzene                   |
| 13.36          | 854                   | 0.16                     | 1,2,4-Trimethylbenzene              |
| 14.84          | 842                   | 0.31                     | 2-Ethyl-p-xylene                    |

The PCA plots for rice (S3) and maize (S5) were close to each other and to the PCA for the control (S0). This may be attributed to the common presence of 2-n-pentylfuran in the three treatments. Despite cymbopogon and rice clustering in different quadrants, the PCAs for both crops were close possibly due to the commonly exudated tert-amylbenzene, pentamethylbenzene and 1-sec-butyl-4-methylbenzene terpenoids and 2,3-dimethylundecane alkane. There are no similar metabolites reported in the root exudates of *M. pruriens* to the ones profiled under
the current study. Nishihara et al. (2004) and Soares et al. (2014) reported L-DOPA to be dominantly exudated from the roots of *M. pruriens*. Kato-Noguchi (2010) identified 3 different allelochemicals, namely: 5-chloro-6-methoxy-2-benzoxazolinone, 6-methoxy-2-benzoxazolinone and 2,4-dihydroxy-1,4-benzoxazin-3-one from the mesocotyls and coleoptiles of rice seedlings.

Generally, the profiled compounds had not been previously identified and reported in the literature. This may be attributed to variation in the genetic characteristics of the test plants and environmental conditions. Jensen et al. (2001) have revealed that allelopathy is quantitatively inherited and identified four main quantitative trait loci (QTL) on three chromosomes of 142 cultivars of upland rice that collectively explained 35% of the allelopathic activity in the population. The potential effects of some bioactive compounds from the test crops have been reported by researchers. Kato-Noguchi (2011) and Poonpaiboonpipat et al. (2013) reported allelochemicals in rice and cymbopogon root exudates to inhibit weed growth. Citral of cymbopogon was reported to cause disruption of microtubules in wheat and *Arabidopsis thaliana* L. roots by Chaimovitsh et al. (2012). Ayeni and Kayode (2014) recorded inhibited seed germination by compounds in root extracts and tassel of maize. Reduced growth of component and subsequent field crops was observed by Pickett et al. (2010) and Soares et al. (2014), in desmodium and mucuna crops, respectively. The effects were attributed to allelochemicals released via root exudates. Cheng and Cheng (2015) reported allelochemicals to inhibit the absorption and transport of ions at the cell plasma membrane in various crops.

**Conclusion**

Bioactive compounds were profiled in soils potted with *C. nardus*, *D. uncinatum*, *M. pruriens*, upland rice (NERICA 1) and *Z. mays* (LONGE 6H). The secondary metabolites included terpenoids, phenols and alkanes. Terpenoids were the principal compounds. The results demonstrate that *Cymbopogon nardus*, upland rice (NERICA 1) *Desmodium uncinatum*, *Mucuna pruriens* and *Z. mays* (LONGE 6H) produced bio-compounds in their root exudates. Some of the compounds are reported to exhibit allelopathic properties and could be significant in the establishment and development of cultivated and natural ecosystems; declines in crop yield due to reduced uptake of nutrients, crop regeneration failure and replant problems. The study crops have been reported to exhibit negative and positive allelopathic influences. Further studies are recommended on the allelopathic potential of the specific compounds identified under specialised crop treatments to allow efficient generation of appropriate allelopathic cultivars. Such cultivars could become important tools in the development of advanced integrated weed management.
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Profili jedinjenja u eksudatima korena pirinča, limun trave, dezmoniuma, stizolobiuma i kukuruza

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Rezime

Korenovi ratarskih biljaka proizvode eksudate sa biološkim aktivnim hemikalijama za koje je poznato da utiču na rast useva i korovskih vrsta. Ogled je sproveden u Nacionalnom državnom institutu za istraživanje ratarskih biljaka u Ugandi, Namulonge tokom 2016. godine kako bi se identifikovala jedinjenja koja se oslobađaju u eksudatima korena biljaka Cymbopogon nardus, Desmodium uncinatum, planinskog pirinča (NERICA 1), Mucuna pruriens i Zea mays (LONGE 6H) gajenih u sudovima četrdeset i petog dana posle setve. Ovo je označavalo period blizu prosečne stacionarne faze za rast ispitivanih useva kada su nivoi sekundarnih metabolita visoki. Organska jedinjenja u zemljištima su ekstrahovana korišćenjem mikroekstrakcije u čvrstoj fazi (engl. solid-phase micro-extraction – SPME) i ekstrakcijom rastvarača. Uzorci su analizirani korišćenjem 7890A gasnog hromatografskog sistema. Datoteke podataka prebačene su u poseban dokument i podaci su preneseni na onlajn platformu XCMS radi poređenja parova i druge statističke analize u biblioteci Nacionalnog instituta za nauku i tehnologiju. Na kontrolnoj varijanti (samo zemljište) identifikovano je 15 terpenoida, dva alkohola i svaki od njih tri halometane, etere, fenole, ketone, furane, alkane i aldehide. Limun trava je izlučila pet terpenoida, jedan fenol i jedan alkan. Korenovi biljke dezmodium izlučili su tri terpenoida, jedan alkan i fenol. Uzev pirinča proizveo je osam terpenoida, dva alkana i jedan furan. Pet terpenoida, jedan fenol i jedan alkan oslobodeni su iz varijante sa stizolobiom, dok je šest terpenoida pronađeno u varijanti sa kukuruzom. Profilisana jedinjenja iz limun trave, dezmodiuma, pirinča, stizolobiuma i kukuruza mogle bi biti odgovorne za alelopatičke osobine koje su se ispoljile kod istraživanih useva u prirodnim i poljoprivrednim ekosistemima, te bi se mogle koristiti u sintezi i stvaranju herbicida.

Ključne reči: alkani, limun trava, dezmodium, eksudati, fenoli, pirinča, terpenoidi.

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