

BIOLOGICAL NITROGEN FIXATION

James Kahindi

United States International University, Nairobi, Kenya

Nancy Karanja

Regional Coordinator Sub Saharan Africa, Urban Harvest-CGIAR System-wide Initiative on Urban and Peri-urban Agriculture, Nairobi, Kenya

Mamadou Gueye

ISRA-MICEN/Laboratoire Commun de Microbiologie (LCM) IRD-ISRA-UCAD, Dakar, Senegal

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Summary

Biological Nitrogen Fixation estimate the amount of fixed nitrogen and to select the most effective rhizobial strain x plant genotype combination. The ¹⁵N techniques are currently the most accurate method to measure the nitrogen fixed in a given system. The elite strains will be then used for the inoculum production.

However, whatever the elite strains are, the quality control of the inoculum must be performed before any use to maximize the BNF process

1. Introduction

Nitrogen is an essential element for plant growth and development and a key issue of agriculture. Most studies indicate that nitrogen fertilizers contribute to resolving the challenge the world is facing, feeding the human population. The Green Revolution was accompanied by an enormous increase in the application of nitrogen fertilizer. There is however a high heterogeneity of its distribution throughout the world: some areas subjected to pollution whereas others to depleted soil, decreased crop production, and other consequences of inadequate supply.

Biological Nitrogen Fixation (BNF) is known to be a key to sustain agriculture and to reduce soil fertility decline. Research on microorganisms and plants able to fix nitrogen contributes largely to the production of biofertilizers. Thus it is important to ensure that BNF research and development will take into account the needs of farmers in the developing countries mainly.

UNESCO has already addressed this challenge through the Microbial Resources Centre (MIRCEN) initiative. Two BNF MIRCENs were thus established in East (Kenya) and West (Senegal) Africa and focused on the diffusion of rhizobium technology including isolation, identification, collection, maintenance and distribution of rhizobial cultures and inoculants for leguminous crops. Considerable experience in the network approach has been gained through these MIRCENs, which functioned as the bases of projects in BNF technology for East and West Africa.

Below are described briefly some key issues of life supporting system related to basics and applied BNF technology emphasized to rhizobial bacteria (Table 1).

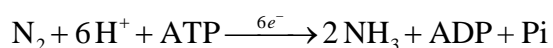
<i>Genres</i>	<i>Espèces</i>	<i>Plantes hôtes</i>	<i>Références</i>
	R. leguminosarum		Jordan, 1984
	biovar viciae	<i>Pisum, vicia, Lathyrus, Lens</i>	Jordan, 1984
	biovar trifolii	Trifolium	Jordan, 1984
	biovar phaseoli	Phaseolus vulgaris L.	Jordan, 1984
Rhizobium	R. galegae	Galega orientalis	Lindström et al, 1989
(croissance rapide)	R. tropici	P. vulgaris L., Leucaena	Martinez-Romero et al, 1991
	R. etli	Phaseolus vulgaris	Segovia et al, 1993
	R. hainanensis	Lég. des régions arides et salées	Chen et al.,1994a;Chen et al.,1997

	R. gallicum	Phaseolus vulgaris L.	Amarger et al., 1997 *
	R. giardinii	Phaseolus vulgaris L.	Amarger et al., 1997 *
	R. mongolense	Medicago ruthenica	Van Berkum et al., 1998
	R. huautlense	Sesbania herbaceae	Wang et al., 1998
	M. loti	Lotus	Jarvis et al., 1982
	M. huakuii	Astragalus sinicus	Chen et al., 1991
Mesorhizobium	M. ciceri	Cicer arietinum	Nour et al., 1994
(croissance	M. hainanensis	Sev. arid reg. pl. sp.	Chen et al., 1994
Intermédiaire)	M. tianshanense	13 tropical pl. sp.	Chen et al., 1995
	M. mediterraneum	Cicer arietinum	Nour et al., 1995
	M. plurifarium	Acacia, Prosopis, Leucaena, Chamaescrista	de Lajudie et al., 1994
	M. amorphae	Amorpha fruticosa	Wang et al., 1999
	S. meliloti (a, b)	Medicago, Melilotus,	Jordan, 1984 ; Eardly et al., 1990
		Trigonella	de Lajudie et al., 1994
Sinorhizobium	S. medicae	Medicago	Rome et al., 1996
(croissance	S. fredii	Glycine max, G. soja	Chen et al., 1988 ; de Lajudie et al., 1994
rapide)			
	S. saheli	Sesbania sp.	de Lajudie et al., 1994
	S. terangaie		
	biovar acaciae	Acacia	de Lajudie et al., 1994; Lortet et al., 1996
	biovar sesbania,	Sesbania,	de Lajudie et al., 1994; Lortet et al., 1996
	S. xinjiangense	Glycine max, G	Chen et al., 1988 ; de Lajudie et al., 1994
	S. kostiense	Acacia, Prosopis	Nick et al., 1999
	S. arboris	Acacia, Prosopis	Nick et al., 1999
Allorhizobium	undicola	Neptunia natans	de Lajudie et al., 1998
(croissance			
rapide)			
Azorhizobium	A. caulinodans	Sesbania rostrata	Dreyfus et al., 1988
(croissance	A. sp.	Sesbania rostrata	Rinaudo et al., 1991
rapide)			
	B. japonicum	Glycine max, G. soja	Jordan, 1982
Bradyrhizobium	B. sp.	Vigna, Lupinus, Mimosa, Acacia,	Jordan, 1982 ; Dupuy, 1994
(croissance lente)		Aeschynomene	Alazard, 1985 ; Young, 1991
	B. elkanii	Glycine max	Kuykendall et al., 1992
	B. liaoningensis	Glycine max, G. soja	Xu et al., 1995

Table 1: Taxonomic evolution of nitrogen fixing bacteria of the family of *Rhizobiaceae* [from Yattara 2000]

2. Nodulation: From the Infection Process to the Functioning of the Nitrogenase

The production of nitrogen fertilizer by industrial fixation generates large quantities of carbon dioxide, contributing to earth warming. The natural process of BNF offers an economic means of reducing environmental problems and improving the internal resources. It is a process that allows microorganisms to convert atmospheric nitrogen (N_2) to ammonia (NH_3) assimilable by associated plants.



Different types of associations are listed in Table 2.

Types of association	Microorganisms	Host plants
Symbiotic	Bacteria (ex. <i>Rhizobium</i>) ^a Actinomycetes (ex. <i>Frankia</i>) Cyanobacteria (ex. <i>Anabaena azollaea</i>)	Legumes Actinorhiza Fern
Non symbiotic	Bacteria (ex. <i>Azotobacter</i> , <i>Azospirillum</i>)	Cereals
Free living systems	Bacteria (ex. <i>Thiobacillus</i> , <i>Clostridium</i>)	

Table 2. Different types of nitrogen fixing systems ^a : *Rhizobium*-leguminous plants is the most studied symbiotic association. There are six main genus of rhizobia : *Allorhizobium* (fast growing), *Azorhizobium* (fast growing) *Bradyrhizobium* (slow growing), *Mesorhizobium* (intermediate growing), *Rhizobium* (fast growing), *Sinorhizobium* (fast growing).

2.1. Nodule Formation

Leguminous plants and rhizobia communicate through the gene expression by reciprocally transmitting signals for the activation of the symbiotic genes in two partners. A type of phenolic called flavonoids, are released by host roots plants into the rhizosphere. Flavonoids act as a chemo-attractant for the bacteria to the plant roots, and eventually colonies of rhizobia attach to the root hairs. Flavonoid signal activates expression of nodulation (nod) genes.

In the rhizobial strains there are numerous nodulation genes including the nod genes nodABC and nodD (Figure 1). On the surface of the rhizobial bacteria the flavonoids are recognized by a expressed nodD protein. Then nodD binds to a promoter DNA sequence, and thereby activates transcription of nod genes of the operons. A group of nod genes encode enzymes synthesise the rhizobial nodulation signal, Nod factor (Figure 2), which triggers development of the root nodules by the plant. The plant roots

recognise Nod factor, through binding to a surface protein receptor at the sub apical root tip. Perception of Nod factor induces a development inside the root, producing pronounced curling of the root hairs entrapping the rhizobia which establish infection of root. Bacteria gain access to plants cell membrane. The plasma membrane invaginates to form novel infection structure known as the infection thread, a tubular structure that extends from the root hair tip to the lower cells of the root cortex.

Rhizobia enter the infection threads in which they actively multiply. At the same time the underlying root cortex cells are quickly proliferated to constitute the nodule primordia. The infection threads branch out into cells of the nodule primordia. The rhizobia are finally released into the nodule cell and enveloped in a membrane derived from the host cell plasma membrane. At this stage, rhizobial bacteria become bacteroids able to fix nitrogen.

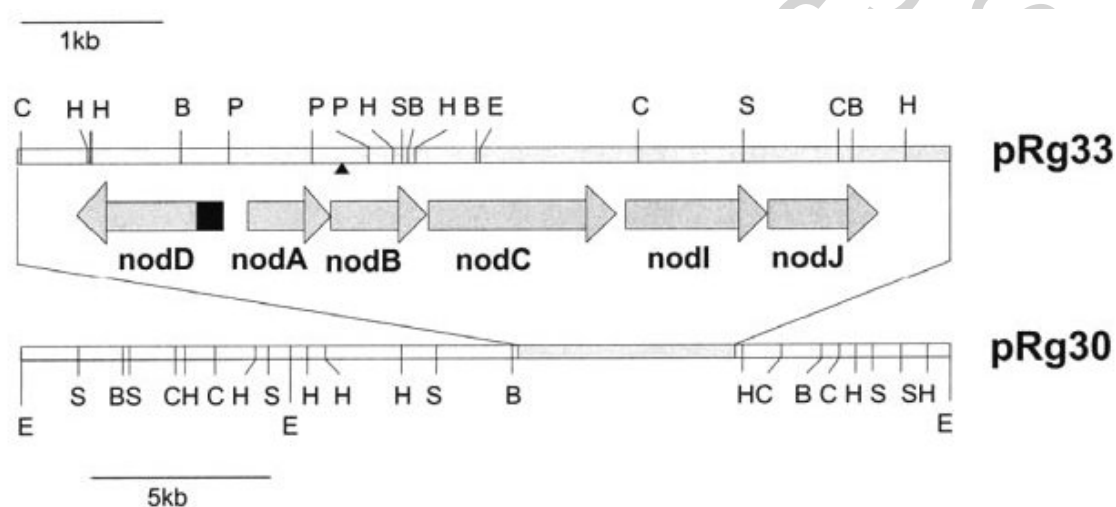


Figure 1. Restriction map of the common *nod* gene region of *Rhizobium galegae* HAMBI 1174. The cosmid clone pRg30 carries the six open reading frames homologous to *nodDABCIJ* genes subcloned in pRg33. ▲ indicates the site of the Tn5 insertion in pRg33. The black square indicates the *nod*-box sequence. Restriction enzymes used were as follows:

E = *EcoRI*; B = *BamHI*; C = *ClaI*; H = *HindIII*; P = *PstI*; S = *SalI*.

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Biographical Sketches

Mamadou Gueye was born in 1950 in Dakar, Senegal, studied microbiology at the University of Lyon, France [1975-1982]. He studied for his doctorate at University of Lyon [1979-1982] on microbial ecology. After receiving his doctorate, he worked in the scope of biological nitrogen fixation (BNF) and

took up an appointment with Institut de Recherché pour le Développement (IRD, formerly ORSTOM) in Dakar [1979 – 1983] and Institut Senegalais de Recherches Agricoles (ISRA) in Senegal in 1983 for building up the West Africa MIRCEN. He participated and conducted numerous BNF training courses in Africa. His research area was BNF technology [*Rhizobium* inoculum production and quality control] and management of fixed nitrogen in cropping systems. He has participated as author or coauthor in numerous scientific publications in international journals. He also is member of editorial board of national and international journals. He is a member of various scientific companies, the Senegalese National Academy of Sciences and Technology (ANSTS) mainly since June 2003.

Nancy Karanja is an Associate Professor, Department of Land Resources Management and Agricultural Technology (LARMAT), University of Nairobi, and a Consultant Urban Harvest Program the International of Potato Centre (CIP) Nairobi. She is also the Director of Microbiological Resources Center (MIRCEN), Nairobi. She obtained her B.Sc. (Agriculture) in 1977 and her M.Sc. (Soil Science) in 1980, both from the University of Nairobi; and her Ph.D. (Soil Science) in 1988 from Department of Soil Science, Reading University, United Kingdom. She has worked as a Principal Research Officer in the Department of Forest Soils, Kenya Forestry Research Institute (KEFRI) from 1990–93 and as a Senior Research Scientist in the Department of Soil and Water of Kenya Agricultural Research Institute (KARI) from 1979–90. Her research interests include: biological nitrogen fixation systems and their applications on farms; integrated nutrient management in particular organic matter dynamics; and soil biodiversity and the management of organic materials including solid waste (household garbage from the urban centers) for soil fertility maintenance.

James H.P. Kahindi is an Associate Professor of Natural Sciences in the School of Arts and Sciences , United States International University-Africa, and a researcher in the Nairobi Microbiological Resources Centre, University of Nairobi. He obtained his B.Sc. (Botany and Zoology) in 1984 and M.Sc.(Botany) in 1987 from the University of Nairobi; and his Ph.D in Microbiology from the Nitrogen Fixation Laboratory, University of Sussex, U.K. His research interests include; the biochemistry and physiology of associative nitrogen fixing systems e.g. *Azotobacter chroococcum* and *Acetobacter diazotrophicus*. He is currently undertaking research in the following areas: the characterization and biodiversity of indigenous strains of Bradyrhizobium-nodulating soyabean in Nitisols; the nitrogen fixation potential of *Acacia drepanolobium*; the development of biopesticides e.g. *Bacillus thuringiensis* for use in plant pest and disease control; and agricultural biodiversity and land use patterns with special emphasis on below ground biodiversity.