

Biosynthesis and Biological Activity of Carbasugars.

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Abstract: The first synthesis of carbasugars, compounds in which the ring oxygen of a monosaccharide had been replaced by a methylene moiety, was described in 1966 by Prof. G.E. McCasland's group. Seven years later, the first true natural carbasugar (5a-carba-R-D-galactopyranose) was isolated from a fermentation broth of *Streptomyces* sp. MA-4145. In the following decades, the chemistry and biology of carbasugars have been extensively studied. Most of these compounds show interesting biological properties, especially enzymatic inhibitory activities and, in consequence, an important number of analogues have also been prepared in the search for improved biological activities. The aim of this review is to give coverage on the progress made in two important aspects of these compounds: the elucidation of their biosynthesis and the consideration of their biological properties, including the extensively studied carbapyranoses as well as the much less studied carbafulranoses.

1. Introduction.

In addition to their well-known role as chemical units for a) release of energy such as sucrose or glucose, b) energy storage such as starch or c) as responsible for structure and strength such as cellulose, carbohydrates are key elements in a variety of biological processes. In fact, the concept of *glycomics* has been defined as “the functional study of carbohydrates in living organism”. [1] Carbohydrates are key elements in a variety of processes such as signaling, cell-cell communication, and molecular and cellular targeting. Many biological processes involve carbohydrates and, in consequence, the biological implications of carbohydrates are strongly related with many diseases. In this context, it should be pointed out that the synthetic-carbohydrate vaccines show potential advantages over those based on carbohydrates from natural sources. Thus, medicinal chemistry techniques can potentially be used to derivatize and modify synthetic carbohydrates to make vaccines that are more immunogenic than those based on natural carbohydrates. For selected, general and recent reviews on these aspects of carbohydrate chemistry, see: (a) general treatises: references [2-5]; (b) synthetic aspects: references [6-7]; (c) carbohydrates in biological and medicinal chemistry: references [8-11]; (d) glycobiology [12]; (d) signaling, cell-cell communication, and molecular and cellular

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targeting: references [13-18]; (e) therapeutic potential of glycoconjugates: references [19-20]; (f) carbohydrate-based vaccines: references [21-25].

On the other hand, novel carbohydrate structures whose biological functions were not always obvious have been discovered. For instance, intriguing compounds such as sialyl Lewis X (sLex) [26-28] or glycosylphosphatidylinositols (GPIs) are now known to play a pivotal role in numerous biological functions.[29-34] Moreover, carbohydrates constitute a very useful source of enantiomerically pure starting materials. They have been used for the synthesis of a wide range of compounds and have been found to be useful chiral auxiliaries which allowed the introduction of a range of functionalities in a highly enantioselective manner.[35-36]

On this basis, the search for new carbohydrate derivatives with analogous or even improved biological properties compared to those of the parent structures (the *carbohydrate mimetics*) [37-40] appears to be an attractive matter of research. The **carbasugars** (initially, the term *pseudosugars* was coined for this family of compounds, although they are currently known as carbasugars [41]), compounds in which the ring oxygen of a monosaccharide had been replaced by a methylene group (Figure 1), fall within this category [42-46]. The structural resemblance of carbasugars to the parent sugars may facilitate their recognition by enzymes or other biological systems in place of the related *true* sugars. On the other hand, these compounds could be more stable toward endogenous degradative enzymes.

The aim of this review is to give coverage on the progress made in the biosynthesis and biological activity of carbasugars until March 2016, including both carbapyranoses and carbafuranoses.

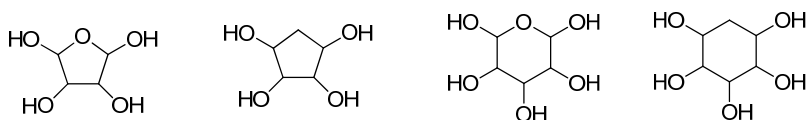


Figure 1. Monosaccharides and Carbamonosaccharides.

2. Natural Occurrence of Carbasugars.

2.1. Natural Carbafuranoses.

Carbafuranoses are scarcely encountered in Nature as free compound. Nevertheless, they are subunits of products isolated from natural sources, in particular carbanucleosides [47-48]. To the best of our knowledge, only two five-membered cyclitol derivatives have been isolated from natural sources (Figure 2): Caryose **1** [49-51], isolated from the lipopolysaccharide fraction of *Pseudomonas caryophylli* (a plant pathogenic bacteria), and calditol **2**, isolated from the thermoacidophilic archaeobacterium *Sulfolobus acidocaldarius*, a thermoacidophilic archaeon belonging to *Sulfolobus* species. These species was found to grow optimally between 75-80° C, with pH optimum in the range of 2-3 [52-55]. The original proposed structure for calditol, an open-chain branched nonitol **3**, was soon questioned by various research groups. To unambiguously clarify this point, four isomeric cyclopentane-based structures were synthesized by Sinaÿ et al. Among them, compound **2** was found to be fully identical to the natural product present in several *Sulfolobus* species [56-57].

2.2. Natural Carbapyranoses

Carbapyranoses have been encountered in Nature rarely being carba- α -D-galactopyranose (4, Figure 3) the only “genuine” carbasugar isolated from natural sources (*Streptomyces* sp) [58].

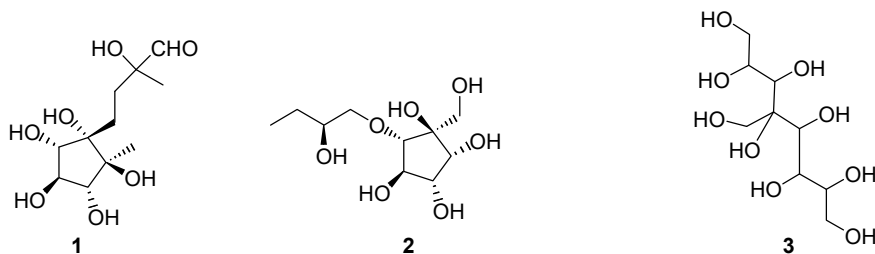


Figure 2. Structure of Caryose **1**, proposed structure of Calditol **3** and structure of Calditol **2**

However they are abundant as subunits of other natural products. On the other hand a large number of highly oxygenated cyclohexane and cyclohexene derivatives, closely related to carbasugars, have been isolated from Nature. Among them, epoxides [59-60] such as cyclophellitol (isolated from *Phellinus* sp)[61-65] (**5**, Figure 3), cyclohexene derivatives such as MK7607 (isolated from *Curvularia eragestrides*) [66], (**6**, Figure 3), streptol (isolated from *Streptomyces* sp) [67-68], (**7**, Figure 3), pericosines A-D (isolated from *Periconia byssoides*) (**8-13**, Figure 4) [69-70], carbonyl compounds such as the gabosine family (isolated from various *Streptomyces* strains) [71-73] (Figure 5, **15-28**), COTC (isolated from *Streptomyces griseosporus*)[74] (Figure 5, **29**) and valienona (isolated from *Strptomyces lincolnensis*) [68] (Figure 5, **30**).

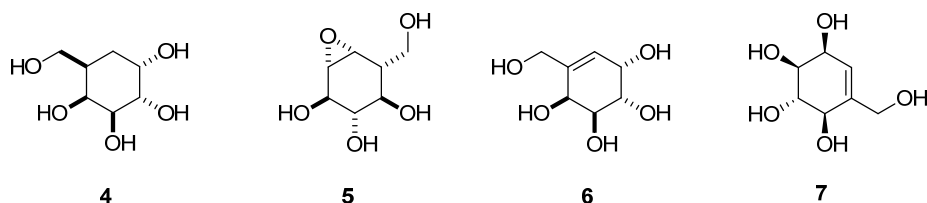


Figure 3. Some natural carbapyranoses: carba- α -D-galactopyranose, cyclophellitol, MK7607 and streptol.

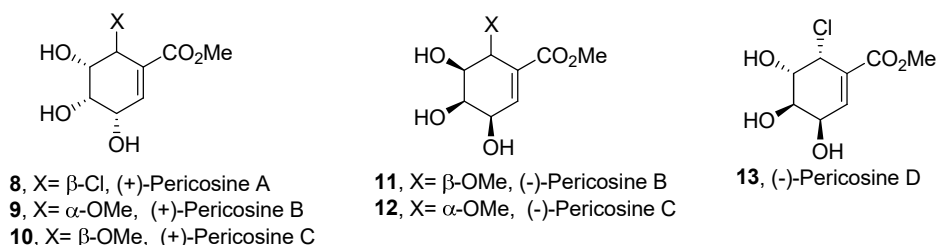


Figure 4. The pericosines.

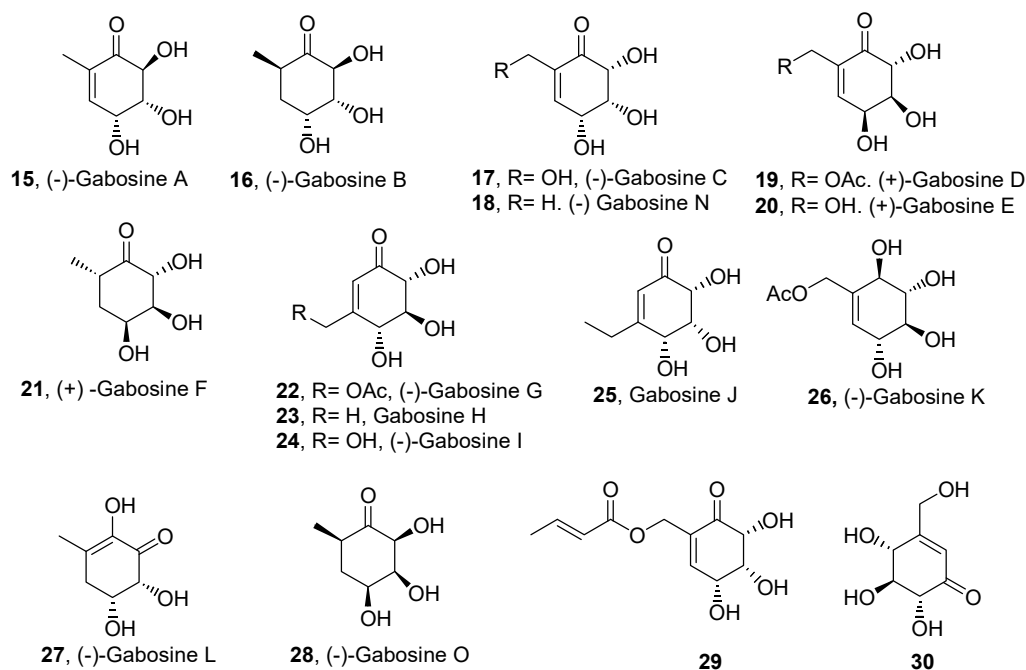


Figure 5. Gabosines, COTC and valienone. The absolute configuration of gabosines H (23) and J (25) remains, to the best of our knowledge, unknown.

Aminocarbasugars, such as valienamine (31) and validamine (32) (natural sources of validamine, include microbial degradation procedures [75-79], chemical degradation of validoxylamine-see below-) using NBS [80-81] and several biotechnological processes [82-84], hydroxyvalidamine [85] (33), and valioline [86-87] (34) (Figure 6), have been mainly found as subunits of more complex molecules (*Vide infra*). These derivatives are secondary metabolites exclusively produced by microorganisms. They have been detected only as minor components in the fermentation broth of *Streptomyces hygroscopicus* subsp. *Limoneus* [87]. Aminocarbasugars are mainly found in validamycins, acarbose, and related carbaoligosaccharides.

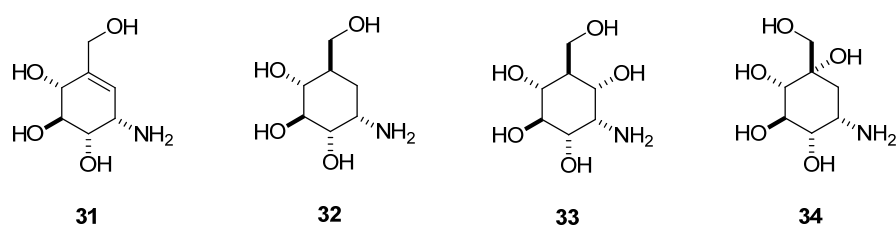


Figure 6. Aminocarbasugars valienamine, validamine, hydroxyvalidamine and valioline.

Validamycins (Figure 7) are a family of antibiotics discovered during the screening for new antibiotics from the fermentation culture of *Streptomyces hygroscopicus*. [88-91] The main component of the complex is Validamycin A (35), a pseudotrissaccharide consisting of a core moiety, validoxylamine A (43), and D-glucopyranose. The core consists of two aminocyclitols, valienamine (31), and validamine (32), which are connected through a single nitrogen atom. Validamycin B (36) differs from validamycin A in the second aminocyclitol unit which, in validamycin B (36), is hydroxyvalidamine (33). The minor components of the validamycins complex, validamycins C-F (37-40)

and validamycin H (**42**), contain validoxylamine A (**43**), as the core unit, but they differ in at least one of the following features: (a) the position of the glucosidic linkage, (b) the number of D-glucopyranose residues, or (c) the anomeric configuration of the D-glucopyranose unit [92-95]. Validamycin G (**41**) contains validoxylamine G (**45**) as its core unit.

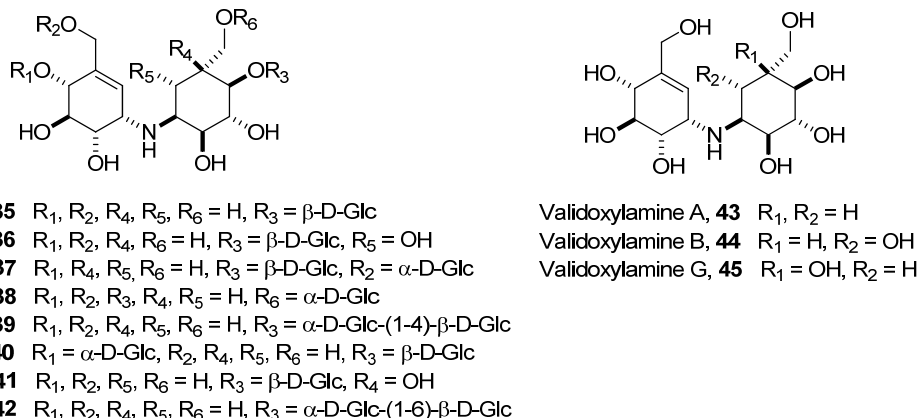


Figure 7. The Validamycins family.

Acarbose (Figure 8, **46**) [96-97] is one of the most clinically important compounds containing carbasugar units, since it is currently used for the treatment of type II insulin-independent diabetes. This disease is a metabolic disorder that is characterized by hyperglycemia in the context of insulin resistance and relative lack of insulin [98-99]. In addition to acarbose, marketed by Bayer, there are two drugs, structurally related with acarbose, which belong to this class of α-glucosidase inhibitors: miglitol **47** –Sanofi- and voglibose **48** –Takeda- (Figure 8). Acarbose is a starch blocker, and inhibits α-amylase, an intestinal enzyme that releases glucose from larger carbohydrates [100-101]. Acarbose is a carbatriasaccharide which was found in a screening of strains of various *Actinomyces* genera and its structure was determined by degradation reactions, derivatization, and spectroscopic analysis. It is composed of valienamine (**31**), a deoxyhexose (4-amino-4,6-dideoxyglucose), and maltose. The carbadisaccharic core of acarbose, known as acarviosine (**49**), is postulated to be essential for its biological activity. The core unit, **49**, is also linked to a variable number of glucose residues, resulting in several other components of the complex mixture of acarbose. The formation of these components is highly dependent on the composition of the carbon source available in the culture medium. Media containing glucose and maltose will result in a specifically high yield of acarbose and the lower components, while media with high concentrations of starch will yield longer oligosaccharide species. The transglycosylation involved in this process was proposed to be catalyzed by an extracellular enzyme, acarviosyl transferase, found in the culture of the acarbose producer [102]. Acarbose has been the subject of interest and excellent reviews have been published, covering various specific aspects on the biochemistry and molecular biology of this compound [103-114].

The amylostatins, with general structure **50** (Figure 9), are related to acarbose analogues due to they contain the acarviosine core **49**. Amylostatins were isolated in the culture filtrate of *Streptomyces diastaticus* subsp. *Amilostaticus* [115-116].

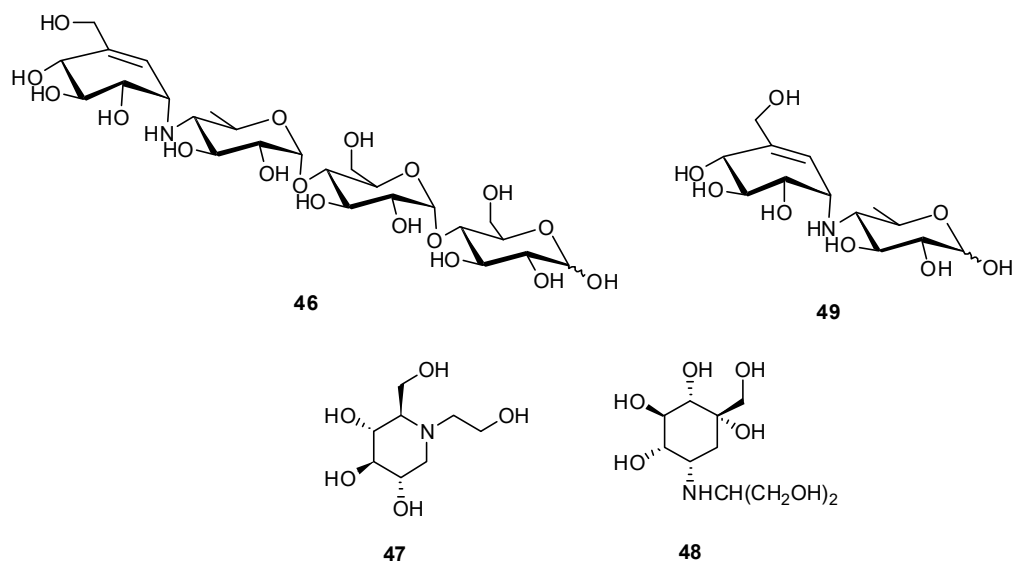


Figure 8. Structures of acarbose, acarviosine and marketed products **47** and **48**.

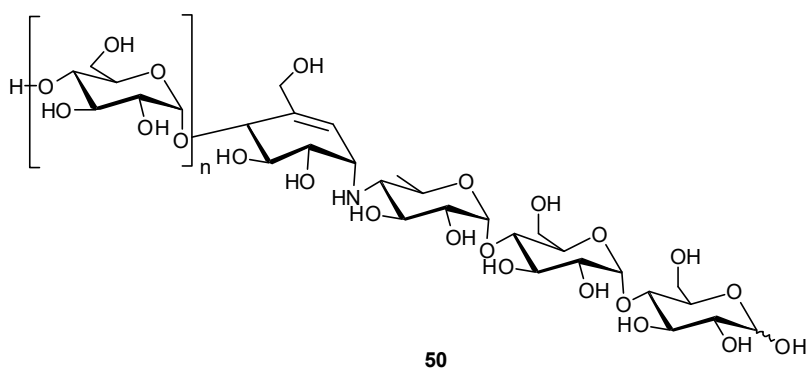


Figure 9. The amylostatins.

Adiposins (**51**, Figure 10) were isolated from *Streptomyces calvus* [117-124]. Structurally, adiposins are related to acarbose (**46**) and amylostatins (**50**). They are formed by an aminocarbasugar (valienamine, **31**) and a deoxy sugar (4-amino-4-deoxyglucose).

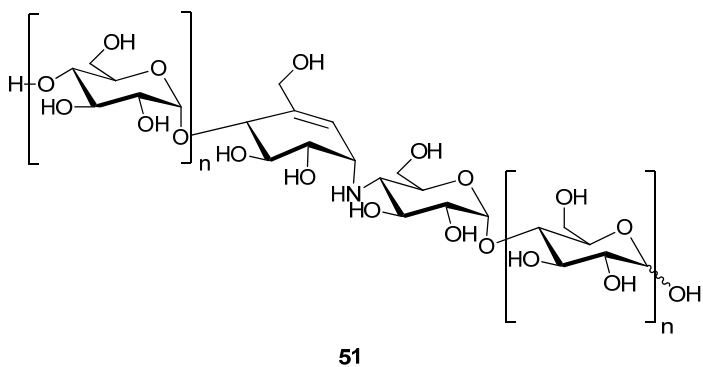


Figure 10. The adiposins.

Oligostatins (**52**, Figure 11) were obtained from culture broths of *Streptomyces myxogenes* [125-129]. They are carbaoligosaccharide antibiotics consisting of penta-, hexa-, and heptasaccharides containing hydroxyvalidamine rather than valienamine.

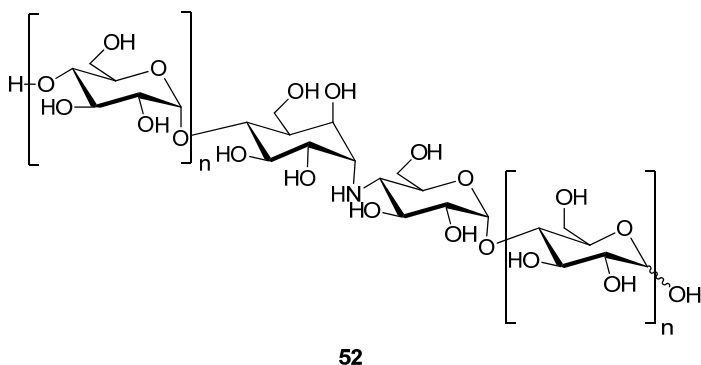


Figure 11. The oligostatins.

Trestatins (**53**, Figure 12) were isolated from fermentation cultures of *Streptomyces dimorphogenes* [130-131]. These carbaoligosaccharides contain one to three dehydro-oligobioamine units and terminate with one residue of α -D-glucopyranose linked 1,1- to the preceding glucose unit. Therefore, unlike the oligostatins **52** and the amylostatins **50**, the trestatins are nonreducing carbohydrates

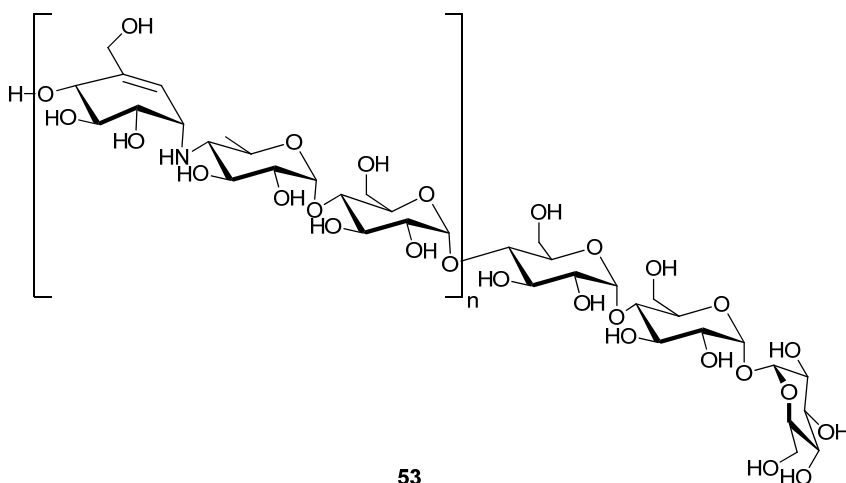


Figure 12. The trestatins.

Trehalase inhibitor salbostatin (**54**, Figure 13) is a metabolite of *Streptomyces albus* species [132-134]. This basic nonreducing carbadisaccharide consisting of valienamine linked to 2-amino-1,5-anhydro-2-deoxyglucitol.

In 1995, the pyralomicins (**55-58**, Figure 14) were isolated from the strain of *Actinomadura spiralis* (which was later renamed *Microtetraspora spiralis*)[135-136]. Their chemical structures consist of benzopyranopyrrole chromophores containing a nitrogen atom which is also shared with 1-epi-valienamine.[137]. Pyralomicins are, thus far, the only examples of natural products having an aminocarbasugar unit, acting as the glycone, attached to a polyketide-derived core structure [138-140].

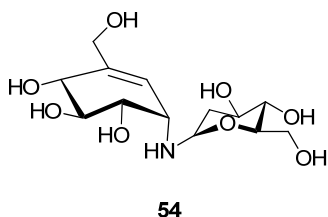
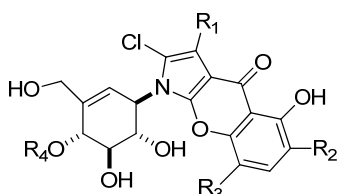


Figure 13. Structure of Salbostatin.



Pyralomicin 1a, **55** R₁ = H, R₂ = Cl, R₃, R₄ = CH₃
 Pyralomicin 1b, **56** R₁ = H, R₂, R₄ = CH₃, R₃ = Cl
 Pyralomicin 1c, **57** R₁, R₄ = H, R₂ = Cl, R₃ = CH₃
 Pyralomicin 1d, **58** R₁, R₂ = Cl, R₃ = CH₃, R₄ = H

Figure 14. The pyralomicins.

3. Biosynthesis of carbasugars.

3.1. Carbafuranoses.

The biosynthesis of carbapentofuranoses has only been considered in the literature, to the best of our knowledge, in the context of the more biologically relevant carbocyclic nucleosides and in the case of the cyclitol calditol **2**.

3.1.1. Carbocyclic nucleosides.

Biosynthetic studies on aristeromycin (**59**) and neplanocin A (**60**) (Figure 15)[141-144] had established that the carbocyclic ribose ring was biosynthesized from D-glucose *via* the enone **61**, the first-formed carbocyclic intermediate. After reduction of the double bond in **61**, the reduction of ketone function of the resulting product **62** in an *anti* fashion and phosphorylation afford the carbocyclic analogue of 5-phosphoribosyl-1-pyrophosphate **63** (Scheme 1). A detailed description of this sequence was described in Reference 42, p. 1923-1924.

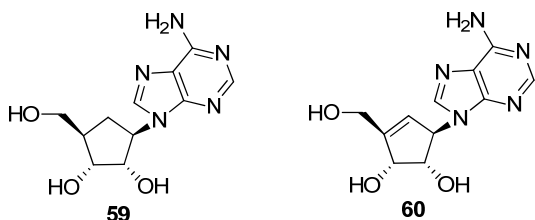
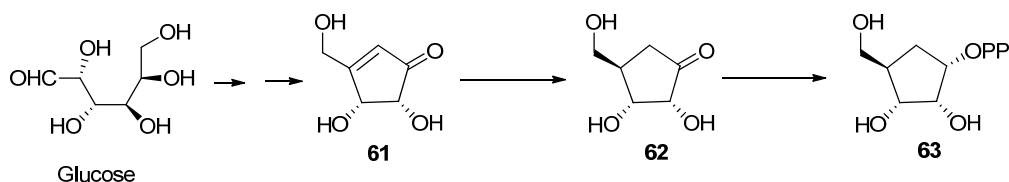


Figure 15. Structures of Aristeromycin **59** and neplanocin **60**.



Scheme 1. Proposed biosynthesis of carbaphosphorybosyl-1-phosphate from glucose.

3.1.2. Biosynthesis of Calditol.

Calditol **2** constitutes the cyclitol moiety of lipids such as **64** (Figure 16) and related compounds which are present in microorganisms belonging to the *Archaea* domain. As shown in Figure 16, the cyclitol fragment is linked to the rest of the molecule by etheral bonding [145].

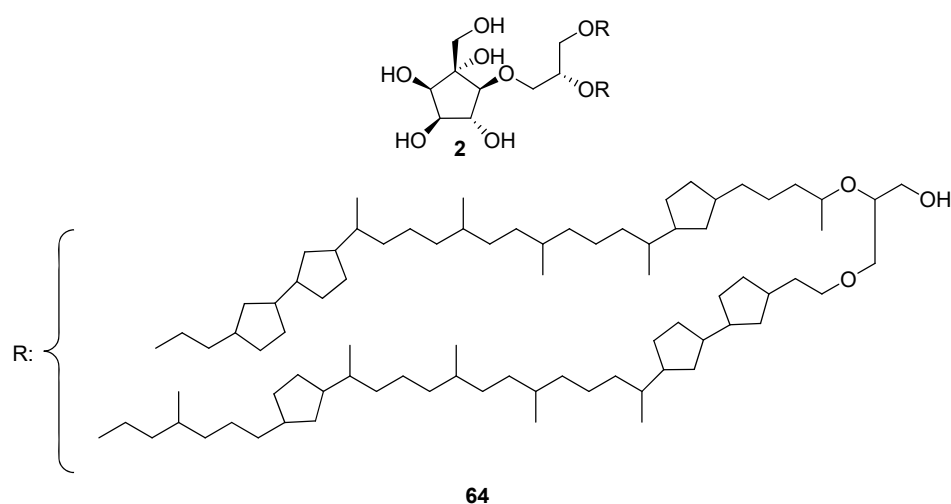


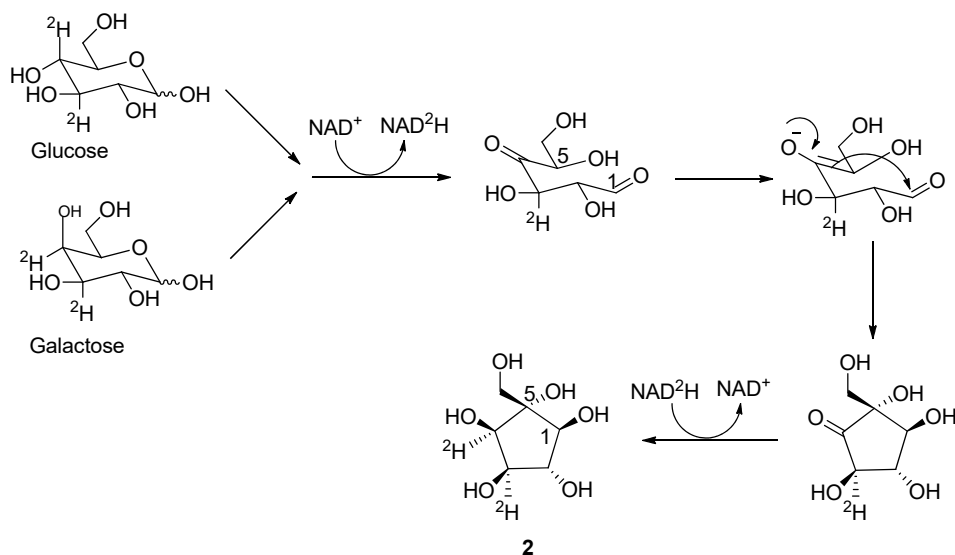
Figure 16. Structure of the lipids isolated from *Archaea*.

From experiments using C-3 and C-4 deuterated glucose and galactose, a biosynthetic ‘inositol like’ pathway for the cyclopentanoid part of calditol has been proposed [146-149]. The sequence involves the formation of a 1,5 carbon bond mediated by a “cyclase” enzyme, followed by a stereospecific reduction at C-4 (Scheme 1). Regarding Caryose **1** no biogenetic proposal has been found in the literature.

3.2. Carbapyranoses.

3.2.1. Sedo-heptulose 7-phosphate.

Sedo-heptulose 7-phosphate (**75**), is a key intermediate in the biosynthetic pathway of valienamine and gabosines A, B, C and H. This compound derives from the pentose phosphate pathway [150-151]. The pentose phosphate pathway is the source of NADPH **68** used in reductive biosynthetic reactions and consists in two phases: the oxidative generation of NADPH (Scheme 3) and the nonoxidative interconversion of sugars (Scheme 4).



Scheme 1. Proposed biosynthesis of Calditol **2**.

In the oxidative phase, NADPH is generated from glucose 6-phosphate **65** and starts with the dehydrogenation **65** at C1 to give 6-phosphoglucono- δ -lactone **67** in a reaction catalyzed by glucose 6-phosphate dehydrogenase and mediated by NADP⁺ (**66**). The next step is the hydrolysis of 6-phosphoglucono- δ -lactone **67** by a specific lactonase (6-phosphogluconolactonase) to give 6-phosphogluconate **69**. This six-carbon sugar is then oxidatively decarboxylated by 6-phosphogluconate dehydrogenase to yield ribulose 5-phosphate **70**. In the non-oxidative phase, ribulose-5-phosphate **70** is transformed into xylulose-5-phosphate **71** and ribose-5-phosphate **72** via epimerization at C-3 and isomerization (through an enolate ion) respectively. Finally, a sequence of retroaldol-aldol reaction mediated by thiamine pyrophosphate **73** results in the formation of sedo-heptulose-5-phosphate **75** and glyceraldehyde-3-phosphate **74**.

3.2.2. Biosynthesis of gabosines.

The cyclization process of sedo-heptulose 7-phosphate (**75**) to a six membered carbocyclic intermediate, 2-epi-5-epi-valiolone **77** [152-155] is catalyzed by a sedoheptulose 7-phosphate cyclase (Scheme 5). These enzymes are phylogenetically related to the dehydroquinase synthases (DHQS) and use Co²⁺ as preferred cofactor. Dehydroquinase synthase (DHQS) is able to perform several consecutive chemical reactions in one active site. There has been considerable debate as to whether DHQS is actively involved in all these steps, or whether several steps occur spontaneously, making DHQS a spectator in its own mechanism. DHQS performs the second step in the shikimate pathway, the transformation of **78** (3-deoxy-D-arabino-heptaluronate-7-phosphate) into **79** (3-dehydroquinase), which is required for the synthesis of aromatic compounds in bacteria, microbial eukaryotes and plants (Scheme 5).[156-157].

The reaction is assumed to be initiated by transient dehydrogenation of C-5 to a ketone **76**, which sets the stage for the elimination of phosphate, followed by reduction of the C-5 ketone and ring-opening to produce the corresponding enolate. The latter then undergoes intramolecular aldol condensation to give 2-epi-5-epi-valiolone **77**. This compound is epimerized at C2 (compound **80**) and dehydrated via a *syn* elimination to

yield valienone **30** (Scheme 6). However, how exactly these final processes take place under the enzymatic point of view remain still obscure.

The transformation of 2-epi-5-epi-valionone **77** into gabosines requires a considerable number of steps such as dehydration, oxidation, reduction and epimerisation as depicted in Scheme 7 for the transformation of 2-epi-5-epi-valiolone **77** into gabosines A, B, C and N through the reduction product **81** (Scheme 7) [158]. It seems possible that the reduction at C-7 and the oxidation at C-1 (gabosines numeration) follow a similar mechanism, as described for the formation of 6-deoxy-4-keto sugars [159-160]. It can expect a considerably high number of specific involved enzymes working in a manner that is really not understood.

In this context a new hypothesis for the biosynthesis of gabosines from **77** has recently been proposed on the basis of an unexpected experimental observation [161]. When compound **82** (Scheme 8) was submitted to a simultaneous oxidation-elimination protocol by reaction with m-CPBA, a separable mixture of the expected α -hydroxymethyl enone **83** (10%) and β -hydroxymethyl enone **84** (68%) was obtained. The formation of **84** may be explained on the basis of a keto-enol equilibrium process followed by sulphide elimination. Considering that a similar keto-enol process had been observed [162] in a previous synthesis of gabosines N and O, a biosynthetic proposal starting from 2-epi-5-epi-valiolone **77** and involving keto-enol equilibrium cascade reactions has been formulated (Scheme 9). This kind of isomerizations has been observed in different biogenetic routes such as the transformation of ribulose-5-phosphate **70** into xilulose-5-phosphate **71** and ribose-5-phosphate **72** (see Scheme 4).

3.2.3. Biosynthesis of Validamycins.

Valienone **30** and they reduction product validone **87** are the more proximate precursor of validoxylamine A **43**, the aglycon moiety of validamycin A **35** (Scheme 10).[171-172] In the transformation of **30** into **87**, the stereochemistry of the reduction probably reflects the result of a nonenzymatic partial epimerization at C-6 of **87** due to enolization of the keto group at C-1.

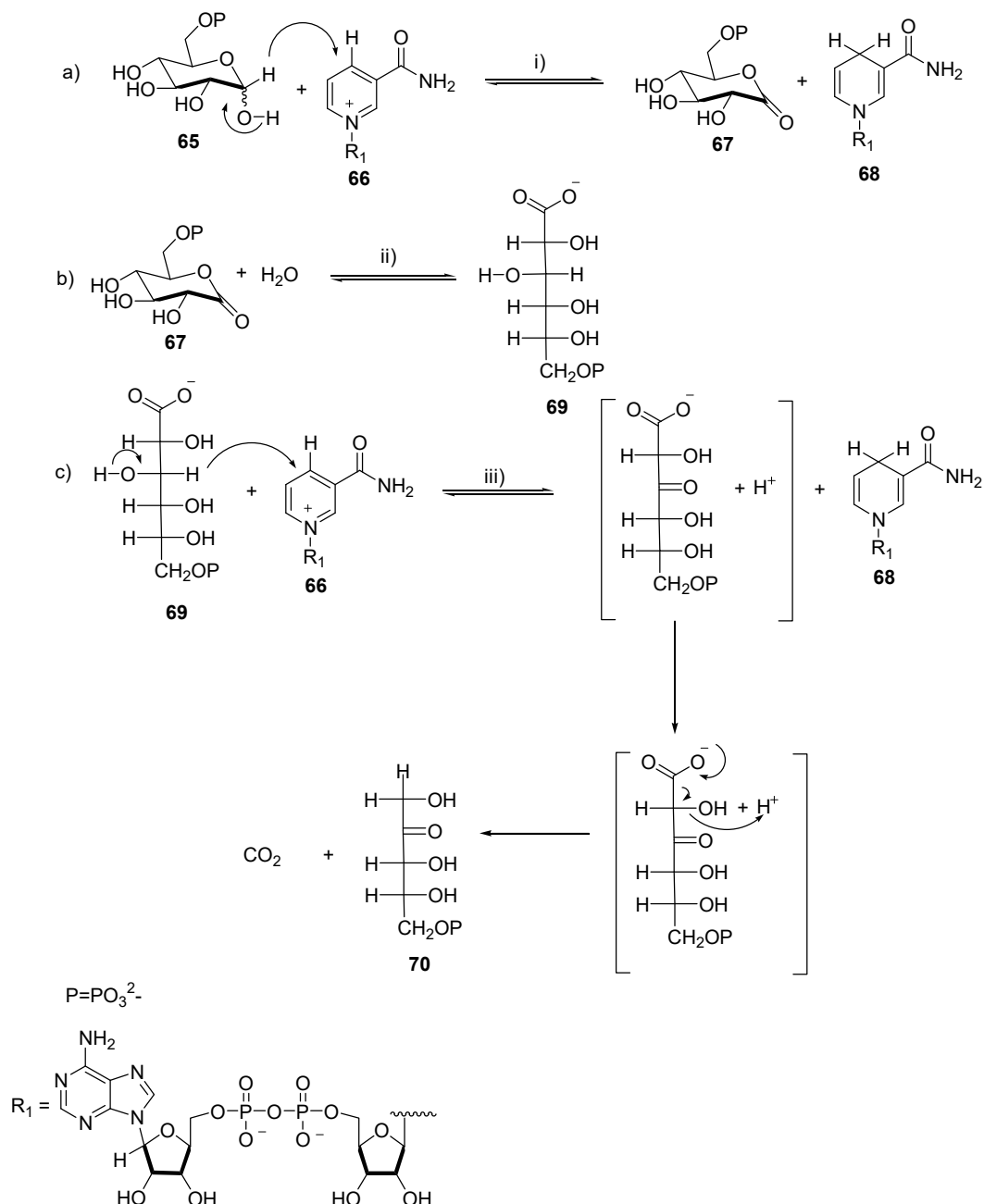
Two alternative possibilities can be envisaged for the formation of validoxylamine **43**, from **30** and **87** (Scheme 10). Either transamination of **30** would give valienamine **31**, which would then reductively couple with **87** or, alternatively, **87** would be transaminated to give validamine **32**, which would then couple with **30**. However, circumstantial evidence in favor of the second of these two scenarios comes from experimental observations using feeding experiments. Finally, incorporation of the glucose moiety should be mediated by a glucosyl transferase enzyme.

On the other hand, studies on *Actinoplanes* sp. have identified glutamate **88**, a typical substrate of transaminases, as the most efficient nitrogen donor. Also aspartate **89** and the α -nitrogens of asparagine **91** and glutamine **90** were also found to be good nitrogen sources in glutamate-depleted cultures [173]. It should be indicated that glutamate, aspartate, glutamine and asparagine are interconnected in typical reactions of the aminoacids metabolism as indicated in Scheme 11.

As we have previously indicated, the validamycin A fermentation also produces a number of minor components. Some of these, such as validamycins C (**37**), D (**38**), E

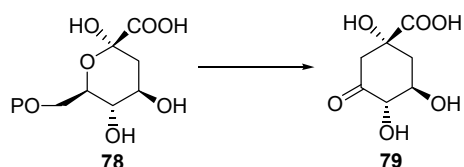
(**39**), and F (**40**), are derived from validamycin A **35**. The formation of the validamycin congeners which differ from **35** in the structure of the second cyclitol moiety would require the transamination of other ketocyclitols, such as 6-hydroxyvalidamine **33** for validamycin B (**36**) and valioline (**34**) for validamycin G (**41**) (Scheme 12).

Oxidative Phase.

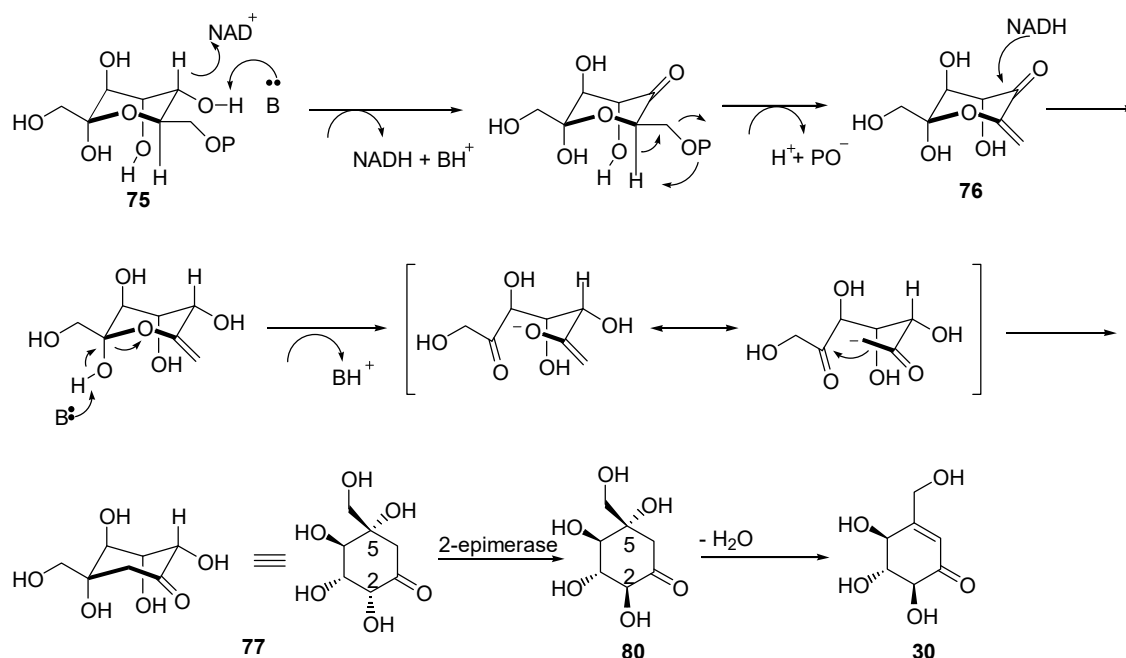


Scheme 3. Oxidative phase. **Legend:** a) *Compounds.* **65**: Glucose-6-phosphate; **66**: NADP⁺; **67**: 6-Phosphoglucono- δ -lactone; **68**: NADPH; **69**: 6-Phosphogluconate; **70**: Ribulose-5-phosphate; b) *Enzymes:* i) Glucose-6-phosphate dehydrogenase [163]; ii) 6-Phosphogluconolactonase [164]; iii) 6-Phosphogluconate dehydrogenase [165].

nucleoside thymidine.[180]. This intermediate is able to transfer the acarviosyl moiety to C6' of maltose. It should be pointed out that acarbose is formed from maltotriose by two routes: (a) 60% of the acarbose is formed by attachment of maltose, produced by removing a glucose exclusively from the nonreducing end of maltotriose, to the pseudodisaccharide core unit. (b) The other 40% of acarbose is formed by direct attachment of maltotriose to the core unit followed by loss of the terminal glucose from the reducing end [181].



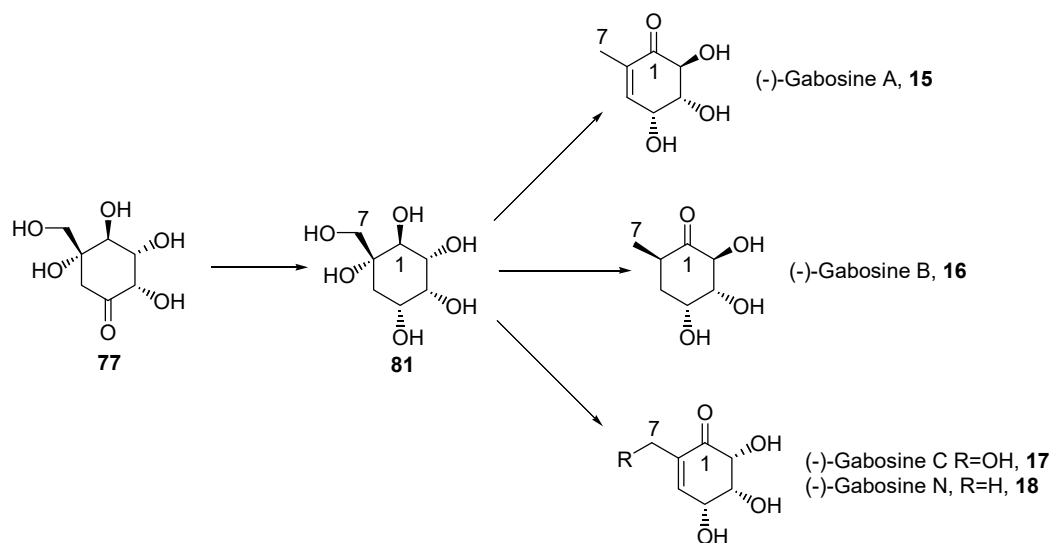
Scheme 5. Transformation of 3-deoxy-D-arabino-heptaluronate-7-phosphate into 3-dehydroquinate.



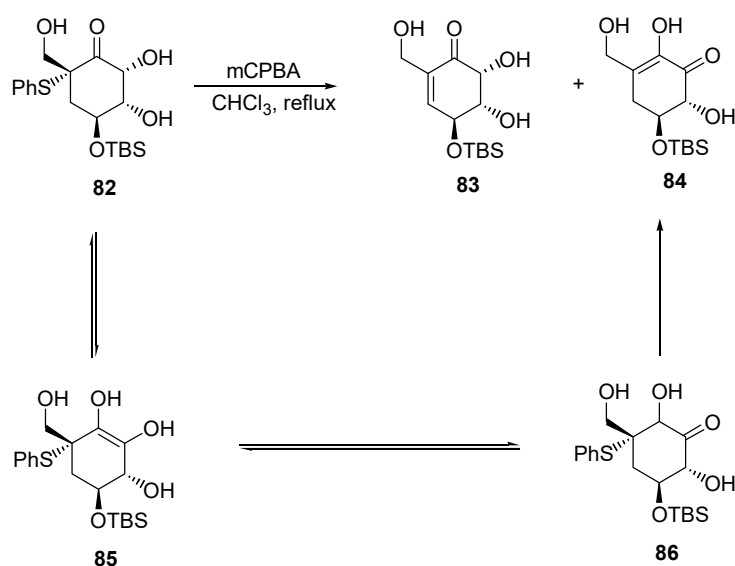
Scheme 6. Transformation of sedo-heptulose-7-phosphate **75** into valienone **30**.

A reasonable route for the formation of dTDP-acarviosine (**93**) involves the introduction of the nitrogen atom into the deoxy sugar moiety via transamination of dTDP-4-keto-6-deoxy-D-glucose (**94**) to dTDP-4-amino-4,6-dideoxy-D-glucose (**95**). This compound then forms a Schiff's base with 2-epi-5-epi-valiolone (**77**) which undergoes 2-epimerization, 5,6-dehydration and final imine double bond reduction to **93** (Scheme 13).

An alternative hypothetical pathway involves the reduction of the keto-sugar **77** to 1-epi-valiol (**99**). Further activation of the C1 hydroxyl group as a phosphate (**100**) and subsequent nucleophilic displacement by the nitrogen of amino sugar **95** would afford pseudosaccharide **101**. This compound, after epimerization at C2 and 5,6-dehydration would give dTDP acarviosine (**93**) (Scheme 14)[182].

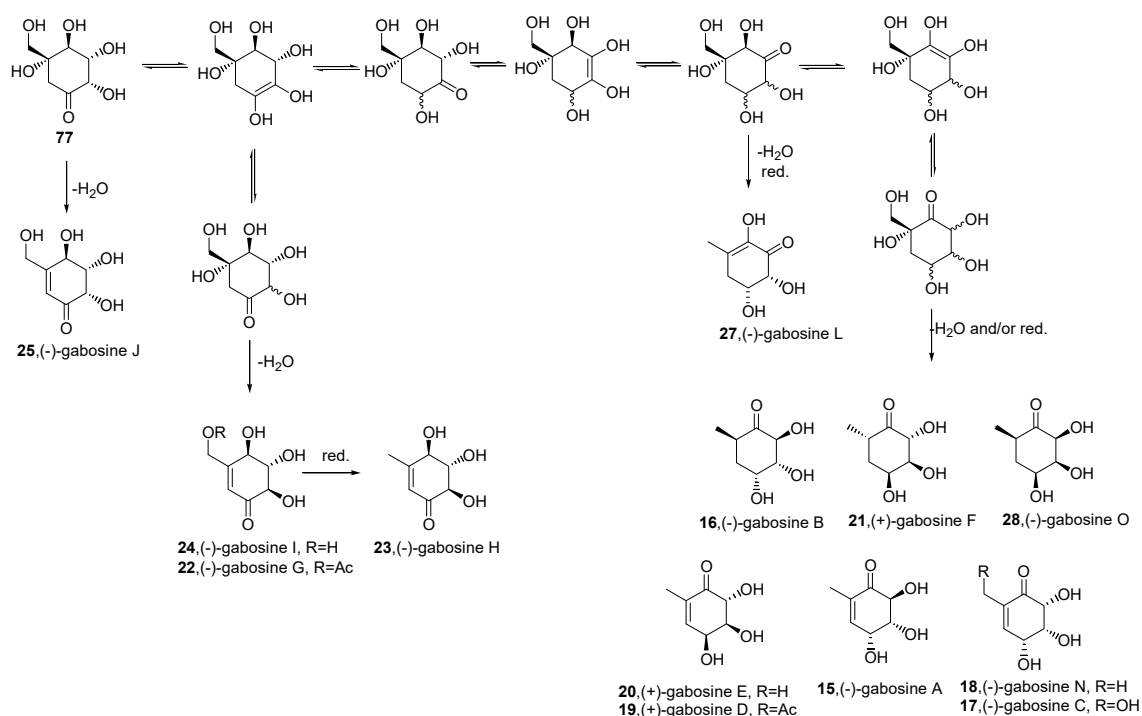


Scheme 7. Proposed transformation pathway of 2-epi-5-epi-valionone **77** into gabosines A, B, C and N.

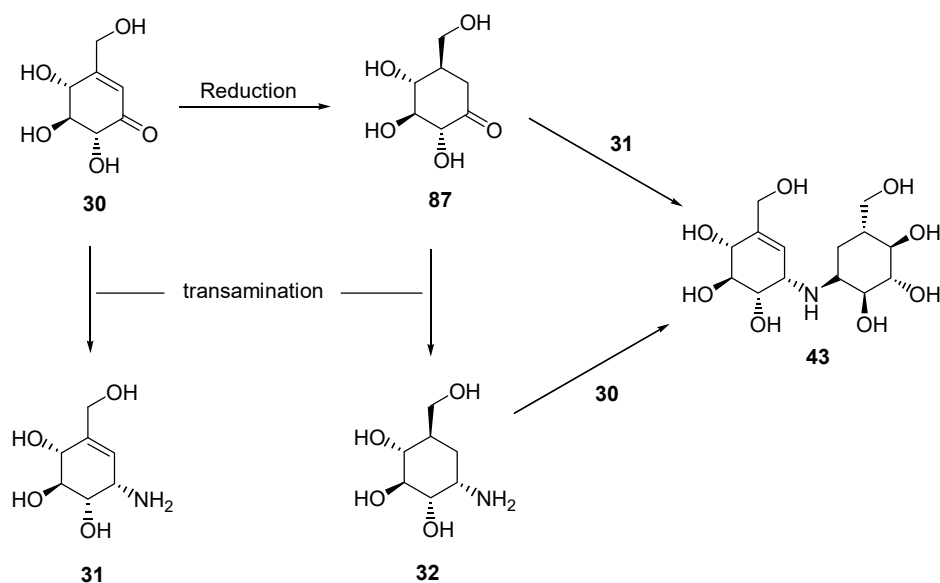


Scheme 8. Proposed mechanism for the formation of compound **84** from **82**.

More recently and on the basis of genetic and biochemical studies, a new mechanism for the biosynthesis of acarbose has been postulated. The Acarbose gene cluster (Acb) [183-186] gene cluster, involved or proposed in the sequence, are also indicated (Schem15). It should be indicated that a gene family is a set of homologous genes within one organism. A gene cluster is part of a gene family. The size of gene clusters can vary significantly from a few genes to several hundred genes. Regardless of the similarity of the DNA sequence of each gene within a gene cluster, the resulting protein of each gene is distinctive from the resulting protein of another gene within the cluster. The Acb corresponds to the 25 known gene cluster from *Actinoplanes* sp. SE50/110 identified and sequenced. Other Acb biosynthetic gene cluster from *Streptomyces glaucescens* has also been identified and sequenced.

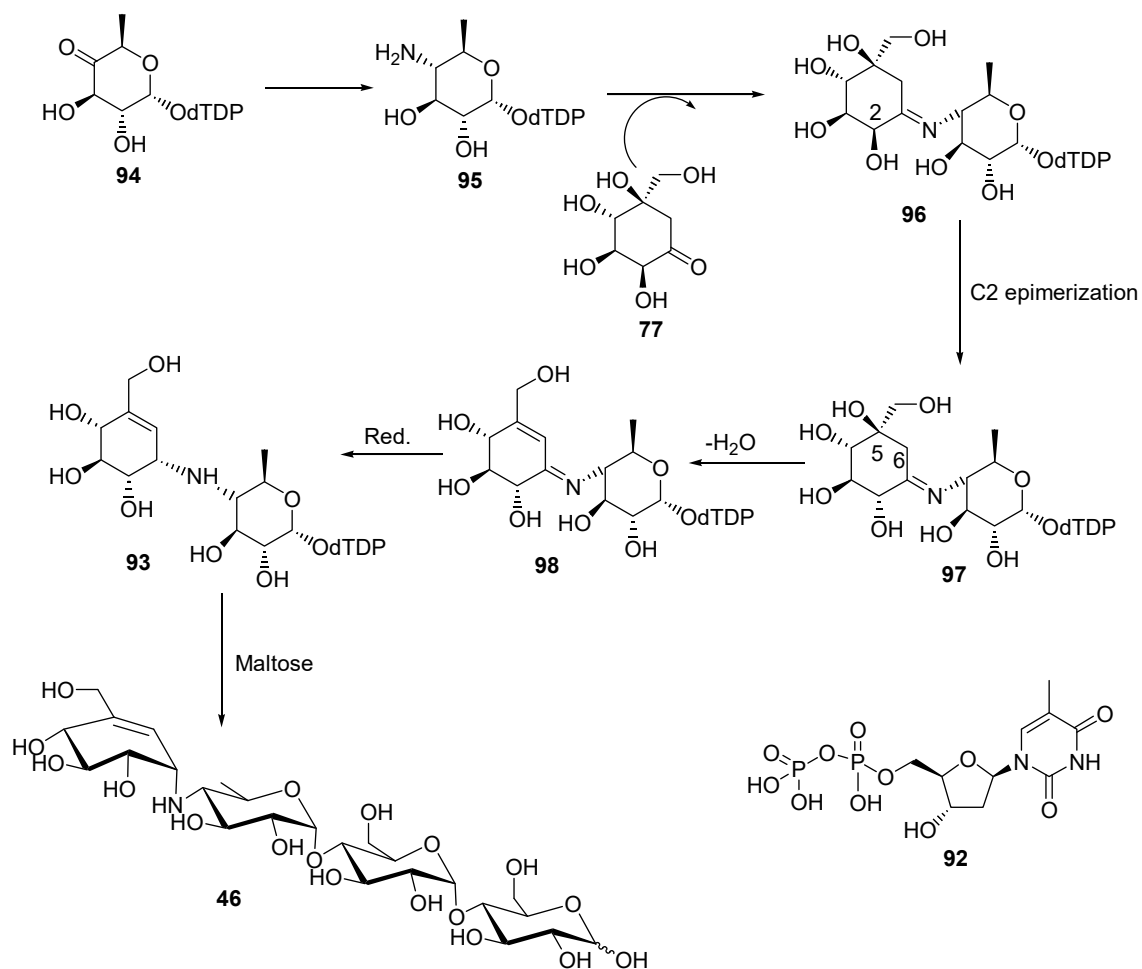


Scheme 9. Biosynthesis of gabosines from 2-epi-5-epi-valiolone **77**.

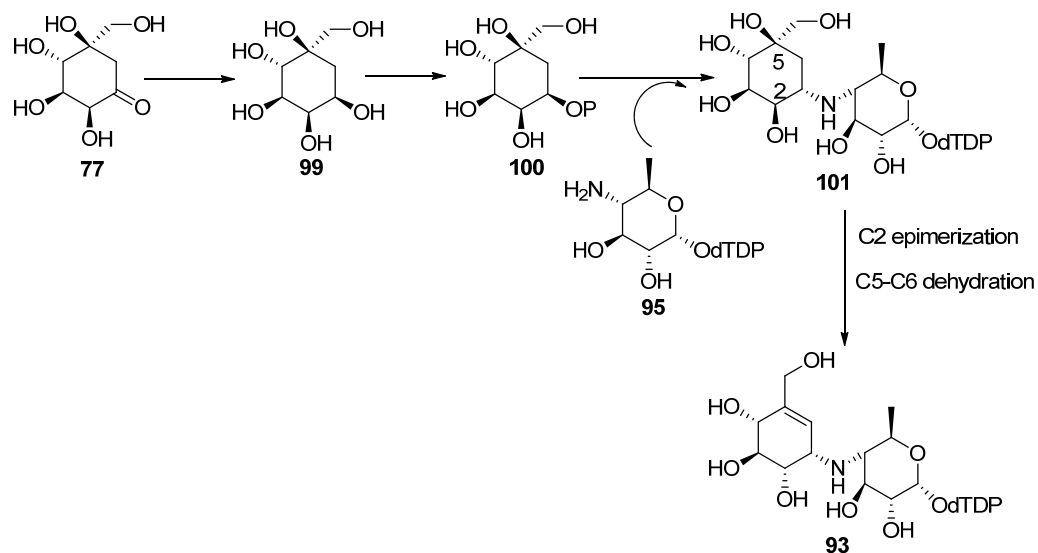


Scheme 10. Biosynthesis of validoxylamine **43** from valienone **30**.

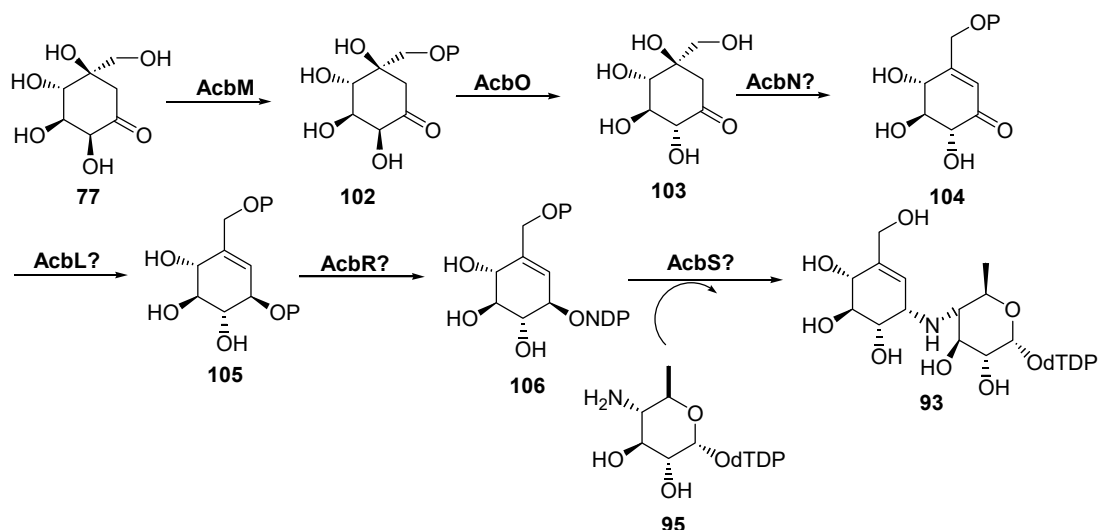
In this mechanism the cyclitol precursor, 2-epi-5-epi-valiolone (**77**), is phosphorylated to give 2-epi-5-epi-valiolone-7-phosphate (**102**) in a process mediated by the enzyme 2-epi-5-epi-valiolone 7-kinase. Compound **102** is then epimerized at C2 to give 5-epivalielone-7-phosphate (**103**). Further steps involving dehydration (**104**), carbonyl reduction and phosphorylations (**105**), nucleotidylation [187] (**106**) and final nucleophilic displacement by the nitrogen atom of **95**, would afford compound **93** [188-191]. In Scheme 15 The transformation **105-106** constitutes a nucleotidylation reaction: the transfer of an entire nucleotidyl unit, rather than just a phospho group [192].



Scheme 13. Proposed biosynthetic pathway to acarbose **46** and structure of dTDP **92**.



Scheme 14. Alternative biosynthesis of dTDP-acarviosine **93**.



Scheme 15. Revised proposal of the biosynthetic pathway to dTDP-acarbose **93**. NDP = nucleotidyl diphosphate.

3.2.5. Biosynthesis of Pyralomicins.

The biosynthetic gene cluster for the biosynthesis of pyralomicin antibiotics (PrI) has been isolated, cloned and sequenced from *Nonomuraea spiralis* IMC A-0156 [193]. The 41 kb (1000 base pairs) gene cluster contains 27 ORFs (the open reading frame –ORF– is the part of a reading frame that has the potential to code for a protein or peptide) [194-195] predicted to encode all of the functions for pyralomicin biosynthesis. This includes nonribosomal peptide synthetases (NRPS, Nonribosomal peptides (NRP) are a class of peptide secondary metabolites, usually produced by microorganisms. While there are a wide range of peptides that are not synthesized by ribosomes (the term *nonribosomal peptide* typically refers to a very specific set of these) and polyketide synthases (PKS) [196-197] required for the formation of the benzopyranopyrrole core unit. The PKS are a multi-domain enzyme complex involved in the biosynthesis of polyketides and fatty acids. The PKS genes for a certain polyketide are usually organized in one operon (an operon is a functioning unit of genomic DNA containing a cluster of genes under the control of a single promoter [198]) in bacteria and in gene clusters in eukaryotes. The biosynthesis of nonribosomal peptides shows several similarities with the polyketide and fatty acid biosynthesis. As consequence, some nonribosomal peptide synthetases contain polyketide synthase modules for the insertion of acetate or propionate-derived subunits into the peptide chain [199-201]. Others enzymes such as four halogenases [202] an O-methyltransferase [203-205] and an N-glycosyltransferase[206-207] necessary for further modifications of the core structure of pyralomicins have also been identified. In particular, the N-glycosyltransferase is involved in the transfer of either glucose or a pseudosugar (cyclitol) to the aglycone.

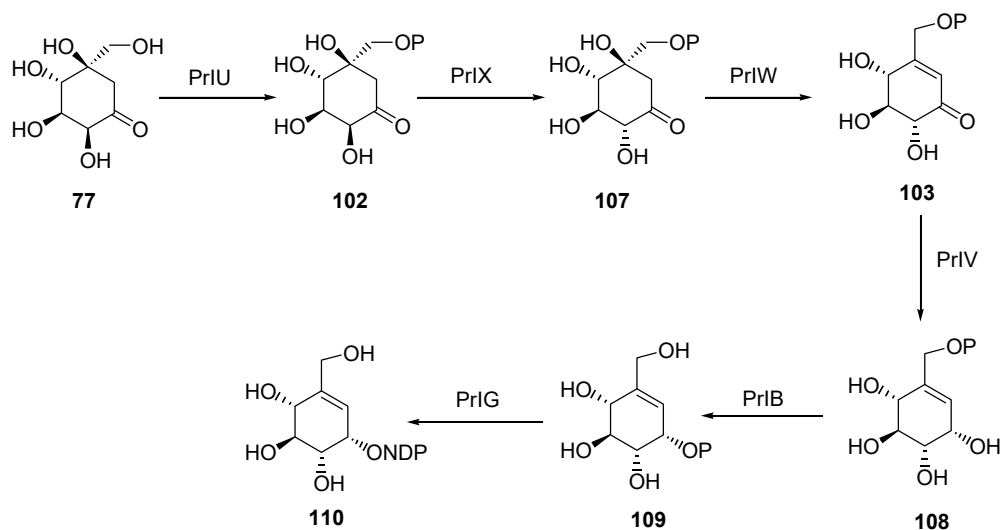
The formation of the cyclitol moiety of pyralomicins is depicted in Scheme 16. This pathway appears to be mediated through the actions of several enzymes including the 2-epi-5-epi-valiolone synthase PrlA, a putative phosphomutase (PrlB), a cyclitol kinase (PrlU), two cyclitol dehydrogenases (PrlV and PrlW), and a 2-epi-5-epi-valiolone phosphate epimerase (PrlX). This cassette of genes shares high homology with the cyclitol biosynthetic genes from the salbostatin [208] and acarbose gene clusters.

On the other hand, the starting material for the biosynthesis of the aglycone portion of pyralomicin is the amino acid L-proline and involves genes that share high identity with some related compounds.

3.2.6. Biosynthesis of Salbostatin.

In silico analysis of the putative biosynthetic gene cluster of salbostatin from *Streptomyces albus* ATCC 21838 revealed 20 open reading frames. The salbostatin genes SalF, SalL, SalM, SalN, SalO, and SalR were found to be homologous to AcbR, AcbM, AcbL, AcbN, AcbO, and AcbP from the acarbose pathway, respectively (see above). That suggests that the biosynthesis of the aminocyclitol moiety of salbostatin may be very similar to that of acarbose (Scheme 17).

Thus, 2-epi-5-epi-valiolone **77** is first converted to its activated form, 2-epi-5-epi-valiolone 7-phosphate **102**, by the action of the 2-epi-5-epi-valiolone 7-kinase (AcbM). Epimerization at the C-2 position by AcbO gives 5-epi-valiolone 7-phosphate **107**. This compound is proposed to be converted to 5-epi-valiolol 7-phosphate **111** or valienone-7-phosphate **103** which were dehydrated (from **111**) or reduced (from **103**) to 1-epi-valienol 7-phosphate **112**. From **112**, 1-epi-valienol-1-phosphate **113**, and then NDP-1-epi-valienol **114** were successively formed. Condensation of NDP-1-epi-valienol **114** with deoxyglucosamine **115** (biosynthesized from N-acetylglucosamine) may finally result in the formation of salbostatin-6'-phosphate **116** which is then converted into salbostatin **54**.



Scheme 16. Proposed mode of formation of the cyclitol moiety of pyralomicins. Legend. **77**: 2-epi-5-epi-valiolone; **102**: 2-epi-5-epi-valiolone-7-phosphate; **107**: 5-epi-valiolone-7-phosphate; **103**: valienone-7-phosphate; **108**: valienol-7-phosphate; **109**: valienol-1-phosphate; **110**: NDP-valienol.

4. Biological Activity of Carbasugars.

As we have previously pointed out (see Introduction) and according to Prof. McCasland “pseudo-sugars may be found acceptable in place of corresponding true sugars to some but not all enzymes or biological systems, and thus might serve to inhibit growth of

malignant or pathogenic cells”. [209] For instance, it, may be indicated that synthetic 6a-carba- β -DL-fructopyranose was found to be almost as sweet as D-fructose. [210-212]

In the context of enzymatic inhibition, [213] the structural similarity between true sugars and carbasugars can cause inhibition of enzymes involved in the digestion of carbohydrates which can lead to important consequences under medically point of view. For instance, the inhibition of carbohydrate digestive enzymes is considered a therapeutic tool for the treatment of type 2 diabetes. [214]. In the next paragraphs some applications of carbasugars and derivatives as enzymatic inhibitory agents wil be highlighted.

4.1. Biological activity of Carbafuranoses.

The carbocyclic analogue of 5-phosphoribosyl-1-pyrophosphate (cPRPP, Figure 17) is the only reported carbafuranose with significant biological activity. [215-217] This compound shows enzymatic inhibitory activity against the enzyme 5-phosphoribosyl R-1-pyrophosphate (PRPP) synthetase [218-220] with values [221] K_i of 186 μ M (human type PRPP synthetase) and a K_i of 3811 mM (*Bacillus subtilis* PRPP synthetase). The enzyme PRPP-synthetase converts ribose 5-phosphate into phosphoribosyl pyrophosphate (PRPP) (Scheme 18). The resulting PRPP acts as an essential component of the purine salvage pathway (used to recover bases and nucleosides that are formed during degradation of RNA and DNA) and the *de novo* synthesis of purines. Mutations that lead to super-activity (increased enzyme activity or de-regulation of the enzyme) result in purine [222] overproduction. Super-activity symptoms include, among others, neurodevelopmental disorders [223]. On the other hand there is evidence that the activity of PRPP synthetase is elevated in tumors. Then, inhibitors of this enzyme show antineoplastic activity [224-225].

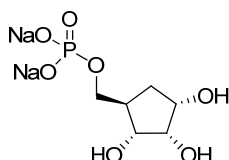
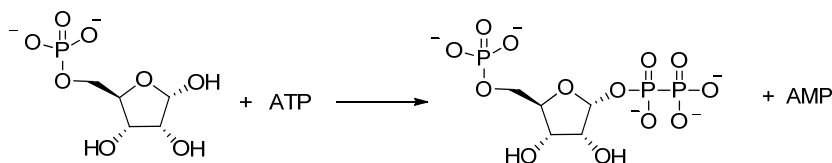
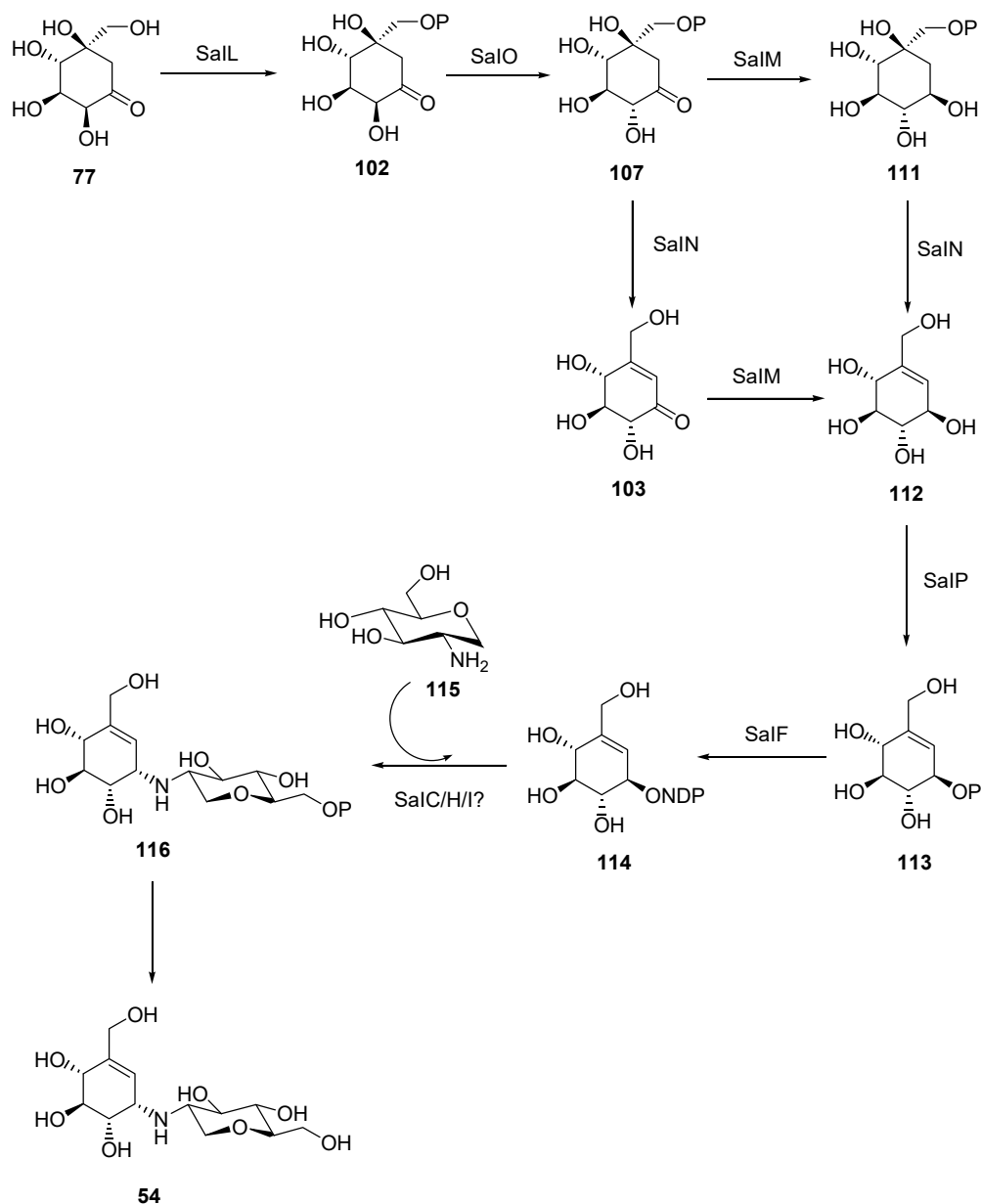


Figure 17



Scheme 18



Scheme 17. Proposed biosynthetic pathway for salbostatin.

4.2. Biological Activity of Carbapyranoses.

4.2.1. Cyclophellitol and derivatives.

(+)-Cyclophellitol (**5**) was found to be a specific inhibitor of β -glucosidases (enzymes that hydrolyze glycosidic bonds to release nonreducing terminal glucosyl residues from glycosides and oligosaccharides [226]) [227-228] with potential inhibition of the human immunodeficiency virus (HIV) and with possible antimetastatic therapeutic activity [229-231]. Several unnatural cyclophellitol derivatives also show interesting biological properties. [232-125]. For instance, (1*R*,6*S*)-cyclophellitol **120** –which is its unnatural diastereomer- inhibits α -glucosidases [236-237] and cyclophellitol aziridines **121** are potent and selective irreversible inhibitors of retaining glycosidases (Figure 18).

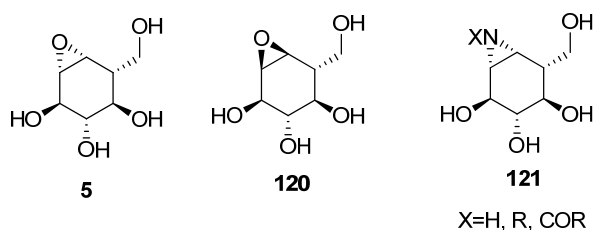


Figure 18. Structures of cyclophellitol **5**, (1*R*,6*S*)-cyclophellitol, **120**, and cyclophellitol aziridines, **121**.

Several natural and synthetic epoxyquinones and epoxyquinols with structures related to both cyclophellitol and gabosines (see below) also show interesting biological properties. The chemistry and biological activities of these compounds have been described in an authoritative reviews and will not be considered here [59].

4.2.2. MK-7067, carba-galactopyranose, carba-glucopyranose, streptol and COTC.

The unsaturated carbapyranose (+)-MK7067 **6** exhibited an effective herbicidal activity [242]. Carba- α -D-galactopyranose (**4**) was found to have a low antibiotic activity against *Klebsiella pneumonia* MB-1264, [243] whereas the L-enantiomer is inactive [244]. 5a-carba- α -DL-glucopyranose ((\pm)-**122**, Figure 19) is a glucokinase (a monomeric cytoplasmic enzyme found in the liver and pancreas. Its main function is regulation of glucose levels in these organs [245-246]) inhibitor. Carbasugar ((\pm)-**122** and the β -anomer ((\pm)-**121**) were used as synthetic analogs of glucose anomers to study the mechanism of glucose-stimulated insulin release by pancreatic islets [247]. It was found that alpha isomer ((\pm)-**122**, but not the beta-isomer ((\pm)-**121**, inhibited both glucose-stimulated insulin release and islet glucokinase activity in a concentration-dependent manner. On the other hand, a cellobiose phosphorylase from *Cellvibrio gilvuse* recognizes only the beta-D-form of 5a-carba-glucopyranose ((\pm)-**121** [248].

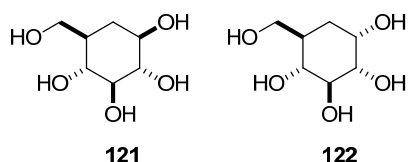
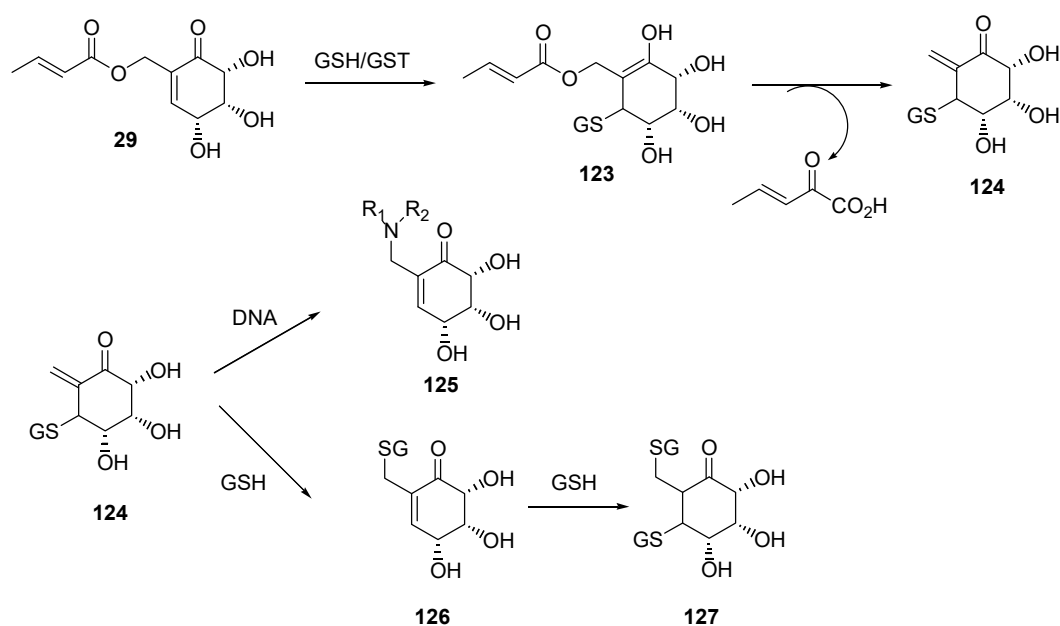


Figure 19. Structures of α - and β -glucopyranose (only D-enantiomers are shown).

Streptol (**7**) inhibited the root growth of lettuce seedlings at a concentration < 13 ppm.

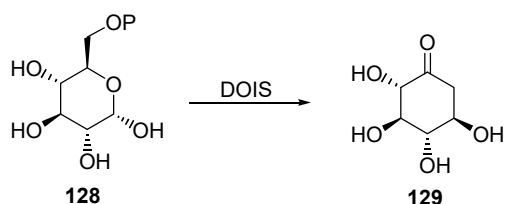
The 2-Crotonyloxy-(4*R*,5*R*,6*R*)-4,5,6-trihydroxycyclohex-2-enone, COTC (**29**) and derivatives have been shown to display notable toxicity towards a range of different cancer cell lines. The general mechanism for anti-cancer activity of COTC is depicted in Scheme 19 [249-253]. After conjugate addition of glutathione (γ -L-glutamyl-L-cysteinylglycine, GSH). Glutathione *S*-transferases (GSTs) comprise a family of isozymes -enzymes that differ in amino acid sequence but catalyze the same chemical reaction- known for their ability to catalyze the conjugation of the reduced form of glutathione (GSH) to xenobiotic -foreign chemical substance found within an organism that is not normally naturally- to the enone moiety of **29**, the resulting enol **123** undergoes expulsion of crotonic acid to generate exocyclic enone **124**. It should be

pointed out that the rate of formation of enol **123** is substantially increased by enzymatic catalysis *via* glutathione transferase (GST). Alkylation of intracellular proteins and/or nucleic acids by **124** then lead to cell death. Other processes may also contribute to the anti-cancer activity of this compound and derivatives. For instance, the GSH conjugate **126**, derived by trapping the exocyclic enone **124** with GSH, and bis-GSH adduct **127** are competitive inhibitor of human glyoxalase 1 (Glo1). This enzyme is vital for cell survival as part of a detoxification system for cytotoxic 2-oxoaldehydes or other toxic species and they inhibitors have previously been demonstrated to have anti-cancer properties [254-255]. On these bases, it seems logical to have carried out extensive efforts for the synthesis of new analogues COTC [256-264].



Scheme 19. Proposed mode of action of COTC and derivatives

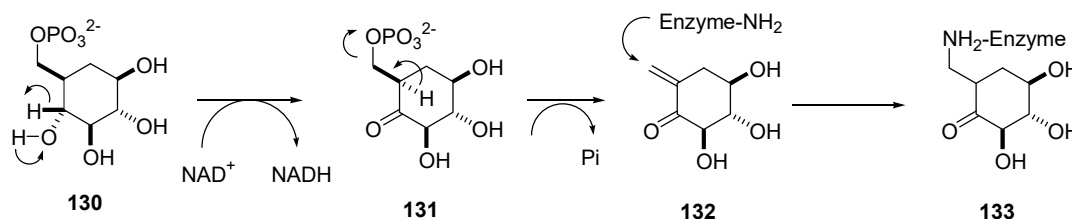
A key enzyme in the biosynthesis of clinically important aminoglycoside antibiotics such as neomycin, kanamycin and gentamicin, [265] among others, is 2-deoxy-scylo-inosose synthase (DOIS), which catalyzes the carbocycle formation from D-glucose-6-phosphate **128** to 2-deoxy-scylo-inosose (DOI, **129**, Scheme 20, [266]).



Scheme 20. Transformation of D-glucose-6-phosphate into 2-deoxy-scylo-inosose.

5a-Carba-DL-glucose-6-phosphate (**130**) is an irreversible inhibitor of DOIS. The proposed reaction mechanism for this inhibitory action is shown in Scheme 21 [267]. Thus, after the initial oxidation at C4 and subsequent elimination of a phosphate, compound (\pm)-**130** was converted within the enzyme into an α,β -unsaturated methylene cyclohexanone (\pm)-**132**. This α,β -unsaturated carbonyl intermediate is attacked by a

specific nucleophilic residue in the active site (Lys-141) through a Michael-type 1,4-addition, resulting in the formation of compound **133**.



Scheme 21. Mechanism of irreversible inhibition of DOIS by 5a-Carba-DL-glucose-6-phosphate.

4.2.3. Pericosines and gabosines.

Pericosines A-C (**8-10**) exhibited significant growth inhibition against several tumor cell lines. In particular, pericosine A (**8**) shows significant *in vitro* cytotoxicity against P388 lymphocytic leukemia cells [268] also showing significant *in vivo* tumor inhibitory activity. In addition, pericosine A inhibited [271] the protein kinase EGFR (the epidermal growth factor (EGF) stimulates cell growth, proliferation, and differentiation by binding to its receptor EGFR. Human EGF is a 6045-Da protein with 53 amino acid residues and three intramolecular disulfide bonds. Mutations that lead to EGFR overexpression or overactivity have been associated with a number of cancers. [269]) and topoisomerase II (topoisomerases are isomerase enzymes that act on the topology of DNA. Type II topoisomerases cut both strands of the DNA helix simultaneously in order to manage DNA. They use the hydrolysis of ATP, unlike Type I topoisomerases which are ATP-independent. [270]) Gabosine E (**20**) showed [273] a weak inhibitory effect on the cholesterol biosynthesis in cell line tests with HEP-G2 (This line has been found to express a wide variety of liver-specific metabolic functions. Among these functions are those related to cholesterol and triglyceride metabolism live cells [272]).

On the other hand, Gabosines A (**15**), B (**16**), F (**21**), N (**18**), and O (**28**) present DNA-binding properties [274-275]. Gabosine C (**17**) is the known antibiotic KD16-U [276] and its crotonyl ester is the previously considered carbasugar COTC. Gabosine J (**25**) inhibits α -mannosidase, an enzyme involved in the cleavage of the alpha form of mannose, [277] and some derivatives such as α -gabosinol **134** and β -gabosinol **135** inhibit β -galactosidase and β -glucosidase respectively (Figure 20) [278].

Some compounds structurally related with gabosines also show interesting biological properties. For instance, compound (+)-**136** has been reported [279] that is a cytotoxic and potential contraceptive agent. On the other hand, nigrospoxydon A (**137**) shows activity against *Staphylococcus aureus* ATCC 25923, a clinical isolate with the designation Seattle 1945 that is used as a standard laboratory testing control strain [280]. It has also been published that the closely related esters (-)-**138** and epoxydine B (**139**) display antibacterial, antifungal, and antialgal activities (Figure 20) [281]. The synthetic compound (+)-RKTS-33 (**140**) has inhibitory activity toward death receptor-mediated apoptosis [282-283]. The racemate of compound **141** is a nuclear factor- κ B (NF- κ B or nuclear factor kappa-light-chain-enhancer of activated B cells, is a protein complex that controls transcription of DNA, cytokine production and cell survival.[284-285])

inhibitor and therefore a suitable candidate as antiinflammatory and anticancer agent [286].

Finally, compound **142** shows [287] synergetic effect with cisplatin against lung cancer cell line A549 (adenocarcinomic human alveolar -terminal ends of the respiratory tree-basal epithelial cells [288], through the inhibition of GSTM1 (Glutathione S-transferase Mu 1 -gene name GSTM1- is a human glutathione S-transferase [289].

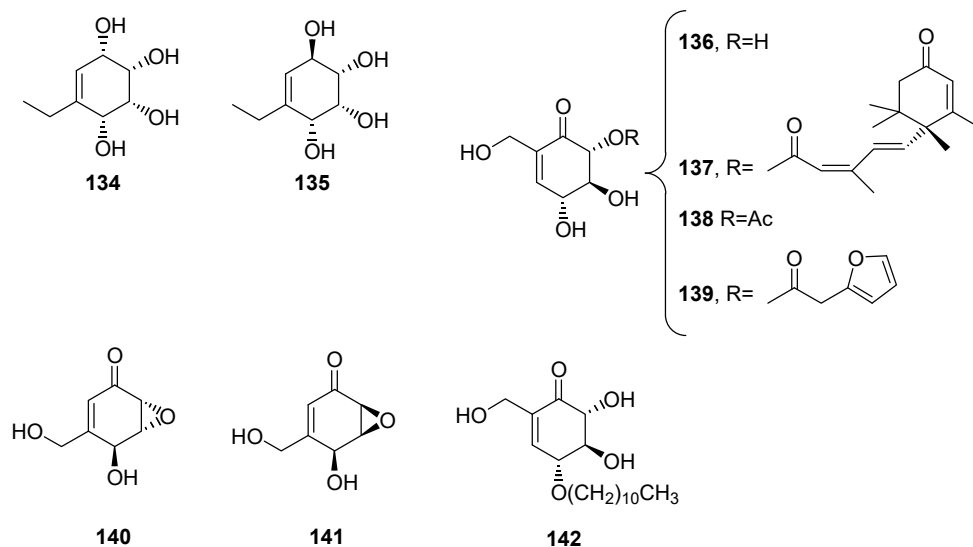


Figure 20. Some biologically active gabosine derivatives.

4.2.4. Carbaglycosides.

O-linked alkyl carba- β -D-glycosides **143** and **144** (Figure 21) have been shown [290] to be useful as primers for biocombinatorial glycosylation involving efficient uptake in B16 mouse melanoma cells, the most frequently used murine melanoma model [291]. Uptake of the carbaglycosides resulted in β -galactosylation and subsequent sialylation of the galactose residues incorporated, to give rise to glycosylated products having a glycan similar to that in ganglioside GM3, a type of ganglioside, molecule composed of a glycosphingolipid with one or more sialic acids linked on the sugar chain. The letter G refers to ganglioside, and M is for monosialic acid as it has only one sialic acid residue. The numbering is based on its relative mobility in electrophoresis among other monosialic gangliosides. Recently, gangliosides have been found to be highly important molecules in immunology. Natural and semisynthetic gangliosides are considered possible therapeutics for neurodegenerative disorders [292-293]. This indicate that carbasugars can be stable and versatile building blocks for the biocombinatorial synthesis using a living cell. In addition, a strong and specific inhibition of β -galactosidase (bovine liver) was found for dodecyl 5a-carba- β -D-galactopyranoside (**144**).

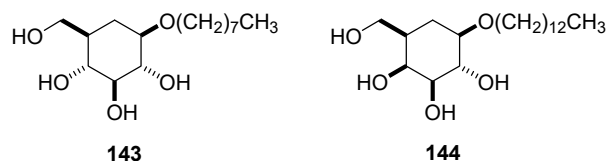


Figure 21. Structures of carba- β -D-glycosides **143** and **144**.

In addition, more complex carbaglycosides have interesting biological activities. Synthetic carbaxylosides of coumarins, i.e., (+)-**145** or (-)-**145**, have significant potential as oral antithrombotic agents [294], and a 5a-carba analogue of glucotropaeolin, (\pm)-**146**, was shown to display a good inhibition power [295] against myrosinase, the only known enzyme found in nature that can cleave a thio-linked glucose [296]. (Figure 22).

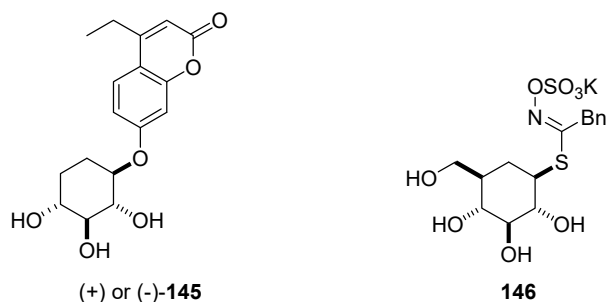


Figure 22. Structures of carba-glycosides **145** and **146**.

4.2.5. Carbanucleotides.

Some synthetic carbasugar-nucleotide displayed biological activity as glycosyltransferase inhibitors. For instance, uridine-5'-(5a-carba- α -D-galactopyranosyl diphosphate) **147** (Figure 23), the carbocyclic analog of UDP-galactose, exhibits inhibitory activity of β -(1 \rightarrow 4) galactosyltransferase from bovine milk [297].

On the other hand, the carbocyclic analogue of GDP-fucose, consisting of 5a-carba- β -L-fucopyranose **148** [298], was found to be a competitive inhibitor of fucosyltransferases, key enzymes in the biosynthesis of the Lewis-x determinant. Interestingly, the carba-fucose analogue **148** showed a K_i value similar to that observed for the GDP-fucose indicating that the ring oxygen of fucose is not critical for the recognition of GDP-Fuc by the enzyme, albeit it is essential for the transfer to occur [299].

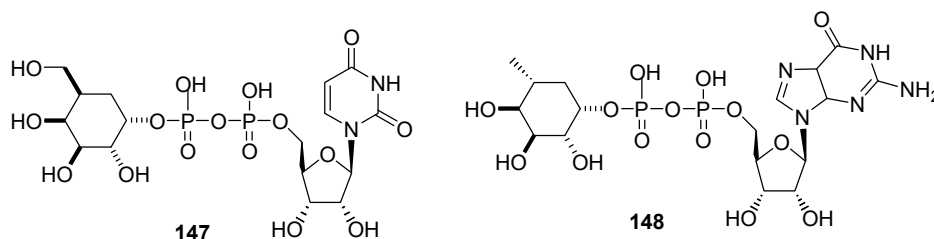


Figure 23. Structure of carbanucleotides **147** and **148**.

4.2.6. Aminocarbasugars.

Amino carbasugars [300] are the most important and appealing carbapyranose derivatives from a biological standpoint.

4.2.6.1. Valienamine, validamine, hydroxyvalidamine, valioline and derivatives.

Simple aminocarbasugars such as valienamine (**31**), validamine (**32**), hydroxyvalidamine (**33**), and valioline (**34**) appeared to be active against several sugar hydrolases [301-302]. Valienamine, validamine and hydroxyvalidamine were reported as microbial oligosaccharide α -glucosidase inhibitors [303-306]. The α -galacto-, β -gluco-, and α -mannovalidamine analogues **149-151** (Figure 24) have been prepared and their glycosidase activity tested [307-309]. These compounds, however, displayed moderate activity as glycosidase inhibitors when compared with α -glucovalidamine. Conversely, valioline (**34**) has more potent α -glucosidase inhibitory activity against porcine intestinal sucrase, maltase, and isomaltase than the rest of the aminocarbasugars [310]. That is why series of *N*-substituted valiolamines were synthesized, resulting in the preparation of the glycohydrolase inhibitor voglibose (**152**) [311-313]. Voglibose was launched as an antidiabetic agent in 1994 to improve postprandial hyperglycemia in diabetes mellitus [314-316]. Voglibose inhibits disaccharidases competitively, suppressing the elevation of the blood glucose concentration after oral sucrose, maltose, or starch administration, but not after oral glucose, fructose, or lactose intake.

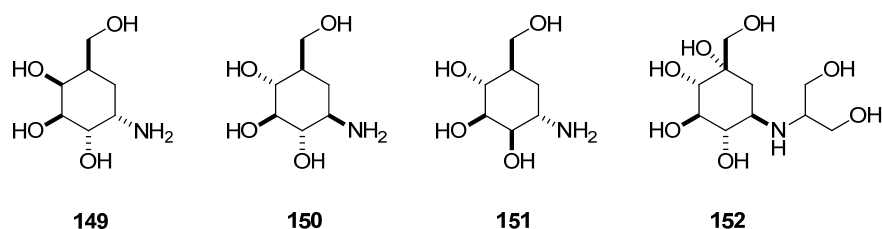


Figure 24. Structures of α -galacto-, β -gluco-, and α -mannovalidamine analogues (**149-151**) and Voglibose (**152**).

Moreover, carbocyclic analogues of glycosylamides [317], which contain the 5a-carba-D-hexopyranose residues (Figure 25), have also been synthesized. 5a-Carba- β -glucopyranosyl- and 5a-carba- β -galactopyranosyl-amides **153** and **154** have been shown to be potent immunomodulators, comparable to the *true* sugars [318], suggesting that the glycolipid analogues may provide appropriate model compounds for biochemical studies in glycolipid chemistry. On the other hand, the glycosidase inhibitory effects of 1,2-bis-epi-valienamine **155** and 1-epi-2-acetamido-2-deoxy-valienamine **156** (Figure 25) have been investigated. 1,2-bis-epi-Valienamine **155** acts as a β -mannosidase [319] inhibitor whereas 2-acetamido-2-deoxy-1-epi-valienamine **156** has been shown [320] to inhibit various β -hexosaminidases, enzymes involved in the hydrolysis of terminal N-acetyl-D-hexosamine residues in N-acetyl- β -D-hexosaminides [321-323].

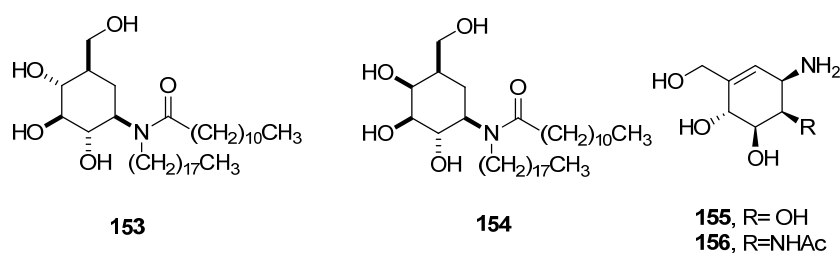


Figure 25. 5a-Carba- β -glucopyranosyl- and 5a-carba- β -galactopyranosyl-amides.

A series of *N*-linked carbocyclic analogues of glycosylceramides, structurally related to glycosphingolipids and glyco glycerolipids, have also been synthesized by replacing the sugar residue with either saturated [324] (**157**, **158**, Figure 26) or unsaturated [325] (**159**, **160**, Figure 26) 5a-carba-D-gluco- or 5a-carba-D-galactopyranoses, respectively. Compounds **157** and **158** are mild immunomodulators and possess a mild inhibitory activity against gluco- and galactocerebrosidases, whereas the unsaturated gluco-**159** and galacto-**160** analogues were shown to be very potent and specific of gluco- and galactocerebrosidase inhibitors, respectively, thus showing the critical role played by the C4 configuration for specificity in inhibition.

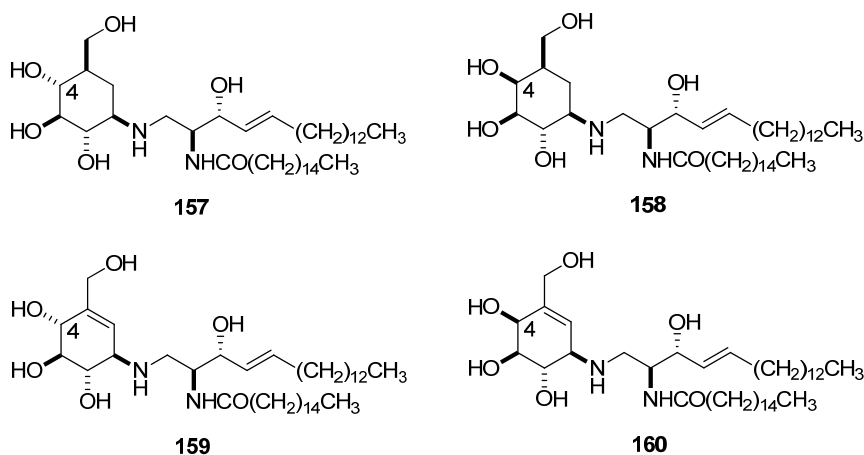


Figure 26. *N*-linked carbocyclic analogues of glycosylceramides **157-160**.

Various *N*-alkyl- and *N,N*-dialkyl- β -valienamines were synthesized and testing as glycosylases inhibitors [326-329]. For instance, *N*-benzylation of valienamine improves significantly their inhibitory activity toward α -glucosidases [330]. In this way, 91 pure *N*-alkylated valienamines **161** (Figure 27) prepared using solid-phase synthesis methodology are new β -glucosidase inhibitors, being most of them more potent than valienamine [331]. On the other hand, the spiroaziridines and spirodiaziridines **162** and **163** were prepared and evaluated as glycosidase inhibitors against β -glucosidases from almonds, β -glucosidase from *Caldocellum saccharolyticum*, and α -glucosidase from yeast with poor results compared with the cyclopentylamine **164** (Figure 27) [332].

Two isomeric bicyclo[4.1.0]heptane **165** and **166** (Figure 27) have been synthesized and evaluated against α -galactosidase enzymes from coffee bean and *E. coli* [333]. The activity of the glycosyl hydrolase family GH27 enzyme (coffee bean) was competitively inhibited by the 1*R*,6*S*-amine with a K_i value of 0.541 μ M. The *E. coli* α -galactosidase exhibited a much weaker binding interaction with the 1*R*,6*S*-amine (IC_{50} = 80 μ M). The diastereomeric 1*S*,6*R*-amine bound weakly to both galactosidases, (coffee bean, IC_{50} = 286 μ M) and (*E. coli*, IC_{50} = 2.46 mM).

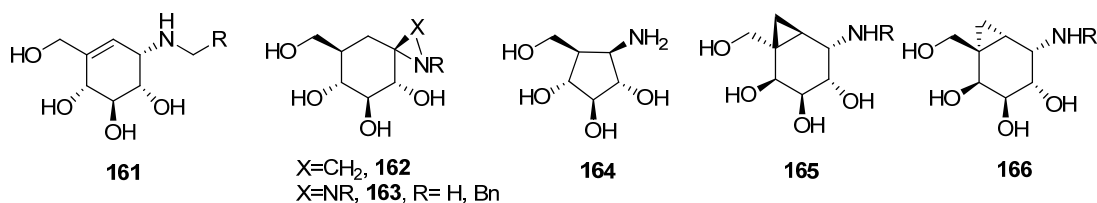


Figure 27. Alkylated valienamine derivatives, spiroaziridines **162**, spiroazirinas **163**, cyclopentylamine derivative **164** and bicyclo[4.1.0]heptane derivatives **165** and **166**.

N-Octyl- β -valienamine derivative **167** (Figure 28) is a potent and specific inhibitors of β -glucocerebrosidases ($IC_{50} = 3 \times 10^{-8}$ M). On the contrary, galacto derivative **168** did not show any improvement in potency. Additionally, it was later demonstrated that **167** and **168** are potent competitive inhibitors of human β -glucosidase and human β -galactosidase, respectively.

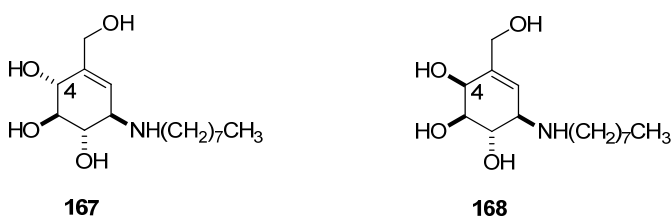


Figure 28. *N*-Octyl- β -valienamine derivatives.

These activities suggest that carbasugar derivatives **167** and **168** work as chemical chaperones [334-337] to accelerate transport and maturation of mutant forms of enzyme proteins and therefore may be useful for certain patients with β -galactosidosis and potentially other lysosomal storage diseases [338-350]. It should be opportune at this point clarify the concept of chemical chaperone [351-353]. Pharmacological or molecular chaperone therapy is among the newest therapeutic ideas for lysosomal storage diseases. Lysosomes are enzymes within cells that digest large molecules and pass the fragments on to other parts of the cell for recycling. This process requires several critical enzymes. If one of these enzymes is defective, because of a mutation, the large molecules accumulate within the cell, eventually killing it. Pharmacological chaperones are small molecules that specifically bind to and stabilize the functional form or three-dimensional shape of a misfolded protein in the endoplasmic reticulum (ER) of a cell. When misfolded due to a genetic mutation, the enzyme is unable to adopt the correct functional shape and, in consequence, the enzyme activity is reduced. The binding of the chaperone molecule helps the protein fold into its correct three-dimensional shape. Pharmacological chaperone therapy is in early stage clinical trials for disease such as Fabry (a rare genetic lysosomal storage disease. Fabry disease can cause a wide range of systemic symptoms such as pain, kidney complications, high blood pressure, cardiomyopathy, fatigue, vertigue, nausea, diarrhea, etc) and Gaucher Type I (a genetic disorder in which glucocerebroside accumulates in cells and certain organs. The disorder is characterized by bruising, fatigue, anemia, low blood platelet count and enlargement of the liver and spleen. It is caused by a hereditary deficiency of the enzyme glucocerebrosidase which acts on glucocerebroside. When the enzyme is defective, glucocerebroside accumulates, particularly in white blood cells and especially in macrophages (mononuclear leukocytes).

In the search for different sugar hydrolase inhibitors, 5a-Carba- α -DL-fucopyranosyl amine [354-355] ((\pm)-**169**) and 5a-carba- β -L-fucopyranosylamine (**170**) [356] were prepared. These compounds have been shown to be strong inhibitors of α -L-fucosidase. α -Fucosidase inhibitors are interesting because they are potential candidates for cancer and HIV drugs, due to their inhibitory effect on the extracellular matrix secreted fucosidases [357]. Different *N*-substituted derivates of (\pm)-**169** were prepared. The

inhibitory activity was increased by incorporation of alkyl and phenylalkyl groups into the amino function of the parent (\pm)-**169**. The change of the *N*-alkyl substituents, from ethyl on **171a** to nonyl on **171e**, improved the inhibitory power. The *n*-octyl derivate (**171d**) was found to be the strongest inhibitor of α -L-fucosidase (bovine kidney) more potent ($K_i = 0.016 \mu\text{m}$) than deoxyfuconojirimicin ($K_i = 0.031 \mu\text{m}$), the most powerful mammalian α -L-fucosidase inhibitor identified [358]. In a similar manner, chemical modifications of **170** generated *N*-substituted derivatives (\pm)-**172a-g**, which were found to be very strong β -galactosidase as well as β -glucosidase inhibitors with no specificity associated with the 4-epimeric structures. This inhibitory activity appeared attributable to D-enantiomers exclusively, that is, *N*-alkyl-6-deoxy-5a-carba- β -D-galactopyranosylamines (D-**172**) [359]. (Figure 29).

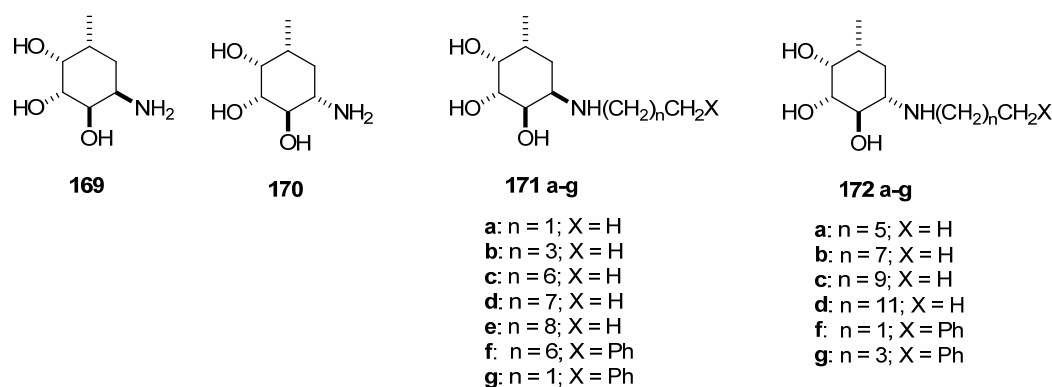


Figure 29. Carba-fucopyranosyl amines **169-172**.

Carbasugar derivatives have also been envisaged to play roles in elucidating and controlling other biological events that involve sugar moieties. This includes the synthesis of analogues of enzyme substrates, which were modified by replacing part of their structures with carbasugar units and which were expected to be used in the elucidation of the mode of action of sugar transferases [360]. These analogues have been recognized as good substrates, thus showing that the ring oxygen in the acceptor is not involved in the specific recognition by the enzyme. For instance, bovine β -(1 \rightarrow 4)-galactosyltransferase was tested with α -galacto- (**173**), α - and β -manno- (**174** and **175**), and α - and β -gluco- (**176** and **177**) 2-acetamido-2-deoxy-5a-carba-DL-hexopyranoses [361]. Of these compounds, only **176** and **177** behave as galactosyl acceptors. The reactions afforded disaccharides **178** and **179**, but half of the material remained unreacted, suggesting that only the D-enantiomers behaved as acceptors. These results indicate that the ring oxygen atom is not used for specific recognition by bovine β -(1 \rightarrow 4)-galactosyltransferase (Figure 30).

4.2.6.2. Validamycins, salbostatin, acarbose, amylostatis, adiposins, oligostatins, tetrastins and related compounds.

Validamycins **35-42** and salbostatin (**54**) have been reported to be mechanistically unique antifungal agents [362-366]. Validamycin A (**35**), the most active compound of the complex, is a fungicida that inhibits trehalases, enzymes that carry out the degradation of the non-reducing disaccharide trehalose [367-369] in plants, insects, and fungi as well as enhance trehalose accumulation in transgenic plants. It is widely used in rice-producing countries in Asia to control sheath blight disease of the rice plants caused by the fungus *Rhizoctonia solani* [370-384].

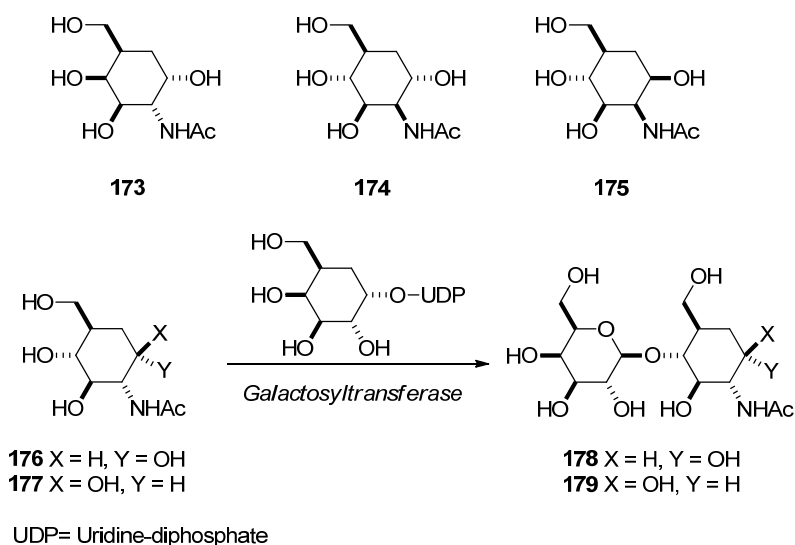


Figure 30. Carbasugars as sugar transferases.

Validamycin A is able to control the spread of the pathogen by inhibiting specifically the hyphal (a long, branching filamentous structure of a fungus, oomycete, or actinobacterium [385]) extension without affecting the specific growth rate. It means Validamycin A is effective against *Pellicularia sasakii* and *Rhizoctonia solani* in plants, but only decreases their virulence instead of exhibiting a fungicidal effect [386-389]. Further extensive studies on the mechanism of action of validamycin in controlling the hyphal extension have been carried out by several research groups, and it seems to be related to the anti trehalase activity [390-392] of the carba-disaccharide validoxylamine (**43**) [393]. For the purpose of developing more potent trehalase inhibitors, several pseudo-trehalosamines, such as **180** and **181**, as well as dicarba analogues of trehalose, **182-184**, composed of valienamine, validamine, and valiolumine moieties, were synthesized and they showed to possess strong inhibitory activity against trehalase (Figure 31) [394-396].

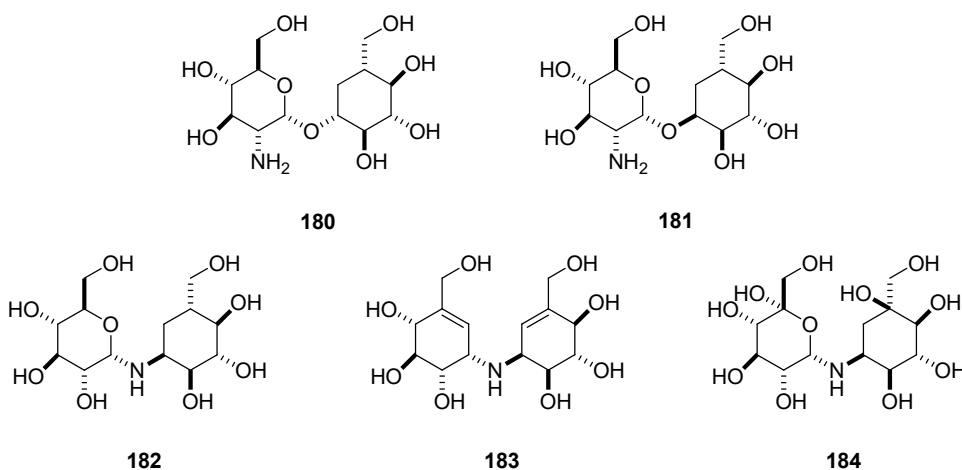


Figure 31. Carbasugars **180-184** with anti-tetrahylase activity

Many members of the carba-oligosaccharidic group, e.g., acarbose (**46**), amylostatis (**50**), adiposins (**51**), oligostatis (**52**), and trestatis (**53**), are known to display potent α -glucosidase inhibitory effects. Among these active metabolites, acarbose is of

considerable pharmacological interest. In addition to its α -glucosidase activity, acarbose also displays potent inhibitory activity against sucrase, maltase, dextrinase, and glucoamilase. This pronounced inhibitory effect has resulted in its use as a clinical drug for the treatment of type II non-insulin-dependent diabetes and, in some countries, prediabetes in order to enable patients to better control blood sugar contents while living with starch-containing diets. It is a starch blocker, and inhibits α -glucosidase, an intestinal enzyme that releases glucose from larger carbohydrates. Inhibition of these enzyme systems reduces the rate of digestion of complex carbohydrates. Less glucose is absorbed because the carbohydrates are not broken down into glucose molecules. Interestingly, individual members of different series of carba-oligosaccharides deactivate α -amylase and sucrase quite differently. Thus, whereas amylase inhibition is maximum with homologues of four and five glucose units, the greatest sucrase inhibition is caused by acarbose containing two glucose residues [397].

Adiposins (**51**) have exhibited potent inhibitory activities against α -glucoside hydrolases such as salivary and pancreatic α -amylases, and intestinal disaccharidases, such as sucrase, maltase, and isomaltase [398]. They have also showed antimicrobial activities against some Gram positive bacteria, Gram negative bacteria, some anaerobic bacteria, and some phytopathogenic fungi, and also showed a synergistic effect on the antibacterial activity with some maltooligosaccharides [399].

Oligostatins (**52**) exhibited not only strong α -amylase inhibitory activity but also they are active against Gram negative bacteria, while Gram positive bacteria are not affected [400].

The acarviosine, which is the core structure of acarbose and related carba-oligosaccharides α -amylase inhibitors, is the responsible of their glycosidase inhibitory activities due to the valienamine portion mimics the glucopyranosyl cation intermediate at the active site for hydrolysis of α -glucosides in the acarviosine moiety. Thereupon, several chemically modified acarviosin analogues, **185-190**, have been prepared and their glycosidase inhibitory activities were tested [401-404]. The results showed that the 4-amino-4,6-dideoxy moiety could be replaced by other simple structures, such as 1,6-anhydrohexoses, without losing its inhibitory power against α -glucosidase. However, modification of the valienamine portion, in order to mimic each substrate structure, did not result in any inhibitory activity against the targeted enzyme; see, for instance, compounds **189** and **190** for β -glucosidase and α -mannosidase activities, respectively (Figure 32).

Carbatriaccharide **191**, an analogue of the “trimannosyl core” which frequently occurs in biologically important glycoconjugates [405-406], was found [407] to be fully active as an acceptor for *N*-acetylglucosaminyltransferase-V, both with the enzyme isolated from hamster kidney and with the one cloned from rat kidney. The kinetic parameters were functionally equivalent with those of the *true* trisaccharide. A preparative glycosylation reaction was performed using **191** as the acceptor with the cloned rat kidney enzyme. A tetrasaccharide formed by the addition of a Glc pNAc residue (**192**) was the sole product detected (Scheme 22).

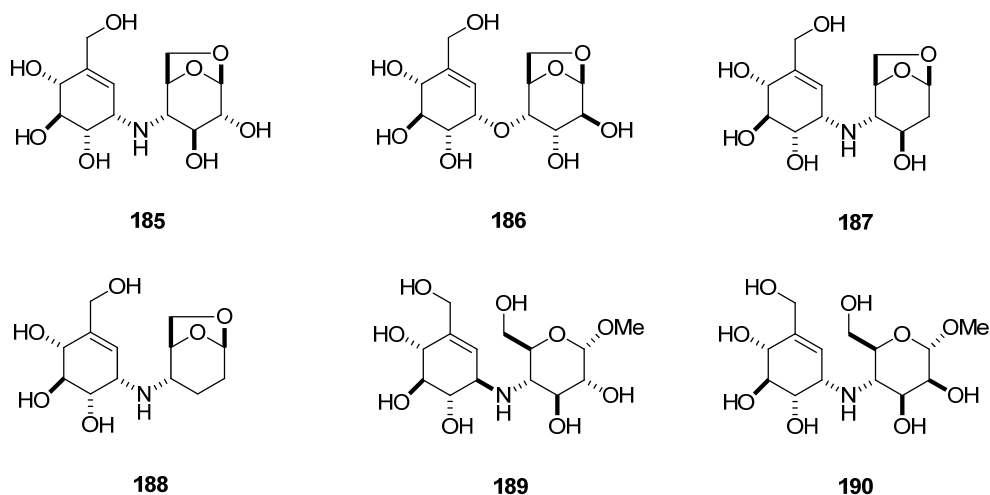
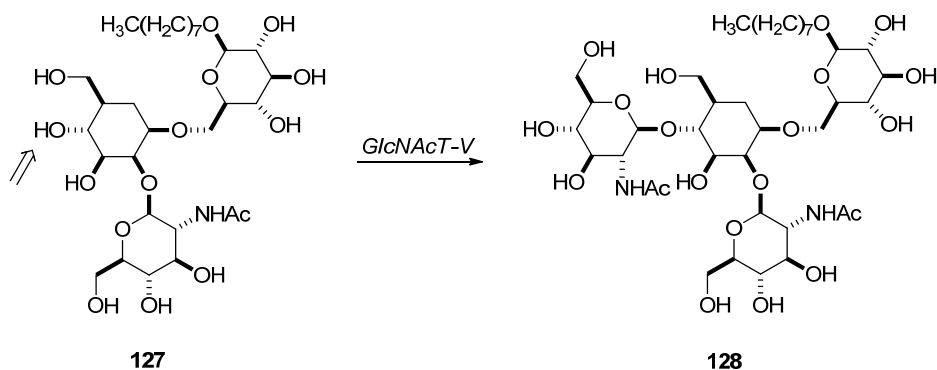


Figure 32. Acarviosine analogues **185-190**.



Scheme 22. Carbatri-saccharides **191** and **192**.

Fucosyl and sialyl transferases are involved in the synthesis of Sialyl Lewis-x, one of the most important blood group antigens, which is a tumor-associated tetrasaccharide, and ligand of *E*-selectin-mediated inflammatory extravasation of granulocytes and monocytes [408]. Fucosyl and sialyl transferases are involved in the last steps of the biosynthesis of Lewis oligosaccharide antigens by transferring α -fucopyranosyl residues [409-411]. Therefore, an area of interest is the design of potential inhibitors of these enzymes involved in the assembly of the Sialyl Lewis-x structure. In the search for inhibitors of the biosynthesis of Lewis oligosaccharide antigens, the synthesis of carbasugar analogues of the disaccharide fragment highlighted in Figure 33 was carried out by Ogawa *et al* [412-413]. They prepared ether- and imino-linked *N*-acetyl-5 α -carba- β -lactosaminides and -isolactiminides, and tested them against fucosyltransferases. Biological assays showed that compounds **193a** and **193b** (Figure 33) are acceptor substrate for human-milk α -(1 \rightarrow 3/4)-fucosyltransferase with kinetic parameters comparable to those observed for standard *true* disaccharides. Small-scale enzymatic synthesis was carried out by treatment of **193a** and **193b** with GDPfucose and milk fucosyltransferase which resulted in the conversion into the corresponding trisaccharides (by fucosylation at O3). Interestingly, compounds **194a** and **194b** were neither acceptors nor inhibitors for milk fucosyltransferase, suggesting that α -(1 \rightarrow 4) transfer is not possible. The milk preparation contains a mixture of two different [α -(1 \rightarrow 3/4)- and α -(1 \rightarrow 3)-] fucosyl transferase enzymes. These enzymes were separated, and it was shown that both forms utilized compounds **193a** and **193b** as acceptor

substrates, whereas **194a** and **194b** were not. This was the first demonstration of a specific substrate for a α -(1 \rightarrow 3)-fucosyltransferase.

In contrast with these results, screening carried out on isomeric octyl 5a-carba- β -lactosaminide (**195b**) and isolactosaminide (**196b**) (where the carbasugar unit is at the reducing end) showed that both compounds were good substrates for α -(1 \rightarrow 3)-fucosyltransferase V (human recombinant, *Spodoptera frugiperda*) as well as α -(2 \rightarrow 3)-(N) sialyltransferase (rat, recombinant, *Spodoptera frugiperda*) when compared to the parent compounds **195a** and **196a** [414].

The inhibitory activity of four new carbadisaccharides (ether-linked methyl 5a'-carba- β -lactoside (**197a**) and imino-linked methyl 5a'-carba- β -lactoside (**197b**), methyl *N*-acetyl-5a'-carba- β -lactosaminide (**197c**), and methyl *N*-acetyl-5a'-carba- β -isolactosaminide (**198**)) toward rat recombinant α -(2 \rightarrow 3)-sialyl and rat liver α -(2 \rightarrow 6)-sialyl transferases with the presence of 4-methylumbelliperyl-labeled Lac-NAc as an acceptor substrate was evaluated [415]. Compounds **197a**, **197b**, and **198** showed more inhibition for α -(2 \rightarrow 3)-sialyltransferase than for α -(2 \rightarrow 6)-sialyltransferase. In addition, the enzyme-inhibition assays showed that compound **197b** possess potent and specific inhibitory activity toward rat recombinant α -(2 \rightarrow 3)-sialyltransferase. Moreover, compounds **197b** (K_m) = 185 μ M) and **198** (K_m) = 245 μ M) presented IC_{50} values similar to that for the acceptor (K_m) = 264 μ M) toward α -(2 \rightarrow 3)-sialyltransferases, whereas compound **133c** displayed less inhibition (K_m) = 419 μ M). Surprisingly, compound **197c**, which was expected to inhibit both enzymes, did not show any appreciable inhibition toward any of them. The authors concluded from this study that the imino function enhances affinity for sialyltransferases but that when two nitrogen atoms exist, the enzymes maintain an equilibrium of interaction between them. They also established that a carbagalactose residue in carbadisaccharides may bind to sialyltransferases, but without the transfer of sialic acid.

4.2.6.3. Pylalomicins.

The pylalomicins **55-58** show activity against various bacteria, particularly strains of *Micrococcus luteus*, an opportunistic Gram-positive bacterium. The antibacterial activity of the pylalomicins appears to be dependent upon the number and the position of chlorine atoms within the molecules and the nature and methylation of the glycone [416]. That suggests a role for the cyclitol moiety in the antimicrobial activity.

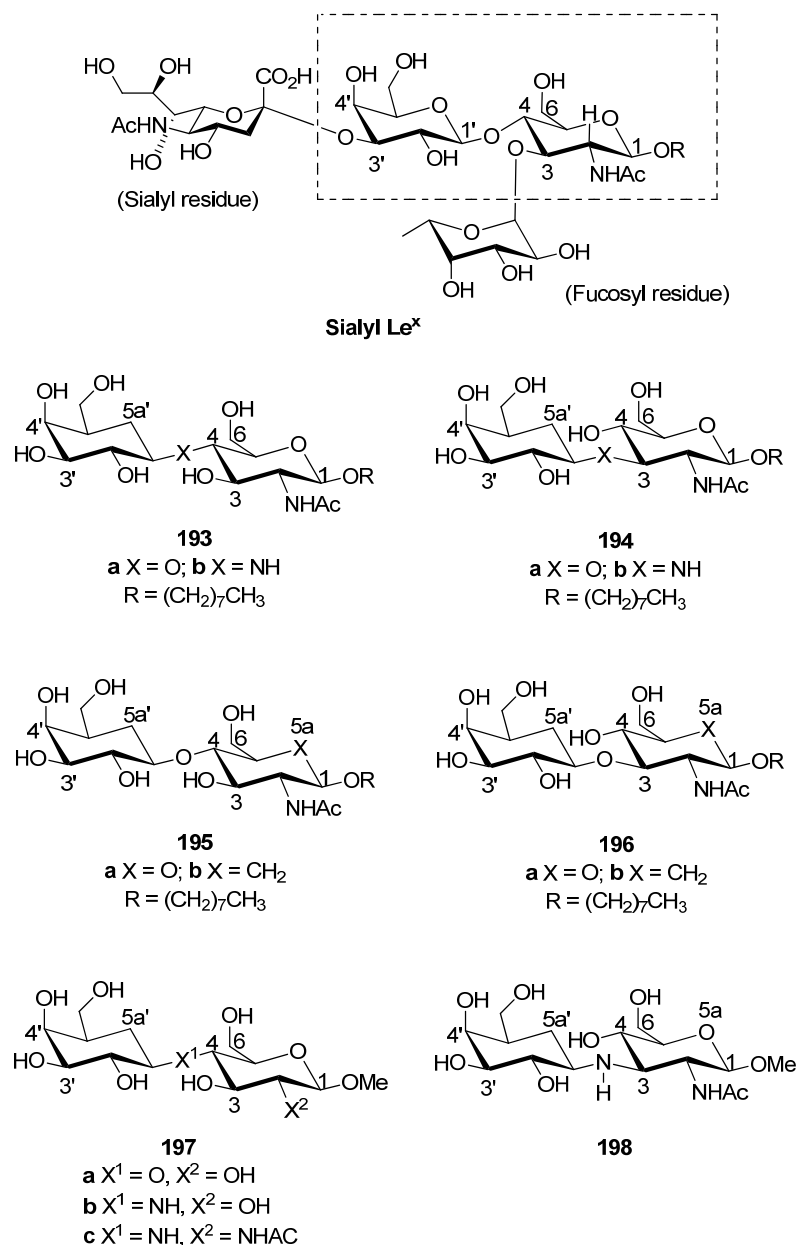


Figure 33. Carbasugars disaccharide analogues as inhibitors of fucosyl- and sialyl transferases.

5. Conclusions.

More than four decades have already elapsed since the first synthesis of a carbocyclic analogue of a carbohydrate: a *carbasugar*. Because these compounds enjoy enhanced chemical stability, the prediction was that these new compounds could replace carbohydrates in their interaction with enzymes thus showing important biological properties. This prediction has been amply confirmed and several biologically active natural products containing *carbasugars* moieties have been discovered and their biosynthesis, synthesis and biological properties were objective of different authoritative research. In addition, many synthetic analogues of these natural products have been synthesized in the search for improved biological properties. It seems fair to predict that the future holds considerable promise for advances in this area.

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Conflict of Interest.

The authors declare that there is not conflict of interests regarding the publication of this paper.

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