ABOUT AJB

The African Journal of Biotechnology (AJB) (ISSN 1684-5315) is published weekly (one volume per year) by Academic Journals.

African Journal of Biotechnology (AJB), a new broad-based journal, is an open access journal that was founded on two key tenets: To publish the most exciting research in all areas of applied biochemistry, industrial microbiology, molecular biology, genomics and proteomics, food and agricultural technologies, and metabolic engineering. Secondly, to provide the most rapid turn-around time possible for reviewing and publishing, and to disseminate the articles freely for teaching and reference purposes. All articles published in AJB are peer-reviewed.

Contact Us

Editorial Office: ajb@academicjournals.org
Help Desk: helpdesk@academicjournals.org
Website: http://www.academicjournals.org/journal/AJB
Submit manuscript online http://ms.academicjournals.me/
Editorial Board

Prof. Sagadevan G. Mundree
Department of Molecular and Cell Biology
University of Cape Town
Private Bag Rondebosch 7701
South Africa

Dr. Martin Fregene
Centro Internacional de Agricultura Tropical (CIAT)
Km 17 Cali-Palmira Recta
AA6713, Cali, Colombia

Prof. O. A. Ogunseyitan
Laboratory for Molecular Ecology
Department of Environmental Analysis and Design
University of California,
Irvine, CA 92697-7070. USA

Dr. Ibrahima Ndoye
UCAD, Faculte des Sciences et Techniques
Departement de Biologie Vegetale
BP 5005, Dakar, Senegal.
Laboratoire Commun de Microbiologie
IRD/ISRA/UCAD
BP 1386, Dakar

Dr. Bamidele A. Iwalokun
Biochemistry Department
Lagos State University
P.M.B. 1087. Apapa – Lagos, Nigeria

Dr. Jacob Hodeba Mignouna
Associate Professor, Biotechnology
Virginia State University
Agricultural Research Station Box 9061
Petersburg, VA 23806, USA

Dr. Bright Ogheneovo Agindotan
Plant, Soil and Entomological Sciences Dept
University of Idaho, Moscow
ID 83843, USA

Dr. A.P. Njukeng
Département de Biologie Végétale
Faculté des Sciences
B.P. 67 Dschang
Université de Dschang
Rep. du CAMEROUN

Dr. E. Olatunde Farombi
Drug Metabolism and Toxicology Unit
Department of Biochemistry
University of Ibadan, Ibadan, Nigeria

Dr. Stephen Bakiamoh
Michigan Biotechnology Institute International
3900 Collins Road
Lansing, MI 48909, USA

Dr. N. A. Amusa
Institute of Agricultural Research and Training
Obafemi Awolowo University
Moor Plantation, P.M.B 5029, Ibadan, Nigeria

Dr. Desouky Abd-El-Haleem
Environmental Biotechnology Department &
Bioprocess Development Department,
Genetic Engineering and Biotechnology Research
Institute (GEBRI),
Mubarak City for Scientific Research and Technology
Applications,
New Burg-Elarab City, Alexandria, Egypt.

Dr. Simeon Oloni Kotchoni
Department of Plant Molecular Biology
Institute of Botany, Kirschallee 1,
University of Bonn, D-53115 Germany.

Dr. Eriola Betiku
German Research Centre for Biotechnology,
Biochemical Engineering Division,
Mascheroder Weg 1, D-38124,
Braunschweig, Germany

Dr. Daniel Masiga
International Centre of Insect Physiology and Ecology,
Nairobi,
Kenya

Dr. Essam A. Zaki
Genetic Engineering and Biotechnology Research
Institute, GEBRI,
Research Area,
Borg El Arab, Post Code 21934, Alexandria
Egypt
Dr. Alfred Dixon  
International Institute of Tropical Agriculture (IITA)  
PMB 5320, Ibadan  
Oyo State, Nigeria

Dr. Sankale Shompole  
Dept. of Microbiology, Molecular Biology and Biochemistry,  
University of Idaho, Moscow,  
ID 83844, USA.

Dr. Mathew M. Abang  
Germplasm Program  
International Center for Agricultural Research in the Dry Areas  
(ICARDA)  
P.O. Box 5466, Aleppo, SYRIA.

Dr. Solomon Olawale Odemuyiwa  
Pulmonary Research Group  
Department of Medicine  
550 Heritage Medical Research Centre  
University of Alberta  
Edmonton  
Canada T6G 2S2

Prof. Anna-Maria Botha-Oberholster  
Plant Molecular Genetics  
Department of Genetics  
Forestry and Agricultural Biotechnology Institute  
Faculty of Agricultural and Natural Sciences  
University of Pretoria  
ZA-0002 Pretoria, South Africa

Dr. O. U. Ezeronye  
Department of Biological Science  
Michael Okpara University of Agriculture Umudike, Abia State, Nigeria.

Dr. Joseph Hounhouigan  
Maître de Conférence  
Sciences et technologies des aliments  
Faculté des Sciences Agronomiques  
Université d’Abomey-Calavi  
01 BP 526 Cotonou  
République du Bénin

Prof. Christine Rey  
Dept. of Molecular and Cell Biology,  
University of the Witwatersand,  
Private Bag 3, WITS 2050, Johannesburg, South Africa

Dr. Kamel Ahmed Abd-Elsalam  
Molecular Markers Lab. (MML)  
Plant Pathology Research Institute (PPathRI)  
Agricultural Research Center, 9-Gamma St., Orman,  
12619,  
Giza, Egypt

Dr. Jones Lemchi  
International Institute of Tropical Agriculture (IITA)  
Onne, Nigeria

Prof. Greg Blatch  
Head of Biochemistry & Senior Wellcome Trust Fellow  
Department of Biochemistry, Microbiology & Biotechnology  
Rhodes University  
Grahamstown 6140  
South Africa

Dr. Beatrice Kilel  
P.O Box 1413  
Manassas, VA 20108  
USA

Dr. Jackie Hughes  
Research-for-Development  
International Institute of Tropical Agriculture (IITA)  
Ibadan, Nigeria

Dr. Robert L. Brown  
Southern Regional Research Center,  
U.S. Department of Agriculture,  
Agricultural Research Service,  
New Orleans, LA 70179.

Dr. Deborah Rayfield  
Physiology and Anatomy  
Bowie State University  
Department of Natural Sciences  
Crawford Building, Room 003C  
Bowie MD 20715, USA
Dr. Marlene Shehata  
University of Ottawa Heart Institute  
Genetics of Cardiovascular Diseases  
40 Ruskin Street  
K1Y-4W7, Ottawa, ON, CANADA

Dr. Hany Sayed Hafez  
The American University in Cairo,  
Egypt

Dr. Clement O. Adebooye  
Department of Plant Science  
Obafemi Awolowo University, Ile-Ife  
Nigeria

Dr. Ali Demir Sezer  
Marmara Üniversitesi Eczacilik Fakültesi,  
Tibbiye cad. No: 49, 34668, Haydarpaşa, Istanbul,  
Turkey

Dr. Ali Gazanchain  
P.O. Box: 91735-1148, Mashhad,  
Iran.

Dr. Anant B. Patel  
Centre for Cellular and Molecular Biology  
Uppal Road, Hyderabad 500007  
India

Prof. Arne Elofsson  
Department of Biophysics and Biochemistry  
Bioinformatics at Stockholm University,  
Sweden

Prof. Bahram Goliaei  
Departments of Biophysics and Bioinformatics  
Laboratory of Biophysics and Molecular Biology  
University of Tehran, Institute of Biochemistry and Biophysics  
Iran

Dr. Nora Babudri  
Dipartimento di Biologia cellulare e ambientale  
Università di Perugia  
Via Pascoli  
Italy

Dr. S. Adesola Ajayi  
Seed Science Laboratory  
Department of Plant Science  
Faculty of Agriculture  
Obafemi Awolowo University  
Ile-Ife 220005, Nigeria

Dr. Yee-Joo TAN  
Department of Microbiology  
Yong Loo Lin School of Medicine,  
National University Health System (NUHS),  
National University of Singapore  
MD4, 5 Science Drive 2,  
Singapore 117597  
Singapore

Prof. Hidetaka Hori  
Laboratories of Food and Life Science,  
Graduate School of Science and Technology,  
Niigata University,  
Niigata 950-2181,  
Japan

Prof. Thomas R. DeGregori  
University of Houston,  
Texas 77204 5019,  
USA

Dr. Wolfgang Ernst Bernhard Jelkmann  
Medical Faculty, University of Lübeck,  
Germany

Dr. Moktar Hamdi  
Department of Biochemical Engineering,  
Laboratory of Ecology and Microbial Technology  
National Institute of Applied Sciences and Technology,  
BP: 676. 1080,  
Tunisia

Dr. Salvador Ventura  
Department de Bioquímica i Biologia Molecular  
Institut de Biotecnologia i de Biomedicina  
Universitat Autònoma de Barcelona  
Bellaterra-08193  
Spain

Dr. Claudio A. Hetz  
Faculty of Medicine, University of Chile  
Independencia 1027  
Santiago, Chile

Prof. Felix Dapare Dakora  
Research Development and Technology Promotion  
Cape Peninsula University of Technology,  
Room 2.8 Admin. Bldg. Keizersgracht, P.O. 652, Cape Town 8000,  
South Africa
Prof. Jean-Marc Sabatier  
Directeur de Recherche Laboratoire ERT-62  
Ingénierie des Peptides à Visée Thérapeutique,  
Université de la Méditerranée-Ambrilia Biopharma inc.,  
Faculté de Médecine Nord, Bd Pierre Dramard, 13916, Marseille cédex 20.  
France

Dr. Fabian Hoti  
PneumoCarr Project  
Department of Vaccines  
National Public Health Institute  
Finland

Prof. Irina-Draga Caruntu  
Department of Histology  
Gr. T. Popa University of Medicine and Pharmacy  
16, Universitatii Street, Iasi,  
Romania

Dr. Dieudonné Nwaga  
Soil Microbiolology Laboratory,  
Biotechnology Center, PO Box 812,  
Plant Biology Department,  
University of Yaoundé I, Yaoundé,  
Cameroon

Dr. Gerardo Armando Aguado-Santacruz  
Biotechnology CINVESTAV-Unidad Irapuato  
Departamento Biotecnología  
Km 9.6 Libramiento norte Carretera Irapuato-León Irapuato,  
Guanajuato 36500,  
Mexico

Dr. Abdolkaim H. Chehregani  
Department of Biology  
Faculty of Science  
Bu-Ali Sina University  
Hamedan,  
Iran

Dr. Abir Adel Saad  
Molecular oncology  
Department of Biotechnology  
Institute of graduate Studies and Research  
Alexandria University,  
Egypt

Dr. Azizul Baten  
Department of Statistics  
Shah Jalal University of Science and Technology  
Sylhet-3114,  
Bangladesh

Dr. Bayden R. Wood  
Australian Synchrotron Program  
Research Fellow and Monash Synchrotron  
Research Fellow Centre for Biospectroscopy  
School of Chemistry Monash University Wellington Rd.  
Clayton,  
3800 Victoria,  
Australia

Dr. G. Reza Balali  
Molecular Mycology and Plant Phthology  
Department of Biology  
University of Isfahan  
Isfahan  
Iran

Dr. Beatrice Kilel  
P.O Box 1413  
Manassas, VA 20108  
USA

Prof. H. Sunny Sun  
Institute of Molecular Medicine  
National Cheng Kung University Medical College  
1 University road Tainan 70101,  
Taiwan

Prof. Ima Nirwana Soelaiman  
Department of Pharmacology  
Faculty of Medicine  
Universiti Kebangsaan Malaysia  
Jalan Raja Muda Abdul Aziz  
50300 Kuala Lumpur,  
Malaysia

Prof. Tunde Ogunsanwo  
Faculty of Science,  
Olabisi Onabanjo University,  
Ago-Iwoye.  
Nigeria

Dr. Evans C. Egwim  
Federal Polytechnic,  
Bida Science Laboratory Technology Department,  
PMB 55, Bida, Niger State,  
Nigeria
Prof. George N. Goulielmos
Medical School,
University of Crete
Voutes, 715 00 Heraklion, Crete,
Greece

Dr. Uttam Krishna
Cadila Pharmaceuticals limited,
India 1389, Tarsad Road,
Dholka , Dist: Ahmedabad, Gujarat,
India

Prof. Mohamed Attia El-Tayeb Ibrahim
Botany Department, Faculty of Science at Qena,
South Valley University, Qena 83523,
Egypt

Dr. Nelson K. Ojijo Olang’o
Department of Food Science & Technology,
JKUAT P. O. Box 62000, 00200, Nairobi,
Kenya

Dr. Pablo Marco Veras Peixoto
University of New York NYU College of Dentistry
345 E. 24th Street, New York, NY 10010
USA

Prof. T E Cloete
University of Pretoria Department of Microbiology
and Plant Pathology,
University of Pretoria,
Pretoria,
South Africa

Prof. Djamel Saidi
Laboratoire de Physiologie de la Nutrition et de
Sécurité
Alimentaire Département de Biologie,
Faculté des Sciences,
Université d’Oran, 31000 - Algérie
Algeria

Dr. Tomohide Uno
Department of Biofunctional chemistry,
Faculty of Agriculture Nada-ku,
Kobe., Hyogo, 657-8501,
Japan

Dr. Ulises Urzúa
Faculty of Medicine,
University of Chile Independencia 1027, Santiago,
Chile

Dr. Aritua Valentine
National Agricultural Biotechnology Center, Kawanda
Agricultural Research Institute (KARI)
P.O. Box, 7065, Kampala,
Uganda

Prof. Yee-Joo Tan
Institute of Molecular and Cell Biology 61 Biopolis Drive,
Proteos, Singapore 138673
Singapore

Prof. Viroj Wiwanitkit
Department of Laboratory Medicine,
Faculty of Medicine, Chulalongkorn University,
Bangkok
Thailand

Dr. Thomas Silou
Université de Brazzaville BP 389
Congo

Prof. Burtram Clinton Fielding
University of the Western Cape
Western Cape,
South Africa

Dr. Brnčić (Brncic) Mladen
Faculty of Food Technology and Biotechnology,
Pierottijeva 6, 10000 Zagreb,
Croatia.

Dr. Meltem Sesli
College of Tobacco Expertise,
Turkish Republic, Celal Bayar University 45210,
Akhisar, Manisa,
Turkey.

Dr. Idress Hamad Attitalla
Omar El-Mukhtar University,
Faculty of Science,
Botany Department,
El-Beida, Libya.

Dr. Linga R. Gutha
Washington State University at Prosser,
24106 N Bunn Road,
Prosser WA 99350-8694
Dr Helal Ragab Moussa  
Bahnay, Al-bagour, Menoufia, Egypt.

Dr VVIPUL GOHEL  
DuPont Industrial Biosciences  
Danisco (India) Pvt Ltd  
5th Floor, Block 4B, DLF Corporate Park  
DLF Phase III  
Gurgaon 122 002  
Haryana (INDIA)

Dr. Sang-Han Lee  
Department of Food Science & Biotechnology,  
Kyungpook National University  
Daegu 702-701, Korea.

Dr. Bhaskar Dutta  
DoD Biotechnology High Performance Computing Software Applications Institute (BHSAI)  
U.S. Army Medical Research and Materiel Command  
2405 Whittier Drive  
Frederick, MD 21702

Dr. Muhammad Akram  
Faculty of Eastern Medicine and Surgery,  
Hamdard Al-Majeed College of Eastern Medicine,  
Hamdard University, Karachi.

Dr. M. Muruganandam  
Department of Biotechnology  
St. Michael College of Engineering & Technology,  
Kalayarkoil, India.

Dr. Gökhan Aydin  
Suleyman Demirel University,  
Atabey Vocational School,  
Isparta-Türkiye,

Dr. Rajib Roychowdury  
Centre for Biotechnology (CBT),  
Visva Bharati,  
West-Bengal, India.

Dr. Gökhan Aydin  
Suleyman Demirel University,  
Atabey Vocational School,  
Isparta-Türkiye,

Dr. Rajib Roychowdury  
Centre for Biotechnology (CBT),  
Visva Bharati,  
West-Bengal, India.

Dr Takuji Ohyama  
Faculty of Agriculture, Niigata University

Dr Mehdi Vasfi Marandi  
University of Tehran

Dr Fügen DURLU-ÖZKAYA  
Gazi University, Tourism Faculty, Dept. of Gastronomy and Culinary Art

Dr. Reza Yari  
Islamic Azad University, Boroujerd Branch

Dr Zahra Tahmasebi Fard  
Roudehen branche, Islamic Azad University

Dr Albert Magrí  
Giro Technological Centre

Dr Ping ZHENG  
Zhejiang University, Hangzhou, China

Dr. Kgomotso P. Sibeko  
University of Pretoria

Dr. Kgomotso P. Sibeko  
University of Pretoria

Dr Jian Wu  
Harbin medical university , China

Dr Hsiu-Chi Cheng  
National Cheng Kung University and Hospital.

Prof. Pavel Kalac  
University of South Bohemia, Czech Republic

Dr Kürsat Korkmaz  
Ordu University, Faculty of Agriculture, Department of Soil Science and Plant Nutrition

Dr. Shuyang Yu  
Department of Microbiology, University of Iowa  
Address: S1 newton road, 3-730B BSB bldg. Iowa City, IA, 52246, USA
Dr. Mousavi Khaneghah
College of Applied Science and Technology-Applied Food Science, Tehran, Iran.

Dr. Qing Zhou
Department of Biochemistry and Molecular Biology, Oregon Health and Sciences University Portland.

Dr Legesse Adane Bahiru
Department of Chemistry, Jimma University, Ethiopia.

Dr James John
School Of Life Sciences, Pondicherry University, Kalapet, Pondicherry
ARTICLES

Current status of Colletotrichum capsici strains, causal agents of Brown blotch disease of cowpea in Burkina Faso 96
Thio I. G., Zida E. P., Sawadogo M. and Séremé P.

In vitro seed germination and seedling development of the orchid Coelogyne stricta (D. Don) Schltr. 105
Gaurav Parmar and Bijaya Pant

Adsorption of copper, zinc and lead on biosurfactant produced from cassava wastewater 110
Larissa Kummer, Natássia Jersak Cosmann, Glaucia Maria Pastore, Ana Paula Resende Simiqueli, Vander de Freitas Melo and Simone Damasceno Gomes

Investigating the antioxidant properties and rutin content of Sea buckthorn (Hippophae rhamnoides L.) leaves and branches 118
Aliye Aras Perk, F. Duygu Ceylan, Onur Yanar, Kadir Boztas and Esra Capanoglu
Full Length Research Paper

Current status of *Colletotrichum capsici* strains, causal agents of Brown blotch disease of cowpea in Burkina Faso

Thio I. G.¹, ²*, Zida E. P.¹, ², Sawadogo M.³ and Sérémé P.¹

¹Institut de l’Environnement et de Recherches Agricoles (INERA), 01 BP 476 Ouagadougou 01, Burkina Faso. 
²LMI Patho Bios (INERA-IRD), Ouagadougou, Burkina Faso. 
³Laboratoire Biosciences, Unité de Formation et de Recherche en Sciences de la Vie et de la Terre (UFR-SVT), Université de Ouagadougou, 09 BP 848 Ouagadougou 09, Burkina Faso.

Received 18 September, 2015; Accepted 13 January, 2016

Brown blotch disease, caused by *Colletotrichum capsici*, is an important disease of cowpea with a significant yield losses ranging from 42 to 100% in West Africa. In this study, a specific polymerase chain reaction (PCR) primer set CC1F1/CcapR was used to characterize and to study the phylogenetic relationship of thirty eight strains of *Colletotrichum* species. This primer set is capable of amplifying only *C. capsici* from different fungal structures and provide a powerful tool for *C. capsici* detection in brown blotch disease in cowpea. Phylogenetic analysis from neighbor-joining (NJ) showed a high genetic variability in the rDNA-ITS region of the isolates. The isolates formed four groups or clusters on the basis of specific fragment analysis. Groups I, II, and III consist of strains containing specific region length of twenty one nucleotides and were considered as variant 1 of *C. capsici*. Group IV was a heterogeneous and consists of variants 1, 2, 3, and 4 of *C. capsici*.

Key words: Cultivars, internal transcribed spacer (ITS) sequence, *Colletotrichum* species.

INTRODUCTION

Cowpea (*Vigna unguiculata* (L.) Walp.) is one of main grain legume crops grown in sub-Saharan Africa in terms of cultivated areas, production, and consumption (Singh et al., 2002; Ajeigbe, 2006). In Burkina Faso, cowpea is a staple food crop, which is grown essentially for human food and nutrition. Cowpea production is subjected to abiotic stresses, such as drought, heat, and poor soil fertility and to various biotic agents including soil borne and seed borne, fungal pathogens, which cause diseases leading to a significant yield losses and reduction in grain density (Katile et al., 2010). Of the diseases, Brown blotch caused by *Colletotrichum capsici/truncatun* has been cited to be of great importance not only in Burkina Faso, but also in other parts of the world. In a worldwide perspective, *C. capsici* pathogen causes a disease commonly known as anthracnose on a wide range of
plants, including legumes, vegetables, and small fruits (Sérémé, 1999; Banerjee et al., 2007; Torres-Calzada et al., 2011). Recently, strains of *C. capsici* and *Colletotrichum dematium f. truncatum* have been described as the same species (Hyde et al., 2009) and are now considered to be synonym of *Colletotrichum truncatum* (Damm et al., 2009). The genus *Colletotrichum* includes several species, such as *Colletotrichum graminicola, C. capsici*, *C. truncatum, Colletotrichum gloeosporioides*, *C. dematium, Colletotrichum destructivum,* and *Colletotrichum coccodes,* which may occur as endophytes, saprobes or pathogens (Hyde et al., 2009). *Colletotrichum* is a cosmopolitan fungus and includes a number of economically important plant pathogenic fungi, occurring predominantly in tropical and subtropical regions on a wide range of crops (Sharma et al., 2014a).

Working on brown blotch disease of cowpea in Nigeria, Emechebe (1986) identified 8 races of *C. capsici.* Four of these races were reported to be specific to habitats in Guinea and Sudan Savannah ecologies. The four other races were reported to be common in rain forest zones. The spread of the pathogen can be facilitated by high humidity and heavy rains during the growing season. The identification of *Colletotrichum* species has been reported to be difficult due to morphological similarities of the pathogen races (Hyde et al., 2009). In Burkina Faso, Sérémé (1999) reported 12 pathogenic groups of *Colletotrichum* spp., including all *C. capsici* which are associated with brown blotch disease. The existence of these pathogen races in Burkina Faso create confusion especially when quick, accurate and proper pathogen identification is needed.

Traditionally, identification and classification of *Colletotrichum* spp. Have been based on the morphological characters, pathogenicity tests, and biochemical approaches (NGuettia et al., 2013; Saxena et al., 2014; Chai et al., 2014; Enyiukwu et al., 2014). In most cases, there were no clear differences in conidial or apressorial size and shape among these species. Thus molecular characterization is essential for completing the morphological description of *Colletotrichum* spp. (Sharma et al., 2014a, b; Enyiukwu et al., 2014). The rDNA region of *Colletotrichum* spp. has been investigated for species identification and phylogenetic relationships (Cannon et al., 2012). The internal transcribed spacer (ITS) markers have also been successfully used for detection of many species including plants, fungi and bacteria (Cros et al., 1993; Shivaprakash et al., 2011). Some ITS markers notably *C.capR/C.capF and CC1F1/CC2R2* have been used for *C. capsici* species detection and phylogenetic analysis (Banerjee et al., 2007; Chandra et al., 2009; Torres-Calzada et al., 2011).

In this paper, species specific polymerase chain reaction (PCR) primer pair CC1F1/CcapR were used to characterize and study the phylogenetic relationship of different strains of *Colletotrichum* spp. responsible of brown blotch disease in cowpea in Burkina Faso.

**MATERIALS AND METHODS**

**Collection of *Colletotrichum* isolates**

*Colletotrichum* isolates were obtained from infected cowpea tissues (leaf, stem and pod) from farmer’s fields in seven different sites, situated in three agro-ecological zones of Burkina Faso, namely Saria, Kamboinse, and Kouare (North Soudanian zone), Farako Ba and Gaoua (Soudanian zone), and Pobe Mengao and Bani (Sahelian zone) during the period from October to November, 2013. The collected tissues materials were surface sterilized in 70% (v/v) ethanol for 1 min followed by immersion in sodium hypochlorite (NaOCl) 1% (v/v) for 5 min and three successive rinses in sterilized distilled water. The samples were left to dry under the laminar air cabinet for 1 h. Then small pieces (approximately 5 × 5 mm) from the margins of infected tissues were transferred to Petri dishes containing three layers of wet blotter papers. Petri dishes containing samples were incubated at 28°C under 12 h/12 h light: dark for 7 to 9 days.

**Identification of *Colletotrichum* spp.**

*Colletotrichum* spp. (complex *C. capsici/truncatum*) were identified based on morphological characters of the acervuli and conidia produced on the infected tissues on the blotter papers under the stereomicroscope and compound microscopes based on the identification key established by Marthur and Kongsdal (2003). Then, using a sterile loop, pure isolates were further placed onto potato dextrose agar (PDA) containing streptomycin (0.3 μg/L of PDA). The plates were incubated at 24°C for 7 days under ultraviolet (UV) light of alternating 12 h light and darkness to obtain pure culture.

**Purification of *Colletotrichum* single spore isolates**

To obtain fresh single spore pure culture of *Colletotrichum* isolates, distilled water (100 ml) was added to PDA and 200 μl of the suspension obtained were spread on new PDA plates and incubated for 24 to 48 h as previously described. Then three to five single cells from each isolate were again transferred onto new PDA. After seven days of growth, single spore pure cultures were stored at 20°C until used.

**Molecular characterization**

**DNA extraction**

The Flinders Technology Associates (FTA) plant cards were used for fungal DNA extraction. The fungal suspension of 100 μl containing approximately 10^4 to 10^5 spores/ml was applied as a single spot on the paper, and the paper was air-dried for 1 to 2 h at room temperature. The spotted FTA plant cards were stored at room temperature until use. Using a Harris Micro Punch instrument, discs of 2-mm in diameter were taken from spots made on the FTA plant card. The sample discs were each placed in separate Eppendorf tubes. The discs from each FTA plant card were washed and air-dried for 1 h at room temperature following the manufacturer’s instruction (www.whatman.com).

**ITS amplification and sequencing**

PCR detection assay was conducted using the genus *Colletotrichum*
specific primer CC1F1 5’ACCTACTGTTGCTTGCG-3’ (Chandra et al., 2009) and the species C. capsici specific primer CcapR 5’-CCCAATGCGAGACGAAATG-3’ (Torres-Calzada et al., 2011), which gave a specific band size of 425 bp. The PCR mixture of 25 µl contained 1 FTA disk, 5 µl of Buffer (Flexer) 5X, 0.5 µl of dNTP (10 µM), 18.42 µl of distilled H2O, 0.5 µl of each primer (5 µm), and 0.08 µl of DNA Go Taq (Promega). The PCR was performed using a thermocycler Master Cycler Gradient at 95°C for 5 min for initial denaturation, followed by 25 cycles of denaturation at 94°C for 30s, primer annealing at 62°C for 30s and extension at 72°C for 2 min. The final extension was set at 72°C for 5 min. Eight microliters of the PCR products was analyzed on 1.5% agarose gel stained with 5 µl of ethidium bromide. After approximately 45 to 60 min of running at 70 to 80 mV, the gel was visualized. The PCR positive products were then sent to Beckman Coulter Genomics service (USA) for sequencing.

Molecular identification and phylogenetic analysis

BioEdit software was used for the Clustal W Multiple sequence alignment, and BLAST for species identification in the NCBI GenBank. Due to complications in distinguishing C. capsici, C. truncatum and C. dematium (Hyde et al., 2009), specific fragment of C. capsici was targeted on the BioEdit multiple sequence alignment software and was compared with that in the NCBI database. The phylogenetic tree was produced using DARwin 6.0.4 software.

RESULTS

The isolates of Colletotrichum spp. which were identified from the lesions of cowpea tissues were identified as C. capsici based on size and shape of conidia. The isolates of C. capsici showed differences in morphological characteristics such as colony color (brown, orange, black or grey or white), conidial shape and size (Figure 1). Conidia of fungal isolates were typically ellipsoidal and hyaline, and produced acervuli. Our results indicated that mycelium of C. capsici, from cowpea varied and could be aerial, compact or cottony (Figure 1). The size of conidia also varied within the isolates (Table 1).

The present study characterized thirty eight isolates of Colletotrichum spp. using molecular approaches; specific region in the International Transcribed Spacer regions of C. capsici was targeted and was used to determine phylogenetic relationships between these fungal strains.

The ITS sequence analysis of the 38 isolates of Colletotrichum spp. showed that all the strains were C. capsici (Table 2). Among the strains, 92% contained the specific sequence of C. capsici (Torres-Calzada et al., 2011) and were designated as variant 1. In total, four variants of C. capsici were identified on the basis of the sequence analysis of species (Table 3).

The four variants of C. capsici identified (Figure 2) in this study are in alignment with four physiological races identified by Emechebe (1986) which are specific to Guinea and Sudan Savanna habitats. The species capsici variant 1 represented the most, with 92% of the strains, and was distributed over all agro-ecological zones of the country. But variants 2, 3 and 4 seemed to be specific to the Sudanian zone (Gaoua).

Based on the phylogenetic relationship of the 38 clones, 4 clusters at a distance coefficient of 0.1 (Figure 3) were formed. The major cluster I had sixteen isolates with 65% similarity. Three of the identified variants of C. capsici belonged to the heterogeneous cluster IV.
Table 1. Comparatives morphological characters of eight *C. capsici* isolates, 10 days on PDA.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Location</th>
<th>Organ</th>
<th>Conidia length (µm)</th>
<th>Colony colour</th>
<th>Acervulus</th>
<th>Mycelia form</th>
</tr>
</thead>
<tbody>
<tr>
<td>03-KO-1</td>
<td>Kouare</td>
<td>Pod</td>
<td>20</td>
<td>Brown</td>
<td>Abundant</td>
<td>Compact</td>
</tr>
<tr>
<td>20-KB-5</td>
<td>Kamboinse</td>
<td>Stem</td>
<td>-</td>
<td>Brown-white</td>
<td>Absent</td>
<td>Cotty</td>
</tr>
<tr>
<td>35-GA-5</td>
<td>Gaoua</td>
<td>Pod</td>
<td>28</td>
<td>Orange</td>
<td>Abundant</td>
<td>Cotty</td>
</tr>
<tr>
<td>42-GA-7</td>
<td>Gaoua</td>
<td>Pod</td>
<td>23</td>
<td>Orange</td>
<td>Abundant</td>
<td>Aeral</td>
</tr>
<tr>
<td>71-FA-6</td>
<td>Farako-Ba</td>
<td>Pod</td>
<td>22</td>
<td>Brown</td>
<td>Abundant</td>
<td>Compact</td>
</tr>
<tr>
<td>74-BA-1</td>
<td>Bani</td>
<td>Pod</td>
<td>21</td>
<td>Brown</td>
<td>Abundant</td>
<td>Aerial</td>
</tr>
<tr>
<td>77-PM-1</td>
<td>Pobe</td>
<td>Pod</td>
<td>21</td>
<td>Black</td>
<td>Abundant</td>
<td>Compact</td>
</tr>
<tr>
<td>96-SA-2</td>
<td>Saria</td>
<td>Stem</td>
<td>20</td>
<td>Orange</td>
<td>Abundant</td>
<td>Cotty</td>
</tr>
</tbody>
</table>

Table 2. Molecular identification of *Colletotrichum* spp. single spores isolates from cowpea in Burkina Faso.

<table>
<thead>
<tr>
<th><em>Colletotrichum</em> spp. isolate</th>
<th>Organ</th>
<th>Location</th>
<th>NCBI identification</th>
<th>GenBank accession number</th>
<th>Specific sequence analysis identification</th>
<th>Variants</th>
</tr>
</thead>
<tbody>
<tr>
<td>001-KO-1</td>
<td>Pod</td>
<td>Kouare</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>003-KO-1</td>
<td>Pod</td>
<td>Kouare</td>
<td><em>C. capsici</em></td>
<td>KM213014 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>005-KB-1</td>
<td>Pod</td>
<td>Kamboinse</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>006-KB-1</td>
<td>Pod</td>
<td>Kamboinse</td>
<td><em>C. capsici</em></td>
<td>KM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>013-KB-3</td>
<td>Stem</td>
<td>Kamboinse</td>
<td><em>C. capsici</em></td>
<td>HQ271457 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>016-KB-3</td>
<td>Stem</td>
<td>Kamboinse</td>
<td><em>C. capsici</em></td>
<td>KM213014 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>020-KB-5</td>
<td>Stem</td>
<td>Kamboinse</td>
<td><em>C. capsici</em></td>
<td>HM197759 (85% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 2</td>
</tr>
<tr>
<td>024-GA-2</td>
<td>Stem</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>025-GA-3</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>KM213014 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>026-GA-3</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>027-GA-3</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>J185787 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>028-GA-3</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>Colletotrichum sp.</em></td>
<td>HQ130691 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>033-GA-4</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>KM213014 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>035-GA-5</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (92% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 3</td>
</tr>
<tr>
<td>036-GA-5</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>042-GA-7</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM191710 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 4</td>
</tr>
<tr>
<td>043-GA-7</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>045-GA-8</td>
<td>Pod</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>047-GA-9</td>
<td>Stem</td>
<td>Gaoua</td>
<td><em>C. truncatum</em></td>
<td>J0936245 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>051-GA-10</td>
<td>Stem</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>053-GA-10</td>
<td>Stem</td>
<td>Gaoua</td>
<td><em>C. capsici</em></td>
<td>HM197759 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
<tr>
<td>058-FA-2</td>
<td>Leaf</td>
<td>Farako-Ba</td>
<td><em>C. capsici</em></td>
<td>KM213014 (99% id.)</td>
<td><em>C. capsici</em></td>
<td>Var. 1</td>
</tr>
</tbody>
</table>
Table 2. Contd.

<table>
<thead>
<tr>
<th>Variant (C. capsici)</th>
<th>Sequence variability in the specific region (C. capsici)</th>
<th>Seq. identity</th>
<th>GenBank</th>
<th>Representative clone</th>
</tr>
</thead>
<tbody>
<tr>
<td>059-FA-3 Leaf Farako-Ba C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>060-FA-3 Leaf Farako-Ba C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271451</td>
<td>Var. 1</td>
</tr>
<tr>
<td>062-FA-4 Stem Farako-Ba C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>064-FA-4 Stem Farako-Ba C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>071-FA-6 Pod Farako-Ba C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>KM213014</td>
<td>Var. 1</td>
</tr>
<tr>
<td>072-FA-6 Pod Farako-Ba C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>074-BA-1 Pod Bani C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>077-PM-1 Pod Pobe-Mengao C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>082-PM-3 Stem Pobe-Mengao C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
<tr>
<td>083-PM-3 Stem Pobe-Mengao C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
<tr>
<td>085-PM-3 Stem Pobe-Mengao C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
<tr>
<td>089-PM-5 Stem Pobe-Mengao C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
<tr>
<td>090-PM-5 Stem Pobe-Mengao C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
<tr>
<td>091-PM-5 Stem Pobe-Mengao C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
<tr>
<td>092-SA-1 Stem Saria C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>096-SA-2 Stem Saria C. capsici</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
</tbody>
</table>

Table 3. rDNA sequence comparison of the specific fragment from the internal transcribed spacer (ITS) region of the 38 Colletotrichum capsici species isolated from cowpea plants.

<table>
<thead>
<tr>
<th>Variant of C. capsici</th>
<th>Sequence variability in the specific region (C. capsici)</th>
<th>Seq. identity</th>
<th>GenBank</th>
<th>Representative clone</th>
</tr>
</thead>
<tbody>
<tr>
<td>Variant 1 (C. capR specific fragment)</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92 to 99%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>Variant 2</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>92%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
<tr>
<td>Variant 3</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>88%</td>
<td>HM197759</td>
<td>Var. 1</td>
</tr>
<tr>
<td>Variant 4</td>
<td>-AACATTTCGTCTCGCATTGG(T)G</td>
<td>85%</td>
<td>HQ271457</td>
<td>Var. 1</td>
</tr>
</tbody>
</table>

Variants 2, 3, and 4 had 71% similarity with variant 1 in cluster IV. The sequences similarities of the 38 strains of C. capsici were consigned in Table 4.

DISCUSSION

In this study, thirty eight Colletotrichum spp. isolates were characterized using molecular approaches. The present findings have revealed that there exist high level of variation between the rDNA-ITS region of Colletotrichum spp. in Burkina Faso. High number of clades obtained on the dendrogram shows a strong intraspecific differentiation within the C. capsici species. All the four clusters were representative of the three agroecological zones and the distribution of the isolates was not depending on the geographic area indicating a high genetic diversity at all locations. Kumar et al. (2010) observed the same results; working with C. falcatum from sugarcane in India. Such variations could be due to similar climatic conditions, which might favor the coexistence of the isolates. The analysis of sequence identity between C.
Capsici strains ranged from 0.773 to 0.974 (Table 3). This similarity indicates a high penalty for closely related sequences. The highest degree of sequence identity was observed between strains 96-SA-2 and 91-PM-5 (0.974), 92-SA-1 and 77-PM-6 (0.961), and the lowest degree (0.773) was observed between strains 20-KB-5 (variant 3) and 28-GA-3 (variant 1). C. capsici isolates from Saria (North soudanian) were very close to those from Pobe Mengao (Sahelian).

Working with Anthracnose disease on chilli fruits, using Randomly Amplified Polymorphic DNA (RAPD), Kumar et al. (2015) demonstrated genetic variability among isolates of C. capsici from different locations in India. Contrary to our study, they found a low value of similarity coefficient. The difference in similarity coefficients between this study and Kumar et al. (2015) could be due to the fact that ITS sequences cannot be used to distinguish closely related species.

The concept of a species in the genus Colletotrichum is not well defined due to insufficient variation in classical descriptive criteria and difficulties in dealing with pathogens of similar morphology, but different host specificity (Sutton, 1992). The molecular study of C. capsici strains provides criteria that permit differentiation of strains or species with similar conidial morphology. The examination of highly conserved rDNA, along with other criteria represents a useful approach of addressing taxonomic uncertainties (Sherriff et al., 1994; Bailey et al., 1996; Sexena et al., 2014). The phylogenetic relationship of the strains of C. capsici showed that the variants 2, 3 and 4 may be evolved from variant 1 from a mutation of two or three nucleotides in the specific fragment region.

In a previous report, C. capsici strains from cowpea in Burkina Faso were different based on both biomorphological and biochemical characters (Sereme, 1999). In the current study, the usefulness of rDNA-ITS markers was demonstrated to distinguish and establish the phylogenetic relationship of different strains of C. capsici isolated from cowpea plants in Burkina Faso. This
research provides a quick and accurate tool for specific PCR detection of *C. capsici*, causative agents of brown blotch disease in cowpea. In this study, the ITS markers were recognized to be phylomarkers for intra and extra-specific relationship within species population as per Lei et al. (2012), and for validation of species status as per the study by Dabert (2006). Thus, findings were presented, which will help future researchers to avoid confusion when distinguishing the *C. capsici* from other *Colletotrichum* spp. infecting cowpea.

Conflict of Interests

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

This research was supported financially by different donors, the West Africa Agricultural Productivity Program (WAAPP), the International
### Table 4. Sequence identity/similarity Matrix of *Colletotrichum capsici* strains from cowpea in Burkina Faso.

<table>
<thead>
<tr>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>01-KO</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>03-KO</td>
<td>0.946</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>05-KB</td>
<td>0.914</td>
<td>0.917</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>06-KB</td>
<td>0.943</td>
<td>0.948</td>
<td>0.926</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>13-KB</td>
<td>0.932</td>
<td>0.948</td>
<td>0.914</td>
<td>0.964</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>16-KB</td>
<td>0.957</td>
<td>0.929</td>
<td>0.919</td>
<td>0.957</td>
<td>0.941</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>20-KB</td>
<td>0.780</td>
<td>0.778</td>
<td>0.758</td>
<td>0.803</td>
<td>0.785</td>
<td>0.797</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>24-GA</td>
<td>0.933</td>
<td>0.928</td>
<td>0.906</td>
<td>0.944</td>
<td>0.933</td>
<td>0.939</td>
<td>0.778</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>25-GA</td>
<td>0.944</td>
<td>0.934</td>
<td>0.924</td>
<td>0.951</td>
<td>0.941</td>
<td>0.953</td>
<td>0.774</td>
<td>0.919</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>26-GA</td>
<td>0.923</td>
<td>0.907</td>
<td>0.913</td>
<td>0.930</td>
<td>0.920</td>
<td>0.935</td>
<td>0.779</td>
<td>0.915</td>
<td>0.910</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>27-GA</td>
<td>0.925</td>
<td>0.916</td>
<td>0.933</td>
<td>0.946</td>
<td>0.936</td>
<td>0.941</td>
<td>0.780</td>
<td>0.927</td>
<td>0.930</td>
<td>0.950</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>28-GA</td>
<td>0.920</td>
<td>0.913</td>
<td>0.906</td>
<td>0.946</td>
<td>0.925</td>
<td>0.932</td>
<td>0.773</td>
<td>0.914</td>
<td>0.928</td>
<td>0.918</td>
<td>0.929</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>33-GA</td>
<td>0.951</td>
<td>0.937</td>
<td>0.910</td>
<td>0.960</td>
<td>0.943</td>
<td>0.957</td>
<td>0.786</td>
<td>0.931</td>
<td>0.949</td>
<td>0.937</td>
<td>0.941</td>
<td>0.955</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>35-GA</td>
<td>0.867</td>
<td>0.846</td>
<td>0.842</td>
<td>0.871</td>
<td>0.855</td>
<td>0.887</td>
<td>0.816</td>
<td>0.854</td>
<td>0.868</td>
<td>0.861</td>
<td>0.872</td>
<td>0.855</td>
<td>0.874</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>36-GA</td>
<td>0.930</td>
<td>0.909</td>
<td>0.910</td>
<td>0.939</td>
<td>0.939</td>
<td>0.948</td>
<td>0.787</td>
<td>0.919</td>
<td>0.933</td>
<td>0.960</td>
<td>0.941</td>
<td>0.916</td>
<td>0.932</td>
<td>0.872</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>42-GA</td>
<td>0.792</td>
<td>0.792</td>
<td>0.779</td>
<td>0.810</td>
<td>0.792</td>
<td>0.800</td>
<td>0.833</td>
<td>0.791</td>
<td>0.782</td>
<td>0.795</td>
<td>0.793</td>
<td>0.783</td>
<td>0.795</td>
<td>0.821</td>
<td>0.786</td>
<td>ID</td>
<td></td>
<td></td>
</tr>
<tr>
<td>43-GA</td>
<td>0.906</td>
<td>0.906</td>
<td>0.909</td>
<td>0.924</td>
<td>0.924</td>
<td>0.921</td>
<td>0.770</td>
<td>0.944</td>
<td>0.907</td>
<td>0.906</td>
<td>0.916</td>
<td>0.907</td>
<td>0.913</td>
<td>0.850</td>
<td>0.906</td>
<td>0.786</td>
<td>ID</td>
<td></td>
</tr>
<tr>
<td>45-GA</td>
<td>0.928</td>
<td>0.916</td>
<td>0.915</td>
<td>0.941</td>
<td>0.932</td>
<td>0.944</td>
<td>0.790</td>
<td>0.917</td>
<td>0.926</td>
<td>0.948</td>
<td>0.948</td>
<td>0.916</td>
<td>0.932</td>
<td>0.865</td>
<td>0.960</td>
<td>0.783</td>
<td>0.906</td>
<td>ID</td>
</tr>
</tbody>
</table>

### Table 4. Contd.

<table>
<thead>
<tr>
<th>Seq-&gt;</th>
<th>47-GA</th>
<th>51-GA</th>
<th>53-GA</th>
<th>58-FA</th>
<th>59-FA</th>
<th>60-FA</th>
<th>62-FA</th>
<th>64-FA</th>
<th>71-FA</th>
<th>72-FA</th>
<th>74-BA</th>
<th>77-PM</th>
<th>82-PM</th>
<th>83-PM</th>
<th>85-PM</th>
<th>89-PM</th>
<th>90-PM</th>
<th>91-PM</th>
<th>92-SA</th>
<th>96-SA</th>
</tr>
</thead>
<tbody>
<tr>
<td>47-GA</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>51-GA</td>
<td>0.907</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>53-GA</td>
<td>0.902</td>
<td>0.978</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>58-FA</td>
<td>0.903</td>
<td>0.921</td>
<td>0.915</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>59-FA</td>
<td>0.873</td>
<td>0.895</td>
<td>0.893</td>
<td>0.917</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>60-FA</td>
<td>0.905</td>
<td>0.928</td>
<td>0.933</td>
<td>0.931</td>
<td>0.898</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>62-FA</td>
<td>0.907</td>
<td>0.926</td>
<td>0.935</td>
<td>0.938</td>
<td>0.902</td>
<td>0.962</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>64-FA</td>
<td>0.939</td>
<td>0.935</td>
<td>0.939</td>
<td>0.939</td>
<td>0.911</td>
<td>0.941</td>
<td>0.941</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>71-FA</td>
<td>0.903</td>
<td>0.932</td>
<td>0.930</td>
<td>0.944</td>
<td>0.900</td>
<td>0.949</td>
<td>0.949</td>
<td>0.939</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>72-FA</td>
<td>0.885</td>
<td>0.905</td>
<td>0.896</td>
<td>0.927</td>
<td>0.927</td>
<td>0.890</td>
<td>0.897</td>
<td>0.919</td>
<td>0.897</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>74-BA</td>
<td>0.888</td>
<td>0.942</td>
<td>0.937</td>
<td>0.932</td>
<td>0.936</td>
<td>0.911</td>
<td>0.913</td>
<td>0.926</td>
<td>0.915</td>
<td>0.928</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>77-PM</td>
<td>0.906</td>
<td>0.943</td>
<td>0.939</td>
<td>0.953</td>
<td>0.915</td>
<td>0.951</td>
<td>0.958</td>
<td>0.948</td>
<td>0.953</td>
<td>0.923</td>
<td>0.937</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>82-PM</td>
<td>0.886</td>
<td>0.920</td>
<td>0.918</td>
<td>0.914</td>
<td>0.895</td>
<td>0.909</td>
<td>0.912</td>
<td>0.921</td>
<td>0.918</td>
<td>0.922</td>
<td>0.914</td>
<td>0.934</td>
<td>ID</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Mixte Laboratory (LMI, INERA-IRD) Patho-bios, and the Kirkhouse Trust Foundation. They thank Dr. Christophe Brugidou and Martine Bangratz for technical support and helpful discussion.

REFERENCES


Full Length Research Paper

**In vitro** seed germination and seedling development of the orchid *Coelogyne stricta* (D. Don) Schltr.

Gaurav Parmar¹* and Bijaya Pant²

¹National Herbarium and Plant Laboratories, Godawari, Lalitpur, Nepal.
²Plant Biotechnology and Plant Biochemistry Unit, Central Department of Botany, Tribhuvan University, Kirtipur, Nepal.

Received 19 July, 2015; Accepted 29 December, 2015

*Corresponding author. E-mail: gaurav_mascot4u@yahoo.com. Tel: 977-9808004464.

**Key words:** *Coelogyne stricta*, *in vitro*, Murashige and Skoog (MS), 6-benzylaminopurine (BAP), α-naphthalene acetic acid (NAA).

**INTRODUCTION**

Nepal, situated in the lap of Himalaya, harbors 451 species of orchids from 107 genera (Rajbhandari, 2015). Orchids as a whole are cited under Appendix II of CITES except *Paphiopedilum insigne* and *Paphiopedilum venustum* in Nepal. They are important aesthetically, medicinally and also regarded as ecological indicator (Joshi et al., 2009). Due to their varied shape, size, colourful-long lasting flowers, shining green leaves and variously shaped pseudobulbs, they are very popular around the world.

A total of 90 species of orchids of Nepal have medicinal value (Pant and Raskoti, 2013). *Coelogyne* represented by 14 plant species (Rajbhandari, 2015), is one of them. It is also the most threatened orchids in Nepal due to its over collection from nature.

*Coelogyne stricta* (D. Don) Schltr., a native orchid of Nepal, is commonly known as 'The Rigid Coelogyne Pseudobulbs'. It is an epiphyte on tree trunks or lithophytes on mossy rocks at elevations of 1400 to 2000 m in Nepal (Raskoti, 2009; Rajbhandari, 2015). It has high aesthetic value (Figure 1), so it is often used as an ornamental plant in many gardens, nurseries, hotels, etc. Its medicinal value is due to paste of its pseudobulb which is applied to the forehead against headache and...
fever (Baral and Kurmi, 2006). Owing to its high demand in the national and international markets, over collection from its natural habitat and slow growth rate in nature, this species is restricted only to narrow pocket areas in the nature.

Orchid seeds lack functional endosperm, so the germination of the seeds requires an aid of suitable fungus. The germination rate of orchid seeds in nature is only 2 to 5% (Rao, 1977); even if they do so, the seeds take a long time to germinate and any disturbance in the habitat may destroys the whole population. The seedlings take 12 years to grow to maturity (Basker and Narmatha Bai, 2006). Vegetative propagation of this orchid through division of clumps of rhizomes, bulbs or by the rooting of off-shoots is slow; so often, that it is difficult to obtain the desired number of plants. These difficulties in natural germination and slow vegetative propagation may drive this species to extinction. In vitro propagation of orchids through seeds can produce large number of orchids in reasonable short time.

Hence, the present study was undertaken to develop an efficient protocol for in vitro propagation of C. stricta through seeds and ultimately assist in its conservation.

MATERIALS AND METHODS

Eight weeks old immature capsule of C. stricta (Figure 2) collected from the orchid house of National Botanical Garden, Godawari, Kathmandu was used in this research.

The capsule was sterilized by washing under running tap water besides 2 to 3 drops of tween 20 solution (Qualigens Fine Chemicals Pvt. Ltd.) for 50 min until the water became totally clear and transparent. The capsule was then rinsed in 70% ethyl alcohol for 2 min and in 1% solution of sodium hypochlorite for 10 min. Finally, it was rinsed with sterile water five times.

Murashige and Skoog (MS) medium was used alone and in different combinations of 6-benzylaminopurine (BAP) and α-naphthalene acetic acid (NAA) (Table 1). The medium was supplemented with 3% sucrose. The pH of the medium was adjusted to 5.8 before autoclaving and solidified with 0.8% (w/v) agar. The medium was autoclaved at 15 psi for 15 min.

The sterilized capsule was then dissected longitudinally into two halves (Figure 3) using sterile surgical blade inside pre-sterilized laminar air flow cabinet. The seeds were then inoculated on the surface of MS medium alone and in different combinations of BAP and NAA using sterile forceps. The cultures were incubated at 25± 2°C under photoperiod of 16/8 h light/dark cycle.

RESULTS AND DISCUSSION

Immature capsule was selected for this research as it shows better germination response and saves time (Pant, 2006). The most effective germination response for C. stricta with complete development of roots and shoots was found to be on MS medium supplemented with BAP (1 mg/L) and NAA (1 mg/L). The quantity and nature of growth regulators have significant effect on the germination of orchid seeds (Arditti, 1979).

The most appropriate medium was selected on the basis of time taken for germination of seeds and their growth and development. Initiation of seed germination was observed after five weeks of culture in five different hormonal combinations of the medium (Table 1). This was supported by the findings of Reddy et al. (1992), who studied the seed germination and seedling growth in four different species of orchids (Cymbidium aloifolium, Dendrobium crepidatum, Epidendrum radicans and Spathoglottis plicata) and found the seed germination after 5 weeks. It was also supported by similar findings of Hoshi et al. (1994) on the seed germination of four species of Cyripedium and Pradhan and Pant (2009) on Dendrobium densiflorum.

Protocorms were obtained after 8 weeks of culture in
Table 1. Effect of growth hormones supplemented to MS medium on seed germination and seedling growth of *C. stricta* (D. Don) Schltr.

<table>
<thead>
<tr>
<th>Medium</th>
<th>Growth hormones</th>
<th>Concentration of hormones (mg/L)</th>
<th>Observation taken in weeks</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Initiation of germination</td>
<td>Protocorm formation</td>
</tr>
<tr>
<td>MS</td>
<td>-</td>
<td>-</td>
<td>5</td>
</tr>
<tr>
<td>MS</td>
<td>BAP</td>
<td>0.5</td>
<td>5</td>
</tr>
<tr>
<td>MS</td>
<td>BAP</td>
<td>1</td>
<td>8</td>
</tr>
<tr>
<td>MS</td>
<td>BAP</td>
<td>1.5</td>
<td>8</td>
</tr>
<tr>
<td>MS</td>
<td>BAP</td>
<td>2</td>
<td>7</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>0.5</td>
<td>5</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>1+0.5</td>
<td>6</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>1.5+0.5</td>
<td>5</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>2+0.5</td>
<td>6</td>
</tr>
<tr>
<td>MS</td>
<td>NAA</td>
<td>1</td>
<td>8</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>0.5+1</td>
<td>7</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>1+1</td>
<td>7</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>1.5+1</td>
<td>7</td>
</tr>
<tr>
<td>MS</td>
<td>BAP+NAA</td>
<td>2+1</td>
<td>7</td>
</tr>
</tbody>
</table>

Culture conditions: 25± 2°C, 32 weeks, 16 h photoperiod and 6 replicates were used in each combination.

Figure 3. Capsule cut longitudinally into two halves.

Figure 4. Clumped protocorms on MS medium supplemented with 0.5 mg/L BAP after 10 weeks of culture.

three different hormonal combinations of the medium (Table 1). Similar findings were also reported by Basker and Narmatha Bai (2010) in the seed germination of *Eria bambusifolia* which took 7 weeks for protocorms formation, Pant et al. (2011) on *Phaius tancarvilleae* which took 9 weeks and Gogoi et al. (2012) on *Cymbidium eburneum* which also took 9 weeks. Clumped protocorms were observed in this case on MS medium supplemented with 0.5 mg/L BAP after 10 weeks of culture (Figure 4). The first shoot initial was obtained after 11 weeks of culture on MS medium supplemented with BAP (0.5 mg/L) and NAA (0.5 mg/L) while it was observed after 13 weeks of culture on hormone-free MS medium (Figure 5). This was supported by the findings of Pant et al. (2011) on *P. tancarvilleae* which took 12 weeks for first shoot formation. Dense shoot formation was common under various hormonal combination of the medium (Figure 7) except on MS medium supplemented with 0.5 mg/L BAP (Figure 6). The first root initial was obtained after 23 weeks of culture on MS
medium supplemented with BAP (1 mg/L) and NAA (1 mg/L) while on MS medium supplemented with 0.5 mg/L NAA it was observed after 25 weeks of culture (Figure 8). Pradhan and Pant (2009) in the seed germination of *D. densiflorum* found 19 weeks needed for the first root formation.

Complete plantlet of *C. stricta* was obtained after 23 weeks of culture. This was supported by the findings of Pant et al. (2011) on *P. tancarvilleae* which took 24 weeks to develop into complete plantlets and Paudel et al. (2012) on *Esmeralda clarkei* which took 25 weeks. MS medium supplemented with BAP (1 mg/L) and NAA (1 mg/L) was found to be the best for seed germination of *C. stricta*. This was supported by the findings of Pant and Swar (2011) in the study of seed germination of *Cymbidium iridioides* who found MS medium supplemented with BAP (1 mg/L) and NAA (1 mg/L) to be best for the protocorms formation and seedlings growth.

Phytohormone NAA was found to be essential for root initiation as the medium combination lacking NAA did not develop root even after 32 weeks of culture (Table 1). It may be due to genetic constitution of explants and the endogenous growth regulators present in them. According to Yam et al. (1989), the nutritional requirements of germinating orchid seeds vary with their physiological state and this may be species specific. This also revealed that the addition of root hormone NAA might be essential in the nutrient medium for the
successful root growth and development. The nutrient requirement of orchid seeds in terms of quantity as well as form may vary at different stages of development for various species (Ernst, 1974; Arditti and Ernst, 1984).

Conclusion

The phytohormones BAP and NAA are both necessary for in vitro seed germination and seedlings growth of *C. stricta*. MS medium supplemented with BAP (1 mg/L) and NAA (1 mg/L) was found to be the best for this purpose.

Conflict of interests

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

The authors would like to express sincere gratitude to Prof. Dr. Pramod K. Jha, Head, Central Department of Botany, Tribhuvan University and Dr. Sushim Ranjan Baral, former Chief, National Herbarium and Plant Laboratories, Godawari for providing necessary laboratory facilities for the research. We would also like to thank National Botanical Garden, Godawari for providing the orchid capsule.

Abbreviations

MS, Murashige and Skoog medium; BAP, 6-benzylaminopurine; NAA, α-naphthaleneacetic acid.

REFERENCES


Full Length Research Paper

Adsorption of copper, zinc and lead on biosurfactant produced from cassava wastewater

Larissa Kummer¹*, Natássia Jersak Cosmann², Glauca Maria Pastore³, Ana Paula Resende Simiqueli³, Vander de Freitas Melo⁴ and Simone Damasceno Gomes²

¹Department of Chemistry and Biology, Federal Technological University of Paraná (UTFPR). Rua Deputado Heitor Alencar Furtado, 5000 - 81280-340 Curitiba-PR, Brazil.
²Center of Exact and Technological Sciences, Western Paraná State University (UNIOESTE/CASCABEL/CCET/ PGEAGRI), Rua Universitária, 2069 - 85819-110 Cascavel, PR, Brazil.
³Department of Food Science, Faculty of Food Engineering, State University of Campinas, Rua Monteiro Lobato, 13083-862 Campinas, SP, Brazil.
⁴Department of Soil Science and Agricultural Engineering, Federal University of Paraná (UFPR), Rua dos Funcionários, 1540 - 80035-050 Curitiba, PR, Brazil.

Received 18 September, 2015; Accepted 1 February, 2016

The remediation of soils contaminated by hydrophobic compounds, especially petroleum derivatives, using surfactants has been fairly studied. The use of these compounds in heavy metal contaminated areas is incipient and their mechanism of action has not been totally elucidated yet. The biosurfactants are compounds with surfactant characteristics produced by living organisms and have several environmental advantages, like greater biodegradability and production from renewable sources. The aim of this study was to evaluate the adsorption potential of the metals copper, zinc and lead onto the biosurfactant structure and to relate it to the Langmuir and Fréundlich physicochemical models of adsorption. The biosurfactant produced presented an emulsification index (EI) around 60%, which was stable even after 72 h of emulsion formation. The analysis of FTIR and HPLC confirmed that the biosurfactant produced is composed mainly of surfactin, found in concentration of 28%. The biosurfactant was capable of adsorbing the metals in its structure. In the adsorption process of Pb²⁺, the biosurfactant was considered as an interesting absorbent, but this behavior did not adjust satisfactorily to Langmuir and Fréundlich models. Thus, the biosurfactant has the potential to be utilized in remediation processes of soils and treatment of effluents contaminated by heavy metals.

Key words: Bacillus subtilis, trace elements, heavy metals, remediation of contaminated areas, agro industrial residue, surfactin.

INTRODUCTION

The surfactants are an important class of chemicals widely utilized in several industrial sectors, as pharmaceutical, cosmetic, fine chemical, food and environmental applications, and are usually synthesized

*Corresponding author. E-mail: lkummer@utfpr.edu.br. Tel: (55 41) 3279-4575.

Author(s) agree that this article remains permanently open access under the terms of the Creative Commons Attribution License 4.0 International License
from petroleum derivatives (Silva et al., 2010). However, the growth of environmental concern between the consumers allied with new legislations of environmental control, lead to the pursuit of natural surfactants as an alternative to the available products. Biosurfactants are bacteria, fungi and yeast metabolic byproducts that show surfactant properties (Barros et al., 2007; Das et al., 2009; Marin et al., 2015; Cortés-Camargo et al., 2016). The application of surfactants produced biotechnologically is restricted to certain areas, since the production process is still not economically competitive as compared to surfactants derived from petroleum (Henkel et al., 2012). Biosurfactant production in industrial scale is usually limited by the high cost of culture media, associated with inefficient downstream methods and to relatively low incomes of the product (Henkel et al., 2012). The use of agroindustrial wastes as substrates for microbial production has been suggested as an alternative to make the process commercially feasible (Colla and Costa, 2003; Barros et al., 2007; Bezerra et al., 2012; Henkel et al., 2012) and enables, as well, the utilization of million tons of environmentally dangerous residues in biotechnological processes (Cortés-Camargo et al., 2016).

Different industrial wastes were studied for biotechnological purposes, such as: cooking oil residues (Haba et al., 2000), effluents of olive oil production (Mercade et al., 1993), molasses and whey (Joshi et al., 2008), okara - solid residue from the production of soy milk (Slivinski et al., 2012), vine-trimming wastes (Cortés-Camargo et al., 2016) and liquor from sisal (Agave sisalana) pulp hydrolysis (Marin et al., 2015).

World cassava production is around 263 million tons (Mt) per year with Africa accounting for about 57% of the supply in 2012. Asia is second with 30.7%, while Latin America and the Caribbean are third with 12.2%. Nigeria is the largest producer of cassava in the world with more than 54 Mt at the end of 2012 and The Democratic Republic of Congo is the second largest producer of cassava in Africa after Nigeria in 2012 (FAOSTAT, 2014). A positive characteristic is that cassava crop is very resilient and can be cultivated in a wide variety of ecological zones, making it ideal for poor farmers to cultivate (Okudoh et al., 2014).

The industrial processing of the cassava generates residues that require different treatments for their disposition that are conditioned to the technological and economic level of each company. The liquid residue, cassava wastewater, is generated during the process of shredded mass pressing for flour production or during cassava starch extraction and purification (Suman et al., 2011). The high concentration of remaining carbohydrates and several important micronutrients can cause a serious problem of environmental pollution if the effluent is not properly treated before disposition (Damasceno et al., 2003). On the other hand, this is also an interesting characteristic in a culture medium, since there might be no need for supplementation to biosurfactant production (Barros et al., 2007; Bezerra et al., 2012).

The application of surfactants in order to remediate soils contaminated with hydrocarbons and/or heavy metals has been widely studied and the biosurfactants are an attractive option because of their biodegradability and lower toxicity (Song et al., 2008; Wan et al., 2011). The efficiency of these compounds for the efficient removal of metals depends on several physicochemical mechanisms of interaction and environmental conditions that have still not been totally elucidated (Franzetti et al., 2009; Singh and Turner, 2009). Among the basic factors involved, the types of surfactant, soil and contaminant, as well the complex interaction between them may be cited (Juwarkar et al., 2007; Asçi et al., 2010; Torres et al., 2012). According to Ramamurthy et al. (2008), anionic surfactants have the largest effects on metals mobilization. Burrows et al. (2010) reported the surfactant acidity as a determining factor for its larger or smaller interaction with the metals, which is stronger for slightly acidic carboxylates than for sulphates or sulphonates. Although these interactions should be due in great part to electrostatic effects, they are also, in some cases, followed by an increase in entropy as a result of the release of water from hydrated cations.

Staliikas (2002) discussed that the interaction of metal species with surfactants occurs through electrostatic interactions with the surfactant polar head, or by hydrophobic interactions of the metal chelates with the micelles hydrophobic chain, which could be a strategy to, for example, promote the removal of metallic ions from an effluent (Costa, 2011).

Rhamnolipid-type biosurfactant interaction with metals was reported by Wang and Mulligan (2009), whose results suggested that the interaction of biosurfactant with soils and/or residues containing heavy metals, may occur due to several factors, such as interfacial tension reduction and solubilization of metals by the formation of micelles or complexes. Das et al. (2009) tested a biosurfactant produced by Bacillus circulans in different critical micellar concentrations (CMC) and concluded that as the concentration of the surfactant increases, the metal removal (Cd and Pb) of the environment (liquid effluent) also increased, reaching a complete removal with a concentration corresponding to 5xCMC.

Thus, this study aimed to evaluate the adsorption capacity of heavy metals (Cu$^{2+}$, Zn$^{2+}$ and Pb$^{2+}$) into the biosurfactant obtained using cassava wastewater, liquid waste from cassava flour production, in order to assess its use as a possible alternative in decontamination of effluents and soils contaminated with metals.

**MATERIALS AND METHODS**

**Biosurfactant production**

The biosurfactant was produced by Bacillus subtilis LB5a isolates pertaining to the culture collection of the Bioflavors Laboratory of
DCA/FIA/Unicamp (Brazil). The liquid wastewater from the cassava flour, the cassava water, was previously treated by heating until boiling point, then chilled and centrifuged to be used as culture medium. The fermentation process was carried out in a pilot fermenter (Pilot New Brunswick 8000 MP 80), at 30°C, 4 rpm (air volume per volume of culture medium per minute) and agitation of 150 rpm (Barros et al., 2008a).

The foam produced during the fermentation process was continuously collected and collapsed (Barros et al., 2007). For biosurfactant extraction, the collapsed foam was centrifuged at 12,700 G for 10 min to get cell-free solution, then had its pH adjusted to 2.0 using 6N HCl and was kept at 4°C overnight for decantation. After the liquid was centrifuged at 12,700 G per 20 min, the precipitate was collected, neutralized with 3 M NaOH, and then dried at 50°C 50°C (Makkar and Cameotra, 1997, 1999; Barros et al., 2007). This material, named raw biosurfactant, was then crushed in mortar and stored for later analysis.

**Emulsification index**

Screw cap test tubes containing 6 mL of hydrocarbon and 4 mL of a 48 mg.L⁻¹ solution of raw biosurfactant were vortexed for 2 min and then left to rest at room temperature. The hydrophobic compounds utilized were sunflower oil, soybean oil and diesel. The emulsification index was determined after 24, 48 and 72 h (EI₂₄h, EI₄₈h and EI₇₂h, respectively) by the difference between the height of the emulsion layer (EL) and the mixture's total height (TH), as shown in Equation 1 (Cooper and Goldenberg, 1987):

\[ EI(\%) = \frac{EL - TH}{TH} \times 100 \]

**Biosurfactant characterization by infrared spectroscopy**

The biosurfactant obtained was characterized by Fourier transform mid-infrared spectroscopy (FT-MIR), using the Shimadzu IR Prestige 21 infrared spectrophotometer with detector DTGS. A quantity of 2 to 5 mg of the samples were diluted in 100 mg of KBr and analyzed by the transmission technique.

The organic attributions for the observed spectroscopic bands were done by the comparative method with the data available in Silverstein and Webster (2007) and other papers in the area to confirm the associations, which were presented during the discussion of the obtained results.

**Biosurfactant characterization by high performance liquid chromatography**

The biosurfactant was analyzed by high performance liquid chromatography (HPLC) utilizing a Shimadzu liquid chromatographer, model LC 20 AT, with a Kromasil C18 column. The mobile phase used was acetonitrile and trifluoroacetic acid (3.8 mmol.L⁻¹) in ratio of 80:20.

To confirm the surfactant type, a co-chromatography with surfactin standard from Sigma- Aldrich was performed. Both the biosurfactant and the standard sample were diluted in acetonitrile: methanol (1:1, v/v) (2 mg.mL⁻¹) and 20 μL were used for the injection. This injection methodology was based on Silivinski et al. (2012).

**Adsorption Isotherms for the ions Cu²⁺, Zn²⁺ and Pb²⁺**

A volume of 20 mL of several solutions containing metallic ions in different concentrations were brought into contact with 50 mg of adsorbent (biosurfactant) at 25°C, agitation of 200 rpm and pH ~ 6.3. The pH of the metallic solutions was adjusted using NaOH (0.1 mol.L⁻¹) and was not corrected during the experiments of adsorption. In order to prevent an increase in competition of the different species for the adsorption spots, a pH buffer was not used. The metallic solutions were prepared from commercial analytical standards of 1,000 mg.L⁻¹ and then diluted to concentrations between 50 and 750 mg.L⁻¹ for Zn²⁺ and from 20 to 200 mg.L⁻¹ for both Cu²⁺ and Pb²⁺. All the tests were performed in triplicate.

After 24 h of shaking to reach the balance, the samples were centrifuged at 3,500 G for 10 min and then filtered through qualitative filter paper. The metal concentration in the supernatants was measured by atomic adsorption spectroscopy (AAS) in a Shimadzu spectrophotometer model AA 6030. Isotherms models of Langmuir and Fréundlich were applied to the obtained data.

The quantity of adsorbed metal (q) was the difference between the initial concentration of metal in each solution and the concentration in the supernatant after contact with the absorbent (Cₑ). The data collected experimentally were applied to the models of Langmuir and Fréundlich whose equations are presented below. The isotherm of Langmuir is given by the Equation 2 where:

\[ q_e = q_m \frac{C_e}{K_L b} + \frac{C_e}{b} \]

The Fréundlich equation is presented in Equation 3, where:

\[ q_e = K_F C_e^{1/n} \]

**RESULTS AND DISCUSSION**

**Emulsification index (EI)**

The EI₂₄h for the biosurfactant solution with the three types of oil evaluated, sunflower oil, soybean oil and gasoline, were about 60% and it was observed that the emulsions formed were stable for at least 72 h (Table 1). Bezerra et al. (2012) who produced ramnolipid from cassava water with *Pseudomonas aeruginosa* obtained the emulsification index of the biosurfactant solution with kerosene ranging from 50 to 68% for the first 24 h. A lot of them are maintained stable for 72 h or more. Batista et al. (2006) that worked with surfactin, got values of 50% of the EI for the commercial kerosene. Barros et al. (2008b) analyzed the surfactin obtained from *B. subtilis* Lb5a and produced under the same conditions as described in the present study with 15 different types of hydrophobic compounds. The emulsions with sunflower...
oil, soybean oil and gasoline were stable for at least 72 h and values of EI\textsubscript{24h} were close to 70%. This difference is probably due to the level of purification of the surfactin used, as the biosurfactant used by Barros et al. (2008b) had gone through an additional process of extraction with solvents. Besides, these same authors verified the relation between the sizes of the fatty acids carbonic chains in the tested oils and the EI\textsubscript{24h} of the emulsions with surfactin and could not identify any relation between the type and the size of the chains. The stability of the emulsions found in the present study and also reported in other papers might indicate that, once the metal is adsorbed into the biosurfactant, the possibility of desorption of the metal to the environment is reduced.

**Biosurfactant characterization**

The results have confirmed that the biosurfactant obtained in this work is really surfactin, once the bands are very similar to the standard of surfactin (Sigma-Aldrich) (Figure 1). The Fourier transform infrared spectroscopy (FTIR) is a methodology that detects similarities or differences in the chemical structures of compounds (Franca et al., 2010). According to Silverstein and Webster (2007), functional groups and structures can be discriminated by their molecular vibrations. This technique can be used for the identification of the biosurfactants because most of them have one radical carbonyl, ester binding or carboxylic acid, which absorb energy in the infrared region of the electromagnetic spectrum (Gartshore et al., 2000).

The absorption spectrum in the infrared zone of the biosurfactant was compared with the spectrum of surfactin standard from Sigma Aldrich (Figure 1), as well as to the data described by Teixeira et al. (2009) and Oliveira et al. (2013) studies that obtained surfactin using different carbon sources. Oliveira et al. (2013) used clarified cashew juice and Teixeira et al. (2009), artificial mineral nutrient broth.

It is possible to observe an absorption in 3.282 cm\textsuperscript{-1}, characteristic of axial strain of the connection N-H present in peptides; absorption in 2.952 cm\textsuperscript{-1} corresponds to the asymmetric stretching of the connection C-H of grouping CH\textsubscript{3} (fatty acids); band in 2.922 cm\textsuperscript{-1} correspondent to the asymmetric stretching of the connection C-H of grouping CH\textsubscript{2}; band of axial strain C=O in 1.720 cm\textsuperscript{-1} of carboxylic acid. This band was observed in all works used as comparison and also in all of them, this strain is discrete (Teixeira et al., 2009; Oliveira et al., 2013). There are two absorptions, one in 1.647 cm\textsuperscript{-1}, that feature the amide I group (C=O; C=\textit{N}); and other in 1.535 cm\textsuperscript{-1} that feature the amide II. Oliveira et al. (2013) also obtained a very similar spectrum, assigning such bands likewise to the amide groups. In the zone of 1.230 to 1.200 cm\textsuperscript{-1}, the vibration C=O in aromatic ring or CH\textsubscript{2} strain in alkyl carboxyl is possible. The strain in 1.056 cm\textsuperscript{-1} can represent the C-O stretch of polysaccharides.

The area obtained from the integration of the 5 peaks of the homologous by HPLC was applied in the regression equation calculated through the calibration curve constructed using different concentrations of surfactin standard from Sigma-Aldrich (R\textsuperscript{2} = 0.9904) to estimate surfactin concentration in the raw biosurfactant. The elution profile in HPLC of the homologous lipopeptide produced presented retention times equivalent to the ones obtained for the standard surfactin. Doing the comparison of the chromatogram obtained for the biosurfactant produced with chromatogram of the standard Sigma-Aldrich sample, as well the results of FTIR and the literature results, it is possible to identify the surfactant produced as surfactin.

Five peaks have been identified: at 6, 14, 18, 25 and 27 min. The integration of the 5 peak areas showed that the concentration of surfactin in the raw biosurfactant was 28%. Since after acid precipitation the biosurfactant did not suffer any other downstream process, a low level of purity was expected. Oliveira et al. (2013) evaluated the biosurfactant production by *B. subtilis* using cashew juice and obtained 11.17% of surfactin in the semi-purified biosurfactant. Franca et al. (2010) produced biosurfactant from *Pseudomonas aeruginosa*. EQ 109 from glycerol and obtained low production yields, and after the purification process, the aforementioned authors obtained about 6.57% of rhamnolipid in biosurfactant.

The choice to avoid further steps of purification was made considering the intended use of this biosurfactant. It was reported that the extraction by solvents, and resulting increase in costs and generation of chemical residues, was not necessary for the process of remediation of soils or effluents.

**Adsorption of metals onto the biosurfactant**

In Figure 2, there are experimental data, as well as the obtained isotherms by the models of Langmuir and Fréündlich for adsorption of Zn, Cu\textsuperscript{2+} and Pb\textsuperscript{2+} by the biosurfactant. Resulting parameters of the isotherms are listed in Table 2.

The high determination coefficients (R\textsuperscript{2}), obtained from

### Table 1. Emulsification index (EI) of different emulsions of hydrocarbons with the biosurfactant produced by *Bacillus subtilis* LB5a.  

<table>
<thead>
<tr>
<th>Hydrophobic compound</th>
<th>EI (%)</th>
<th>24h</th>
<th>48h</th>
<th>72h</th>
</tr>
</thead>
<tbody>
<tr>
<td>Soybean oil</td>
<td>59.4</td>
<td>59.4</td>
<td>59.4</td>
<td></td>
</tr>
<tr>
<td>Sunflower oil</td>
<td>59.7</td>
<td>59.7</td>
<td>59.7</td>
<td></td>
</tr>
<tr>
<td>Gasoline</td>
<td>60.3</td>
<td>60.3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
the linearized equations of Langmuir and Fründlich (Table 2), indicate that both adsorption models are significantly able to demonstrate the adsorption of Zn$^{2+}$ and Cu$^{2+}$ into the studied biosurfactant.

Table 2. Langmuir and Fründlich parameters for adsorption of Zn$^{2+}$, Cu$^{2+}$ and Pb$^{2+}$ into the biosurfactant.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Langmuir</th>
<th>Fründlich</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>$K_L$ ($L,mg^{-1}$)</td>
<td>$B$ ($mg,g^{-1}$)</td>
</tr>
<tr>
<td>Zinc</td>
<td>0.25</td>
<td>5.00</td>
</tr>
<tr>
<td>Copper</td>
<td>0.11</td>
<td>10.00</td>
</tr>
<tr>
<td>Lead</td>
<td>0.05</td>
<td>3.33</td>
</tr>
</tbody>
</table>

$K_L$: Langmuir isotherm constant; $B$: maximum monolayer coverage capacity; $R^2$: coefficient of determination; $K_F$: Fründlich isotherm constant.

**Figure 1.** Infrared spectrum of the biosurfactant obtained by the bioprocess (a) and surfactin standard Sigma-Aldrich (b).
Figure 2. Isotherms obtained from the adsorption data obtained experimentally for Zn\(^{2+}\) (a) Cu\(^{2+}\) (b) and Pb\(^{2+}\) (c) in the equilibrium solution.

Langmuir model represented better the behavior of adsorption of Zn\(^{2+}\) into the biosurfactant, and Freundlich model overestimated the experimental values (Figure 2).

Based on the b values obtained by the Langmuir isotherm, that estimates the maximum capacity of adsorption (MCA), it is possible to affirm that the biosurfactant has high affinity for the studied metals. The value for Cu\(^{2+}\) was the highest, 10 mg.g\(^{-1}\), followed by Zn\(^{2+}\) (5 mg.g\(^{-1}\)). For Pb\(^{2+}\), the curves showed that the
system did not adjust well to the Langmuir model in the studied concentration range, which makes the MCA value not valid. Fréundlich model was the most appropriate to describe the adsorption of this element.

The experimental values were important to confirm that the biosurfactant produced from cassava wastewater have shown high capacity to adsorb metals, independent whether an adjustment to the evaluated physicochemical models has been observed. According to Zeraik and Nitischke (2010) and Seydlová and Svobodová (2008), the surfactin is characterized as an anionic biosurfactant is a result of the negative charges in its polar group, which is due to the presence of functional groups as amide and carboxylic acids.

Therefore, this capacity to adsorb metals on the cation forms occurs because of the anionic nature of the surfactin, which allows the interaction between the negatives charges of the biosurfactant and the positives charges of the metallic ions. According to Piron and Domard (1997), who studied the uranium adsorption into different types of chitosans, the adsorption capacity increases with the average degree of acetylation (DA). The DA measures the percentage of amino groups available in the chitosan chain and is one of the main parameters that affect the adsorption properties.

Colla et al. (2012), in a study that compared the Cd removal in liquid containing biosurfactant and different species of filamentous fungi, concluded that in those liquids containing biosurfactant, the metal removal was better. The association between Aspergillus fungi and biosurfactant promoted 100% removal of the Cd existence in the solution. The authors concluded that the presence of biosurfactants in liquids improves the metal removal efficiency.

The difference between the adsorption potential for the three metals studied is due to the properties of each one of them. According to Vieira et al. (2011), concentration, pH and ionic strength of the solution, beyond the effect of competitors ions, widely influences the adsorption properties, besides contributing to the protonation of the amino groups from the biopolymers. Thus, the knowledge of the behavior of these metallic species in solution, may contribute to the understanding of the adsorption mechanism (ionic change, electrostatic action, chelation, etc).

According to Miller (1995), the biosurfactant presents potential to increase the efficiency of metal removal in soils because they facilitate sorption processes, mass transfers and resistance to transport in aqueous phase. The addition of biosurfactants may promote the desorption of heavy metals of solid phases through the complexation of free forms of metals in solution or by the accumulation of the biosurfactants in the liquid-solid interface, caused by the reduction of interfacial activities, which promotes a direct contact between the biosurfactants and the metals. Moreover, Valdman et al. (2005) demonstrated that an exopolysaccharide extracted from the microorganism Serratia sp., with biosurfactant activities, presented a high efficiency in the Cd removal from liquids. In these experiments 50 mg.L⁻¹ of Cd²⁺ and 0.1 g.L⁻¹ of the previously purified biosurfactant were used, achieving a Cd removal of 170 mg.g⁻¹ of biosurfactant.

Conclusions
The biosurfactant produced presents emulsifier properties and stability, and the emulsification index was about 60% even after 72 h. The biosurfactant produced consists fundamentally of surfactin with 28% of purity.

The biosurfactant produced from cassava wastewater has shown capability to adsorb Cu²⁺, Zn²⁺ and Pb²⁺ into its structure. The maximum capacity of adsorption of Cu²⁺ and Zn²⁺ was estimated at 10 and 5 mg.g⁻¹, respectively.

In the adsorption process of Pb²⁺, the biosurfactant presented as a good adsorbent, however the satisfactory adjustment has not been observed for the Langmuir model. The Fréundlich model presented better adjustment. Further studies are recommended to verify the behavior of the biosurfactant in liquid effluents and soils containing heavy metals.

Conflicts of interest
The authors declare that there is no conflict of interest.

REFERENCES
Cooper DG, Goldenberg BG (1987). Surface-active agents from
Cortés-Camargo S, Pérez-Rodríguez N, Oliveira RPS, Huerta BEB, Domínguez JM (2016). Production of biosurfactants from vine-
trimming byproducts using the halotolerant strain Bacillus licheniformis ZSB10. Ind. Crop. Prod. 79:258-266.
Costa PBA (2011). Síntese e propriedades de surfactantes di-
aniónicos: interação com íons trivalentes. MS Dissertation, University of Coimbra, Portugal.
Juwarkar AA, Nair A, Dubey KV, Singh SK, Devotta S (2007). Biosurfactant technology for remediation of cadmium and lead
Makkar RS, Cameotra SS (1997). Biosurfactant production by a ther
Marin CP, Kaschuk JJ, Frollini E, Nitschke M (2015). Potential use of the
Miller RM (1995). Biosurfactant-facilitated remediation of metal-
Okudoh V, Trois C, Workneh T, Schmidt S (2014). The potential of cassava biomasses and applicable technologies for sustainable biogas
Slivinski CT, Mallmann E, Araújo JM, Mitchell DA, Krieger N (2012). Production of surfactin by Bacillus pumilus UFPEDA 448 in solid-
Full Length Research Paper

Investigating the antioxidant properties and rutin content of Sea buckthorn (*Hippophae rhamnoides* L.) leaves and branches

Aliye Aras Perk¹*, F. Duygu Ceylan², Onur Yanar¹, Kadir Boztas¹ and Esra Capanoglu²

¹Istanbul University, Faculty of Science, Department of Botany, Istanbul 34460, Turkey.
²Istanbul Technical University, Faculty of Chemical and Metallurgical, Food Engineering Department, Istanbul 34469, Turkey.

Received 29 April, 2015; Accepted 10 December, 2015

The present study focused on the antioxidant properties and rutin content of leaves and branches of *Hippophae rhamnoides* L. (Sea buckthorn) in Turkey. Dried leaves (leaf tea), processed (PB) and unprocessed branches (UB) of Sea buckthorn (SBT) were extracted with ethanol and prepared in forms of aqueous extract (AE). All samples were analyzed for their contents of rutin, total phenolics (TPC), total flavonoids (TFC) and total antioxidant capacity by using DPPH and CUPRAC methods. TPC of leaves from ethanolic extracts (EE) were significantly higher than UB and PB extracts. The DPPH scavenging activity of extracts ranged from 41.93 ± 3.57 and 132.43 ± 6.57 mg trolox equivalent (TE)/g, and the antioxidant capacity measured with CUPRAC method were in between 129.4 ± 18.1 and 538.5 ± 34.8 mg TE/g. Both EE and AE of leaf samples had significantly higher rutin content compared to the UB and PB samples. Taking the high antioxidant and rutin content of leaves into account and with respect to their positive health effects, consumption of SBT as a herbal tea should be investigated.

**Key words:** Sea buckthorn, *Hippophae rhamnoides*, leaves, antioxidant, phenolic profile, rutin content.

INTRODUCTION

Sea buckthorn (SBT) (*Hippophae rhamnoides* L.) is a species of flowering plant in the family Elaeagnaceae, deciduous shrub with good adaptability to various climate conditions and extensive genetic variability with numerous greenish-yellow flowers and bright orange, globular, ellipsoid fruit. It is native to Europe and Asia and has been domesticated in several countries (India, China, Nepal, Pakistan, Myanmar, Russia, Britain, Germany, Finland, Romania, France, etc.) (Khan et al., 2010; Yogendra Kumar et al., 2011; Pop et al., 2013). In Turkey, SBT is widely distributed throughout North and East Anatolia and known locally as ‘Yalancı igde, Cicirgan, Diijirgan, Cicilik’ or ‘Sincan Çalısı’ (Aras-Tayhan, 1997). All parts of the plant are considered to be a good source of large number of bioactive substances like vitamin, carotenoids, and flavonoids, organic acids, sterols and some essential amino acids. For instance, berries and seeds of SBT are well known for their antioxidative properties, attributed to hydrophilic and lipophilic compounds including ascorbic acid, flavonoids,
proanthocyanidins and carotenoids. The leaves of SBT are also considered for their antioxidant potential correlated to flavonoids and phenolic acids derivatives, and they have been used in some countries to make extracts, tea, animal feed, pharmaceuticals and cosmetics (Michel et al., 2012; Wani et al., 2013).

Flavonoids are the widest group of secondary metabolites involved in many biological functions in plants. They are classified into flavonols, flavones, flavanones, catechins, anthocyanidins and chalcones (Gupta et al., 2011). Rutin is one of the bioactive flavonoid compound, which is present in substantial amounts in various plants (Attanassova and Bagdassarian, 2009). Grapes and buckwheat are the most important rutin containing foods between fruits, vegetables and grain crops (Kreft et al., 2006). Rutin, a naturally occurring flavonol consisting of aglycone quercetin and a rutinoside moiety in position 3 of the C ring, is found in many food substances. It has been reported to exhibit beneficial effects against several types of liver diseases (Pan et al., 2014). Within the group of flavonoids, many studies have been conducted on rutin, since this flavonoid is of great therapeutic importance. Rutin causes an increase in pancreatic lipase with consequent reduction in triacylglyceride levels in rats. It has also been described in events associated with the immune system, as seen with other flavonoids. Rutin has been shown to inhibit neoplasia induced by immunonosuppression with azoxymethanol and to reduce oxidative stress in leukocytes in rheumatoid arthritis (Marcarini et al., 2011). H. rhamnoides is generally reported to be rich in a wide range of biologically active substances. Due to the antioxidant properties of sea buckthorn leaves the number of studies investigating their potential utilization has grown in recent years, but there are limited number of studies on SBT branches in the literature and therefore, this study was focused mainly on leaves and branches of SBT. The aim of the present study is to investigate the antioxidant properties and rutin content of sea buckthorn leaves, processed branches and unprocessed branches.

**MATERIALS AND METHODS**

**Plant material**

Wild Sea buckthorn (*H. rhamnoides* L.) were harvested from Central Anatolia, particularly Sivas region (Table 1). The leaves and branches were separated from each other and ventilated. In order to inhibit the activation of oxidation enzyme, leaves and branches were subjected to shocking procedure. For this purpose plant materials were shocked with 90 to 100°C vapor in rotary evaporator. Output materials of the shocking unit were cooled with dry air. Cooled materials were subjected to folding procedure for 25 to 30 min. After folding unit, leaves and branches were transferred into the drying chamber and dried at 110°C. At the end of this treatment dried leaf tea and processed branch were obtained. These materials were cut into small pieces and stored in the dark at room temperature before use (up to 1 week).

Dried leaves, processed (PB) and unprocessed branches (UB) of *H. rhamnoides* were extracted with ethanol as described below, also prepared in forms of infusion of leaf tea and decoction technique was used for PB and UB. All samples were analyzed for their contents of total phenolics and total flavonoids as well as their total antioxidant capacity by using two different methods including 1,1-diphenyl-2-picrylhydrazyl (DPPH) and Copper Reducing Antioxidant Capacity (CUPRAC). The samples were also analyzed by using HPLC to identify their phenolic profiles.

**Table 1. Some characteristics of the sampling sites.**

<table>
<thead>
<tr>
<th>Sampling site</th>
<th>Latitude/altitude longitude</th>
<th>Annual precipitation (Mm)</th>
<th>Annual temperature (°C)</th>
<th>Climate type</th>
<th>Sampling dates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sivas-Sincan stream</td>
<td>39°54’N- 2000 m 37°59’E</td>
<td>794</td>
<td>2.8</td>
<td>Humid</td>
<td>June 2013</td>
</tr>
</tbody>
</table>

**Extraction procedure**

**Ethanolic extraction**

Ethanolic extractions were carried out for dried leaves, PB and UB samples as described previously by Maheshwari et al. (2011) with slight modifications. 2.0±0.01 g of each sample was extracted with 15 ml of 70% aqueous-ethanol in a cooled ultrasonic bath (Azakli, Turkey) for 15 min. After 24 h incubation, the treated samples were centrifuged (Hettich Zentrifugen Universal 32R, UK) for 10 min at 4000 rpm at 4°C and the supernatant were collected. Then 15 ml of 70% aqueous-ethanol was added to the pellet and this extraction procedure was repeated two more times. All four supernatants were combined and adjusted to a final volume of 50 ml. Prepared extracts were stored at -20°C until analysis.

**Aqueous extraction**

To improve the efficiency of extractions, different methods were used for aqueous extraction of leaves, UB and PB. Dried leaf tea samples were prepared in forms of infusions. For the preparation of infusions, 2±0.01 g of dried leaves were weighed and dissolved in 200 ml of pure water at 90°C. After waiting for 30 min, the leaves were removed and the infusion was filtered, and further analyzed. Because of the woody structure of UB and PB, similar technique to the preparation of wood for microscopic examination was applied. 2±0.01 g of UB and PB were weighed and 75 ml of water added. It was heated until boiling. At the boiling point 25 ml of pure water was added and was reboiled. This procedure repeated four more times until final volume of 200 ml. Branches were removed and extract was filtered and further analyzed (Aras-Tayhan, 1997).
Determination of total phenolic content (TP)

The TP of extracts was determined using Folin-Ciocalteu reagent according to the method modified from Velioglu et al. (2006) using gallic acid as a standard. A mixture of 100 μl of the extract, 900 μl of distilled water and 1.5 ml of 0.2 N Folin-Ciocalteu reagents were prepared and allowed to react for 5 min. Then 1.2 ml of 7.5% Na₂CO₃ solutions added into the reaction mixture. After incubation for 90 min at room temperature, the absorbance was measured at 765 nm using Optima SP-3000 nano spectrophotometer. The TP of extracts was expressed as mg of gallic acid equivalent (GAE) per g sample.

Determination of total flavonoid content (TF)

The TF was measured colorimetrically as described by Kim et al. (2003). Mixture of 0.25 ml of each extract, 1.25 ml of distilled water and 75 μl of 5% NaNO₂ were prepared and allowed to react for 6 min. Then 150 μl AlCl₃·H₂O was added and mixed. After 5 min 0.5 ml of 1 M NaOH was added. The total volume was adjusted to 2.5 ml with distilled water. Absorbance of the mixture was measured at 510 nm versus prepared blank. The TF of extracts was determined by a rutin standard curve and expressed as milligram of rutin equivalent (RE) per gram sample.

Determination of total antioxidant capacity (TAC)

Antioxidant capacity of plant extract cannot be evaluated by only a single method due to the complex nature of phytochemicals. Therefore, in this study the TAC was estimated by two different assays. The DPPH and CUPRAC assays were performed according to Kumaran and Karunakaran (2006) and Apak et al. (2005) respectively. Trolox was used as a standard and results were expressed in terms of milligram of Trolox equivalent (TE) per gram sample.

DPPH-radical scavenging activity assay

The free radical scavenging activity of sea buckthorn leaves, UB and PB aqueous and ethanolic extracts on DPPH radical were determined according to the method introduced by Kumaran and Karunakaran (2006) and Rai et al. (2006). 0.1 mM of DPPH was prepared by dissolving 3.943 mg DPPH with 100 ml ethanol. 100 μl of each extract was mixed with 2 ml ethanolic solution of DPPH (0.1 mM). Extracts were substituted by methanol and distilled water blanks. Decolourisation of purple free radical DPPH solution was measured at 517 nm after 30 min incubation in the dark and at room temperature. A trolox calibration curve was done between 0.01 and 0.2 mg/ml. Results were expressed in mg of trolox equivalents/g of sample (mg TE/g).

Copper reducing antioxidant capacity (CUPRAC) assay

CUPRAC assay was carried out according to Apak et al. (2005) which is based on the absorbance measurement of Cu(I)-neocuproine (Nc) chelate formed as a result of the redox reaction of chain- breaking antioxidants with the CUPRAC reagent, Cu(II)-Nc, where absorbance is recorded at the maximal light-absorption wavelength of 450 nm. 10⁻² M of CuCl₂ solution was prepared by dissolving 0.4262 g CuCl₂·2H₂O in distilled water, and diluted to 250 mL. Ammonium acetate buffer at pH = 7.0, 1.0 M, was prepared by dissolving 19.27 g NH₄Ac in distilled water and diluted to 250 mL. Neocuproine (Nc) solution was prepared daily by dissolving 0.078 g Nc in 96% ethanol, and diluted to 50 mL with ethanol. 100 μl of extract was mixed with 1 ml of CuCl₂ solution, 1 ml of Nc solution, 1 ml of ammonium acetate buffer and 1 ml of distilled water. After 30 min absorbances were measured at 450 nm against reagent blank. Results were expressed in milligram of TE per gram of sample.

HPLC analysis of rutin and other flavonols

Rutin and major flavonols were determined following the method of Capanoglu et al. (2008). Extracts were filtered through a 0.45 μm membrane filter and analyzed using a Waters 2695 HPLC system with a PDA (Waters 2996) detector. A Supelcosil LC-18 (25 cm x 4.60 mm, 5 μm column Sigma-Aldrich, Steinheim, Germany) was used. The mobile phase consisted of solvent A, Milli-Q water with 0.1% (v/v) Trifluoroacetic acid (TFA) and solvent B, acetonitrile with 0.1% (v/v) TFA. A linear gradient was used as follows: At 0 min, 95% solvent A and 5% solvent B; at 45 min, 65% solvent A and 35% solvent B; at 47 min, 25% solvent A and 75% solvent B; and at 54 min returning to initial conditions. The flow rate was 1 ml/min. Detection was done at 360 nm. Identification was based on the retention times and characteristic UV spectra. Quantification was done using external standards (rutin, quercetin-3-O-galactoside, kaempferol) as well as taking the information from the literature into account.

Statistical analysis

All the experiments were replicated three times and the data were represented as mean ± SD. For multiple comparisons, data were subjected to statistical analysis using SPSS software (version 16.0 for Windows, SPSS Inc.) for the analysis of variance (ANOVA). Duncan’s new multiple range test was used to analyze differences between treatments (p<0.05).

RESULTS

Total phenolic content (TPC) and total flavonoid content (TFC)

The TPC of SBT leaves, unprocessed branches (UB) and processed branches (PB) were reported in the range of 25.8±2.9 to 75.9±6.5 mg GAE/g (Table 2). The TPC of leaves from ethanolic extracts (EE) were significantly higher than UB and PB extracts (p<0.05). It was observed that TPC of PB extracts were higher than UB extracts. When considering PB and UB extracts with respect to the differences between aqueous and ethanolic extraction methods, the TPC of aqueous extracts (AE) were substantially higher than ethanolic extracts (Figure 1). This circumstance was interpreted, as decocion was a more efficient extraction technique vis-à-vis ethanolic extraction.

The TPC of SBT leaves, UB and PB were indicated in the range of 21.2±3.8 to 74.0±3.0 mg RE/g. In contrast with TPC results, TFC of all EE was higher than the AE content. The highest level of flavonoids was found in EE of leaves (74.0±3.0 mg/g) followed by UB and PB extracts (p<0.05). But there is no significant difference between EE of UB and PB statistically (p>0.05).
### Table 2. Total phenolic content (TPC), total flavonoid content (TFC), Free radical scavenging activity (DPPH) and Copper reducing antioxidant capacity (CUPRAC) of SBT ethanolic and aqueous extraction.

<table>
<thead>
<tr>
<th>Variables</th>
<th>Sample</th>
<th>Total phenolics (mg GAE/g)</th>
<th>Total flavonoids (mg RE/g)</th>
<th>DPPH (mg TE/g)</th>
<th>CUPRAC (mg TE/g)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Leaf</td>
<td>Ethanolic extraction</td>
<td>75.9 ± 6.5&lt;sup&gt;a&lt;/sup&gt;</td>
<td>74.0 ± 3.0&lt;sup&gt;a&lt;/sup&gt;</td>
<td>89.6 ± 2.0&lt;sup&gt;c&lt;/sup&gt;</td>
<td>538.5 ± 34.8&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td></td>
<td>Aqueous extraction</td>
<td>66.9 ± 5.9&lt;sup&gt;a&lt;/sup&gt;</td>
<td>21.2 ± 3.8&lt;sup&gt;a&lt;/sup&gt;</td>
<td>132.4 ± 6.6&lt;sup&gt;a&lt;/sup&gt;</td>
<td>293.5 ± 26.7&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Processed</td>
<td>Ethanolic extraction</td>
<td>43.1 ± 5.7&lt;sup&gt;c&lt;/sup&gt;</td>
<td>59.4 ± 6.8&lt;sup&gt;b&lt;/sup&gt;</td>
<td>83.3 ± 9.8&lt;sup&gt;c&lt;/sup&gt;</td>
<td>291.3 ± 17.2&lt;sup&gt;b&lt;/sup&gt;</td>
</tr>
<tr>
<td>Branch</td>
<td>Aqueous extraction</td>
<td>53.8 ± 8.9&lt;sup&gt;b&lt;/sup&gt;</td>
<td>45.2 ± 0.6&lt;sup&gt;c&lt;/sup&gt;</td>
<td>113.1 ± 6.1&lt;sup&gt;b&lt;/sup&gt;</td>
<td>235.5 ± 34.1&lt;sup&gt;c&lt;/sup&gt;</td>
</tr>
<tr>
<td>Unprocessed</td>
<td>Ethanolic extraction</td>
<td>25.8 ± 2.9&lt;sup&gt;d&lt;/sup&gt;</td>
<td>64.6 ± 4.5&lt;sup&gt;b&lt;/sup&gt;</td>
<td>41.9 ± 3.6&lt;sup&gt;d&lt;/sup&gt;</td>
<td>129.4 ± 18.1&lt;sup&gt;e&lt;/sup&gt;</td>
</tr>
<tr>
<td>Branch</td>
<td>Aqueous extraction</td>
<td>43.2 ± 3.6&lt;sup&gt;e&lt;/sup&gt;</td>
<td>30.5 ± 3.4&lt;sup&gt;d&lt;/sup&gt;</td>
<td>71.1 ± 7.9&lt;sup&gt;d&lt;/sup&gt;</td>
<td>181.7 ± 27.6&lt;sup&gt;d&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

*Data represent average values ± standard deviation of three independent samples. Different letters in the columns represent statistically significant differences (p < 0.05).

---

A. **Ethanolic Extraction**

B. **Aqueous Extraction**

*Figure 1. Total phenolic content (TPC), total flavonoid content (TFC), free radical scavenging activity (DPPH) and copper reducing antioxidant capacity (CUPRAC) of both ethanolic (A) and aqueous (B) extracts.*
Table 3. Flavonol profile of ethanolic and aqueous extracts of SBT.

<table>
<thead>
<tr>
<th>Compound (µg/g)</th>
<th>Leaf</th>
<th>Processed branch</th>
<th>Unprocessed branch</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ethanolic</td>
<td>Aqueous extraction</td>
<td>Ethanolic</td>
</tr>
<tr>
<td>Rutin</td>
<td>8377 ± 96a</td>
<td>6939± 46b</td>
<td>1229 ± 98d</td>
</tr>
<tr>
<td>Quercetin-3-O-galactoside</td>
<td>703 ± 13a</td>
<td>586 ± 37b</td>
<td>164 ± 23d</td>
</tr>
<tr>
<td>Kaempferol</td>
<td>129 ± 2a</td>
<td>65 ± 1b</td>
<td>Nd*</td>
</tr>
</tbody>
</table>

*Data represent average quantities ± standard deviation (determined by HPLC) of three independent samples. Different letters in the rows represent statistically significant differences (p < 0.05). **Nd: not detected.

Antioxidant activity

To investigate the antioxidant activities of SBT leaves UB and PB two different in vitro assays including 1,1-diphenyl-2-picrylhydrazyl (DPPH) and Copper Reducing Antioxidant Capacity (CUPRAC) were used. The DPPH scavenging activity of extracts ranged from 41.9 ± 3.6 and 132.4 ± 6.6 mg TE/g. EE of leaf (89.6±2.1 mg TE/g) had significantly higher antioxidant properties than PB (83.3±9.8 mg TE/g) and UB (41.9±3.6 mg TE/g). But statistically there is no significant difference between EE of leaves and PB (p>0.05). This correlation was also valid for AE. When compared to extraction methods, higher scavenging activity was observed in AE of leaves, UB and PB (Figure 1). The CUPRAC values of extracts ranged from 129.4±18.1 to 538.5±34.8 mg TE/g. Higher antioxidant capacity was observed in EE of leaf, PB and AE of UB.

HPLC analysis

The results as shown in Table 3 indicated that the extracts are rich in rutin, Quercetin-3-O-galactoside and kaempferol.

DISCUSSION

In the present study, relatively higher phenolic compounds were observed from EE in comparison to AE of SBT leaves (Figure 1). These results were in accordance with previous studies (Upadhyay et al., 2010; Yogendra Kumar et al., 2013). Leaves were found to contain maximum TPC followed by processed branches and unprocessed branches.

In a study performed by Michel et al. (2012), different SBT extracts were evaluated for their antioxidant activity. The DPPH scavenging activity of extracts ranged from 174.8 and 528.6 mg TE/g.

In another study, Yogendra Kumar et al. (2011), evaluated antioxidant activity of the leaf extracts of SBT using DPPH and FRAP assays. The trolox equivalent antioxidant capacity (TEAC) values reported for the extracts by using FRAP assay were in the range of 2.03 to 182.13 mg/g, while the values for the DPPH assay were 6.97 to 282.75 mg/g. In addition, according to the researchers the higher antioxidant activity exhibited by the sub critical water extracts (SWE) over the other Soxhlet and decoction extraction methods clearly demonstrated the relative advantage of SWE for obtaining formulations with high antioxidant compounds.

The profile of lipophilic antioxidants (LA) was also studied in SBT leaves, harvested in summer (June) and autumn (October) from plants of both sexes (female and male) by Górnas et al. (2014). According to this study, results indicated a greater significance of plant sex rather than harvest time; however, autumn samples of both plant sexes had a slightly higher antioxidant activity than summer samples. But an opposite phenomenon was observed in the case of isolated LA fraction from SBT leaves extracts. The higher antioxidant activity of the isolated LA fraction from 80% ethanol extracts of SBT harvested in autumn, compared with the summer samples, were explained by an increase in the content of lipophilic compounds during leaf development in plants of both sexes.

According to the results, there are differences between DPPH and CUPRAC assays; higher values were obtained by the CUPRAC method. This might be related with the diversity of the reaction conditions including the required reaction time, and the wavelength at which the measurements are performed (Antolovich et al., 2002; Capanoglu et al., 2010). It is known from the literature that the chromogens of CUPRAC method have a good solubility in solvent systems (both aqueous and organic) (Apak et al., 2007), which can be the reason of high TE values. The differences are basically as a result of the non-standardized assay techniques with different radicals that is generated, time of reaction or mechanism. Especially, with regard to the antioxidant capacity tests, it will be beneficial to apply different test procedures for a full evaluation of antioxidant activity (Antolovich et al., 2002; Capanoglu et al., 2010). Moreover, in order to investigate these metabolites in detail it is recommended to use more comprehensive methods such as LC-MS.
Several authors have determined the profile of major phenolic compounds of SBT (Zu et al., 2006; Arimboor et al., 2008; Upadhyay et al., 2010; Arimboor and Arumughan, 2012; Pop et al., 2013, etc). In these studies, compounds belonging to groups of phenolic acids, flavonol, and flavone were identified. In the group of phenolic acids, gallic acid (GA) was the dominant phenolic acid for SBT leaves. Bittova et al. (2014) monitored the HPLC profiles of polyphenolic compounds in different SBT plant parts during annual growth cycle and estimation of their antioxidant potential. Their results showed that catechin, epicatechin and gallic acid were the most abundant analytes in annual green shoots and leaves, and their content varied significantly during the studied period. Besides, according to the result of Pop et al. (2013) leaves had higher levels of flavonol glycosides than berries, at average 1118 mg/100 g dry weight. On the other hand, isorhamnetin were the predominant flavonoid for berries, but rutin, quercetin-3-glucoside and kaempferol were found to be predominant in leaves.

This study also focused on the analysis of flavonols, particularly rutin, from sea buckthorn leaves and branches. In the literature, there is limited information on the content of rutin in SBT. According to our results, rutin content changed between 418 ± 108 and 8377 ± 96 µg/g. Rutin content is critical since it was reported to have positive health effects against several types of liver diseases and it has great therapeutic importance. It also causes an increase in pancreatic lipase with consequent reduction in triacylglyceride levels in rats. It has also been described in events associated with the immune system, as seen with other flavonoids (Marcarini et al., 2011). The highest rutin amounts were determined in EE of leaf (8377 ± 96 µg/g). Both EE and AE of leaf had significantly higher rutin content compared to processed branches and branches. On the other hand rutin content of all samples were significantly different (p<0.005).

The quercetin-3-O-galactoside amounts of SBT leaves, processed branches and branches were reported between the range of 85 ± 31 and 703 ± 13 µg/g. The highest quercetin-3-O-galactoside amounts were determined in EE of leaf too (703 ± 13 µg/g). But there is no significant difference between EE of UB and PB (p>0.005). But kaempferol was only observed in EE (129 ± 2 µg/g) and AE (65 ± 1 µg/g) leaf extracts.

HPLC results indicated that parallel to the spectrophotometric analysis results, infusion resulted with lower flavonol content. Ethanolic extraction presented the highest concentration of flavonoids except processed branches. Martins et al. (2014), evaluated and compared the antioxidant and antibacterial activities, and phenolic compounds of the infusion, decoction and hydroalcoholic extract of oregano. According to their results, both preparations, mostly decoction, gave higher antioxidant activity than the hydroalcoholic extract. The antioxidant properties seem to be related to phenolic compounds, mainly flavonoids, since decoction presented the highest concentration of flavonoids and total phenolic compounds, followed by infusion and hydroalcoholic extract, respectively.

Conclusion

According to the results of the current study, leaves, UB and PB of SBT acquire high amounts of phenolics, flavonoids and also present some degree of antioxidant activities. Taking the high antioxidant and rutin content of leaves into account and with respect to their positive health effects, consumption of SBT in forms of an herbal tea should be investigated. Wide variations in the flavonoid profile and antioxidant activity of samples were observed which is probably related with the effect of type and variety of leaves and branches and other related factors as well as processing conditions including temperature, relative humidity, etc. Further studies should be performed in order to establish bioactive properties in vivo and in vitro.

Conflict of Interests

The authors have not declared any conflict of interests.

ACKNOWLEDGEMENTS

This study was financially supported by Istanbul University, Scientific Research Project (BAP) Unit, Project no. 35978.45891 and Ministry of Science, Industry and Technology, Techno-initiative Project no. 0239.TGDS.2013.

REFERENCES

Bittova M, Krejzová E, Roblová V, Kubaň P, Kubaň V (2014). Monitoring...


African Journal of Biotechnology

Related Journals Published by Academic Journals

Biotechnology and Molecular Biology Reviews
African Journal of Food Science
African Journal of Plant Science
Journal of Bioinformatics and Sequence Analysis
International Journal of Biodiversity and Conservation