

(²II) is a pair of vertical transitions, one to the ground state of NH (³Σ⁻) and the other to the excited singlet state, ¹Δ. The extended Franck–Condon contour in our photodetachment spectra with excitation of ring-breathing modes implies that the ground state of the C₆H₅N⁻ ion is \tilde{X}^2B_2 and that much of the charge is delocalized from the N atom onto the phenyl ring. This contrasts with the \tilde{A}^2B_1 ion which localizes the extra electron in the b₂ nonbonding orbital, on the N atom. Preliminary UHF calculations¹⁰ on both states of the C₆H₅N⁻ ion in a 6-311++G** basis lead to the ²B₂ state being stabilized by about 10 kcal/mol below the ²B₁ state. Figure 3 is a symbolic drawing which contrasts the electronic states of NH with those of C₆H₅N.

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Registry No. C₆H₅N₃, 622-37-7; C₆D₅N₃, 85770-99-6; C₆H₅N⁻, 74586-02-0; C₆D₅N⁻, 143332-33-6; C₆H₅N, 2655-25-6; C₆D₅N, 143332-34-7.

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Total Synthesis of the NodRm-IV Factors, the Rhizobium Nodulation Signals

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NodRm-IV (S) (1) and NodRm-IV (Ac,S) (2) are sulfated lipooligosaccharides of *N*-acetyl-D-glucosamine secreted by the microorganism *Rhizobium meliloti*.^{1–6} These remarkably specific

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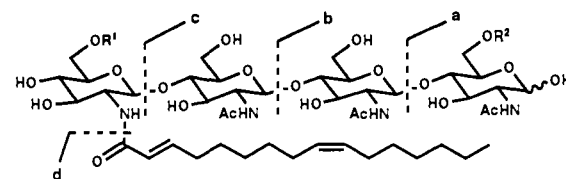
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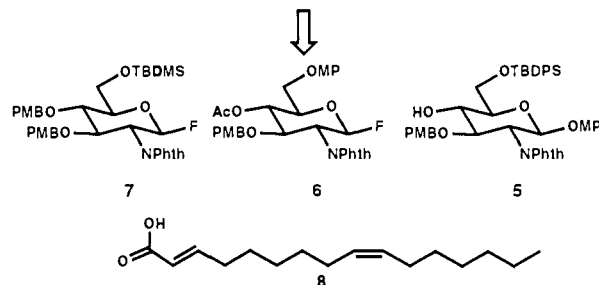
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
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Scheme I. Structures and Retrosynthetic Disconnections of NodRm-IV Factors (1–4)



- 1: NodRm-IV (S); R¹ = H, R² = SO₃⁻
 2: NodRm-IV (Ac,S); R¹ = Ac, R² = SO₃⁻
 3: NodRm-IV (Ac); R¹ = Ac, R² = H
 4: NodRm-IV; R¹ = R² = H



PMB = 4-methoxybenzyl Phth =  TBDMS = *t*-BuMe₂Si
 MP = 4-methoxyphenyl TBDPS = *t*-BuPh₂Si

compounds play a crucial role in the *Rhizobium*–legume symbiosis by eliciting the formation of nitrogen-fixing root nodules and root hair deformation on alfalfa but not on vetch. Interestingly, the non-sulfated compounds NodRm-IV (Ac) (3) and NodRm-IV (4) elicit the same organogenesis and root morphology on vetch but not on alfalfa.^{5,6} Experiments with mutant strains of *R. meliloti* identified the genes responsible for the sulfation of these lipooligosaccharides.⁷ The important actions of these molecules coupled with their fascinating specificity, natural scarcity, and challenging molecular structures prompted us to target them for chemical synthesis. Herein we report the first total synthesis of these substances (1–4) in their naturally occurring forms.

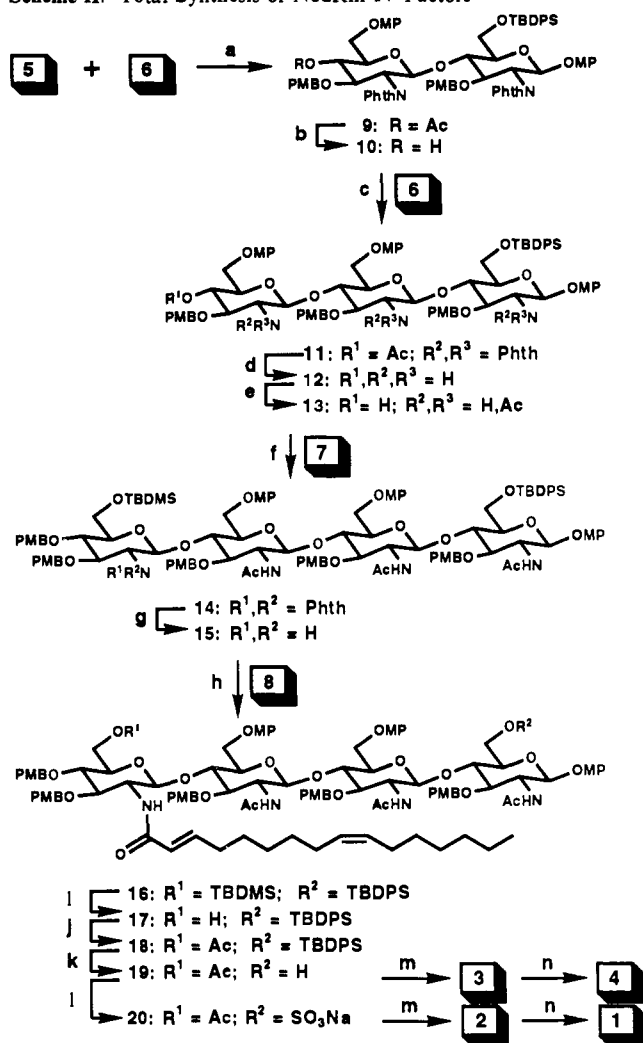
Despite their repetitive nature in glucosamine units, the structures of NodRm-IV factors (1–4) are synthetically quite challenging due to the presence of unsaturation, nitrogen, and sulfur. This variety of functional groups required a carefully designed and executed strategy. Scheme I presents the retrosynthetic analysis on which the synthesis was based. Thus, disconnections at the indicated bonds led to key building blocks 5–8. The projected construction called for an a, b, c, d sequence of coupling reactions and selective deblocking of hydroxyl groups.

Coupling of glucosamine derivative 5 with glycosyl fluoride 6 under the Mukaiyama–Suzuki⁸ conditions led to disaccharide 9 with a β-glycoside linkage as expected from the directing effect of the *N*-phthalimido group (Scheme II). Liberation of the 4'-OH group followed by attachment of a second glucosamine unit 6 as above resulted in the stereospecific formation of trisaccharide 11. Having performed their function as activating and β-directing groups, the phthalimide moieties were removed with hydrazine, leading to the triamine 12, which was acetylated to afford the triacetamide 13. Introduction of the final glucosamine unit was accomplished using derivative 7 and the above mentioned conditions, furnishing tetrasaccharide 14 stereoselectively. Generation of the free amine functionality from 14 as described above allowed the incorporation of the unsaturated fatty acid chain 8 through intermediate 15 and the action of 2-chloro-1-methylpyridinium

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Scheme II. Total Synthesis of NodRm-IV Factors^a

^a Reagents and conditions: (a) 1.0 equiv of **5**, 1.75 equiv of **6**, 5.0 equiv of AgOTf, 5.0 equiv of Cp₂ZrCl₂, 1.0 equiv of 2,6-di-*tert*-butyl-4-methylpyridine, 4-Å molecular sieves, CH₂Cl₂, 0–25 °C, 16 h, 56% (plus 36% recovered **5**); (b) 1.0 equiv of K₂CO₃, MeOH–THF (1:1), 25 °C, 2 h, 90%; (c) 2.0 equiv of **6**, 5.0 equiv of AgOTf, 5.0 equiv of Cp₂HfCl₂, 1.0 equiv of 2,6-di-*tert*-butyl-4-methylpyridine, 4-Å molecular sieves, CH₂Cl₂, 0–25 °C, 16 h, 60% (plus 37% recovered **10**); (d) excess of hydrazine hydrate, EtOH–benzene (20:1), 100 °C, 16 h; (e) excess of Ac₂O, MeOH–CH₂Cl₂ (1:1), 25 °C, 30 min, 72% for two steps; (f) 5.0 equiv of **7**, 5.0 equiv of AgOTf, 5.0 equiv of Cp₂HfCl₂, 0.2 equiv of 2,6-di-*tert*-butyl-4-methylpyridine, 4-Å molecular sieves, CH₂Cl₂, 25 °C, 16 h, 50% (plus 25% recovered **13**); (g) excess of hydrazine hydrate, EtOH, 100 °C, 6 h, 87%; (h) 3.0 equiv of **8**, 3.0 equiv of 2-chloro-1-methylpyridinium iodide, 3.3 equiv of Et₃N, MeCN, 25 °C, 2 h, 73%; (i) 1.3 equiv of pyridinium *p*-toluenesulfonate, EtOH, 25 °C, 16 h; (j) 1.5 equiv of Ac₂O, 1.1 equiv of Et₃N, DMAP (cat.), CH₂Cl₂, 25 °C, 10 min, 72% for two steps; (k) 3.0 equiv of TBAF, THF, 25 °C, 1.5 h, 88%; (l) excess of SO₃·NMe₃, pyridine, 25 °C, 1 h, 85%; (m) 20.0 equiv of ceric ammonium nitrate (CAN), MeCN–H₂O (4:1), 25 °C, 1 h, 30%; (n) excess of NaOMe, MeOH, 25 °C, 3 h, 75%.

iodide.⁹ Selective removal of the *tert*-butyldimethylsilyl group from compound **16** proceeded smoothly on exposure to PPTS¹⁰ to afford **17**. Acetylation of **17** followed by desilylation with ⁿBu₄NF gave compound **19**. Sequential deprotection of **19** with ceric ammonium nitrate (CAN) and NaOMe led to the targeted NodRm-IV (Ac) (**3**)¹¹ and NodRm-IV (**4**), respectively. Al-

ternatively, sulfation of **19** with SO₃·NMe₃ and ion exchange (Na⁺) gave compound **20**. Sequential deprotection of **20** under the above conditions gave NodRm-IV (Ac,S) (**2**)¹¹ and NodRm-IV (S) (**1**). Final products **1–4** were purified by reverse-phase HPLC as described in the supplementary material.

The described chemistry renders these scarce bioactive compounds readily available for further biological studies. Molecular design and structure–activity studies are also now feasible, and so is the isolation of the receptors of these compounds.

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Supplementary Material Available: Schemes for the synthesis of building blocks **5–8**, including reagents, conditions and yields, and listing of selected physical data for compounds **9**, **11**, **14**, **16**, **19**, **20**, **4**, **3**, **2**, and **1** (12 pages). Ordering information is given on any current masthead page.

Kinetic Importance of Conformations of Nicotinamide Adenine Dinucleotide in the Reactions of Dehydrogenase Enzymes

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Suggestions regarding the relationship of cofactor conformation to stereospecificity¹ and to rates² of dehydrogenase enzymes have emerged. Our objectives have been to evaluate the potential energies of ground-state conformations and their influence on reaction trajectories and the structures of transition states. To assess the importance of conformational features, we have employed semiempirical (AM1)³ and molecular dynamics (CHARM_m)⁴ calculations using single-crystal X-ray structures of both nicotinamides and 1,4-dihydronicotinamides⁵ and dehydrogenase enzymes.⁶ The virtual angles X_n, X_{am}, α_C, and α_N define the conformations of interest (Charts I and II).

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