BIOPOLYMERS

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DEFINITION

In its general acceptation, biopolymers are polymers produced by living organisms. Two main characteristics encounter here: to be a polymer, e.g. to have repeating (monomer) units and to be produced by living organisms e.g. to be produced from a DNA (deoxyribonucleic acid) encoded information.

KEYWORDS:

DNA; RNA; polysaccharide; proteins; nucleic acids

HISTORICAL ORIGIN(S)

It was not concluded if RNA (Joyce 2002[1]) or DNA (Vreeland et al. 2000[2]; Vreeland et al. 2002[3]) acted first to replicate for life. The convenient supposition is that the prebiotic world was made by a mixture of small organic molecules (such as short-chain fatty acids and amino acids) that produced relatively short peptides (Andras & Andras 2005[4]). The emergence of proteins (as polypeptides) possibly it brought to the emergence of the encapsulated reproduction of sequences of proteins later turned into advanced function of it by developing memories of replication. The biological memories as we know are made from nucleic acids (Walker 1972[5]).

Biopolymers groups together the polymers of biological origin (see Figure 1).

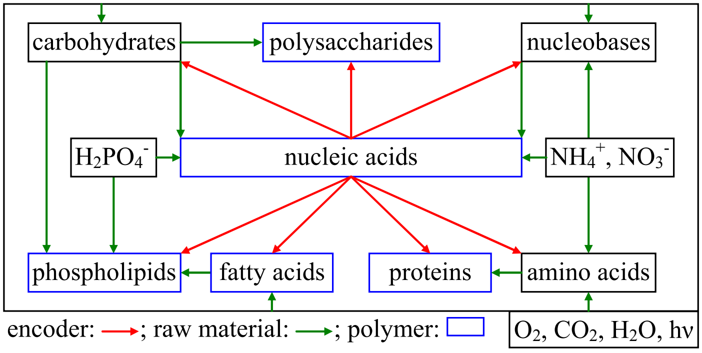


Figure 1. Biopolymers and their biosynthetic routes

In the natural context, the trophic chain is responsible for synthesis of BioPoly from simpler ones to complex ones (see Figure 2).

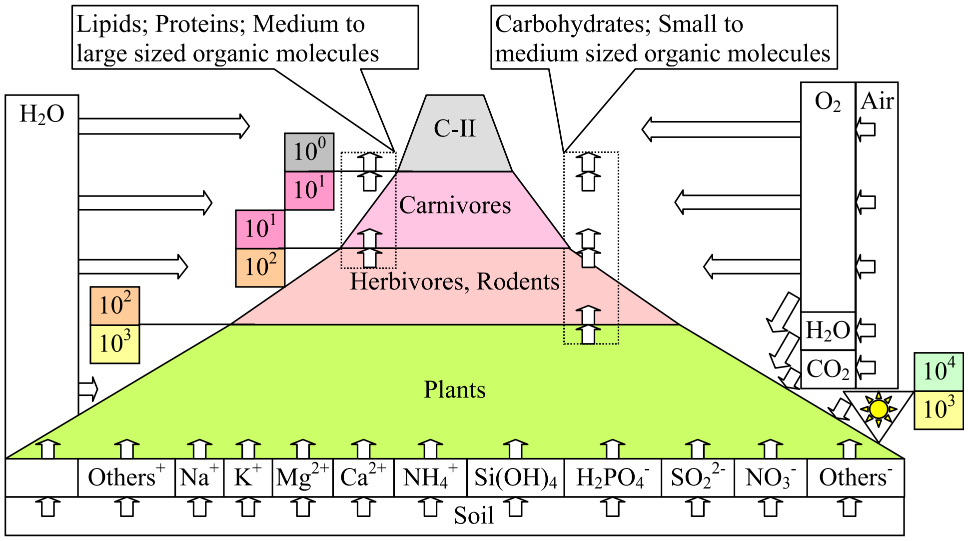


Figure 2. Trophic chain, biomass and energy conversion

It was identified about 100 amino-acids till 1966, and about 240 to 1979 (Fowden et al. 1979[6]), most having a rather restricted distribution, and many of them appear to be products of interaction of one or other of 21 classical amino acids (for lists of 21(A), 16(B), and 13(C), see Vickery 1972[7]). Other grouping include 22 being genetically encoded (Srinivasan et al. 2002[8]), which are usually contained in the human amniotic fluid (Levy & Montag 1969[9]), from which and 21 are usually found in proteins (Vickery & Schmidt 1931[10]).

NANO-SCIENTIFIC DEVELOPMENT(S)

Cytosine (C), guanine (G), adenine (A), and thymine (T) are used for building of the biological memories in DNA (deoxyribonucleic acid) and Cytosine (C), guanine (G), adenine (A), and uracil (U) - a demethylated form of thymine (T) are used for building of the biological memories in the RNA (ribonucleic acid) being paired when the nucleic acids have double strands (see Figure 3). Ccytosine (C), thymine (T), and uracil (U) are pyrimidine ($C_4H_4N_2$) derivatives.

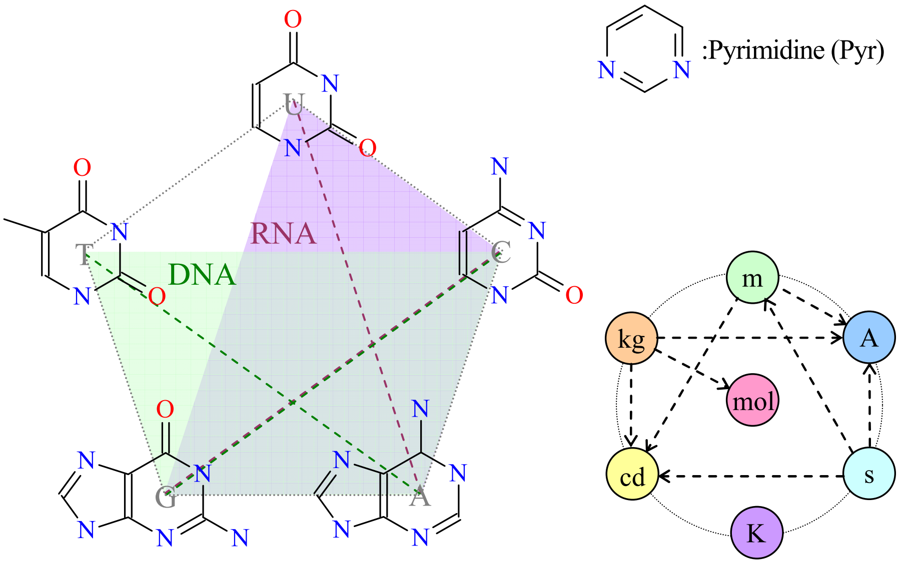


Figure 3. Nucleobases (left) and fundamental physical units (right) and their linkages

The pairing is made via two (in the case of A and T/U) or three (in the case of C and G) hydrogen bonds (see Figure 4).

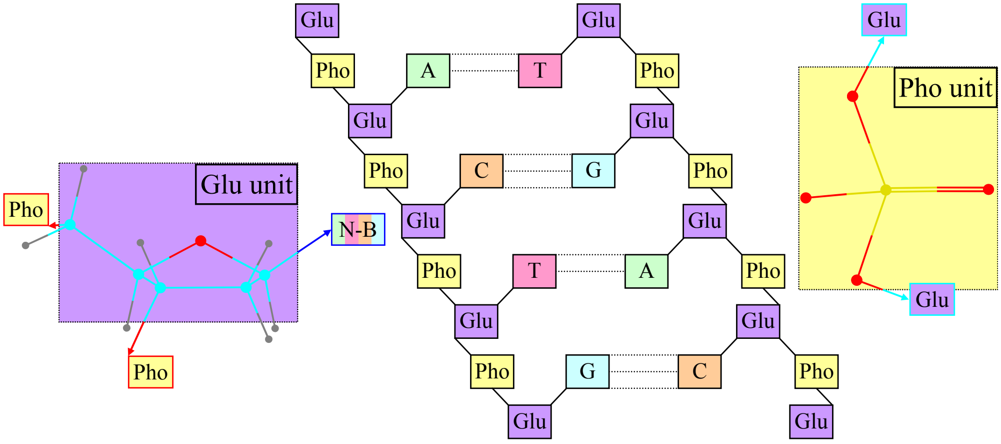


Figure 4. Pairing of the nucleobases in DNA

The presence of the double bonds (see Figure 3) produces an almost planar arrangement for the pair (see Figure 5) and the Glu-Pho strain arranges in a 3D form of a helix (see Figure 6).

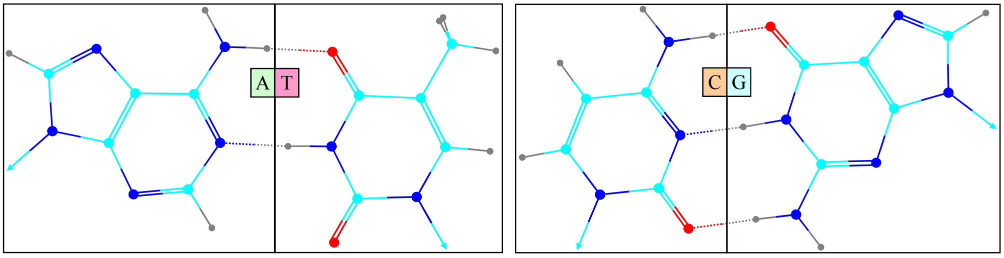


Figure 5. Bridging of the bases in DNA

The helix of the DNA (see Figure 6; for simplicity, only the phosphorus atoms were depicted to scale) was constructed from crystallographic experimental data providing the arrangement of a DNA decamer (Qiu et al. 1997[11]).

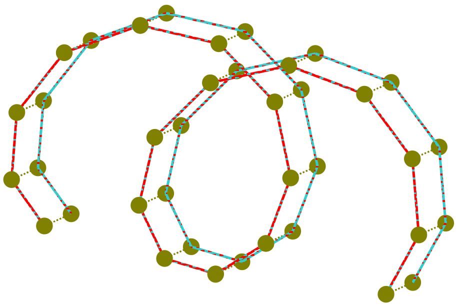


Figure 6. Helix shape of the DNA

A series of math were used in order to determine the equation(s) of the helix(es). Thus, firstly relative to its direction of the propagation, the helix can be rotated and therefore three angular variables must be used to parameterize this rotation (see Equation 1):

$x'_i = \cos(c_1)\cdot x_i - \sin(c_1)\cdot z_i$	**Equation 1.** Equations to be used to align the helix relative to a arbitrary z' axis
$y'_i = \sin(c_0)\cdot\sin(c_1)\cdot x_i + \cos(c_0)\cdot y_i + \sin(c_0)\cdot\cos(c_1)\cdot z_i$	
$z'_i = \cos(c_0)\cdot\sin(c_1)\cdot x_i - \sin(c_0)\cdot y_i + \cos(c_0)\cdot\cos(c_1)\cdot z_i$	
$x''_i = \cos(c_2)\cdot x'_i + \sin(c_2)\cdot y'_i$	
$y''_i = -\sin(c_2)\cdot x'_i + \cos(c_2)\cdot y'_i$	
$z''_i = z'_i$	

Then, the z" coordinates must be aligned on a line (first constrain in Equation 2) and the x" and y" coordinates relatively to a shift (c_4 and c_5) should be on a circle (the last two constrains in Equation 2):

$z"_i \sim c_3 + c_6 \cdot t_i$	**Equation 2.** Constrains to be used to obtain the helix equations
$x"_i \sim c_4 + c_7 \cdot \sin(2 \cdot \pi \cdot c_8 \cdot t_i)$	
$y"_i \sim c_5 + c_7 \cdot \cos(2 \cdot \pi \cdot c_8 \cdot t_i)$	

The helix parameters (c_6, c_7, and c_8), the translation shifts (c_3, c_4 and c_5) and the rotation ones (c_0, c_1 and c_2) can be determined by minimizing the residuals corresponding to constrains from Equation 2).

The DNA has a double helix shape (see Figure 4). Because of this, other series of eight parameters (from c_{0+9} to c_{8+9}) must be used to parameterize the second helix. Fortunately, the two helixes are linked (via hydrogen bonds, see Figure 2, Figure 3, and Figure 4) which allows the defining of a series of identities (see Equation 3), and thus only the translation shifts (c_3, c_4 and c_5) are actually supplementary variables to be identified.

$c_{0+9} = -c_0$	$c_{6+9} = c_6$	**Equation 3.** Identities linking the helixes equations of the DNA
$c_{1+9} = c_1 - \pi$	$c_{7+9} = c_7$	
$c_{2+9} = c_2 + \pi$	$c_{8+9} = c_8$	

By using these equations (Equation 1, Equation 2, and Equation 3) all variables (from c_0 to c_{8+9}) were identified for the data given in (Qiu et al. 1997[11]), as given in Equation 4, when explained variance was 503.97 $Å^2$, unexplained variance was 24.71 $Å^2$, and the probability of a wrong model is $p_F = 7.2 \cdot 10^{-6}$.

$c_0 = -1.74438 \cdot 10^{-2}$	$c_1 = 4.33624 \cdot 10^{-1}$	$c_2 = -9.84365 \cdot 10^{-1}$	**Equation 4.** Identified parameters for the used data to depict Figure 4
$c_9 = -c_0$	$c_{10} = c_1 - \pi$	$c_{11} = c_2 + \pi$	
$c_3 = -1.75024 \cdot 10^{1}$	$c_4 = -1.09980 \cdot 10^{1}$	$c_5 = -1.27403 \cdot 10^{1}$	
$c_{12} = -2.28491 \cdot 10^{1}$	$c_{13} = -7.15844 \cdot 10^{0}$	$c_{14} = -1.49852 \cdot 10^{1}$	
$c_6 = 2.94075 \cdot 10^{0}$	$c_7 = 9.33651 \cdot 10^{0}$	$c_8 = -1.02345 \cdot 10^{-1}$	
$c_{6+9} = c_6$	$c_{7+9} = c_7$	$c_{8+9} = c_8$	

A number of usually 20, sometimes 22 (see Table 1) amino-acids are decoded from the nucleic acids by the genetic code, when groups of three bases (a 'codon') encodes the amino-acid to be build (Crick et al. 1961[12]).

Table 1. Decoding of the amino acids from the nucleic acids

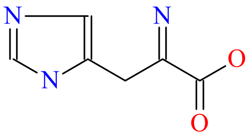
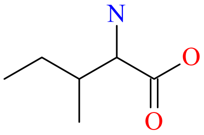
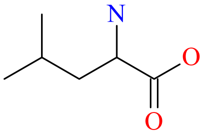
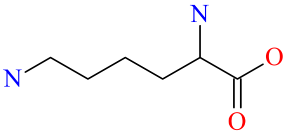
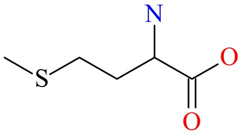
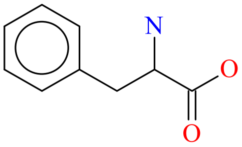
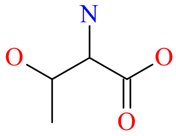
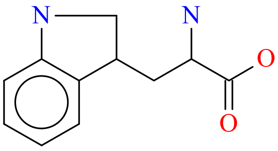
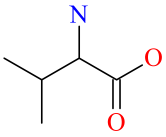
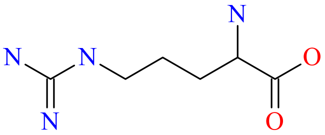
1	3\2	U	C	A	G
U	U	UUU → Phe	UCU → Ser	UAU → Tyr	UGU → Cys
	C	UUC → Phe	UCC → Ser	UAC → Tyr	UGC → Cys
	A	UUA → Leu	UCA → Ser	UAA → Xxx or Stop	UGA → Zzz or Stop
	G	UUG → Leu	UCG → Ser	UAG → Yyy or Stop	UGG → Trp
C	U	CUU → Leu	CCU → Pro	CAU → His	CGU → Arg
	C	CUC → Leu	CCC → Pro	CAC → His	CGC → Arg
	A	CUA → Leu	CCA → Pro	CAA → Gln	CGA → Arg
	G	CUG → Leu	CCG → Pro	CAG → Gln	CGG → Arg
A	U	AUU → Ile	ACU → Thr	AAU → Asn	AGU → Ser
	C	AUC → Ile	ACC → Thr	AAC → Asn	AGC → Ser
	A	AUA → Ile	ACA → Thr	AAA → Lys	AGA → Arg
	G	AUG → Met or Start	ACG → Thr	AAG → Lys	AGG → Arg
G	U	GUU → Val	GCU → Ala	GAU → Asp	GGU → Gly
	C	GUC → Val	GCC → Ala	GAC → Asp	GGC → Gly
	A	GUA → Val	GCA → Ala	GAA → Glu	GGA → Gly
	G	GUG → Val	GCG → Ala	GAG → Glu	GGG → Gly

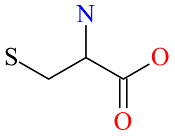
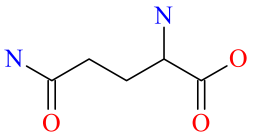
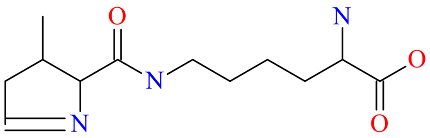
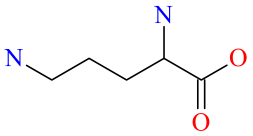
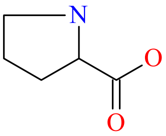
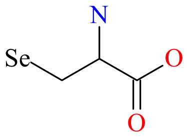
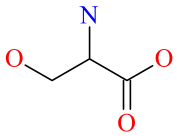
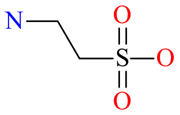
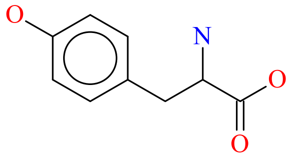
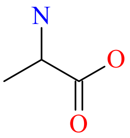
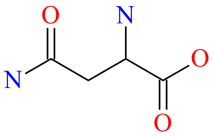
Remark: generics Xxx, Yyy, and Zzz (and Stops) are differently decoded by different ribosomes

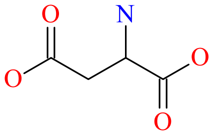
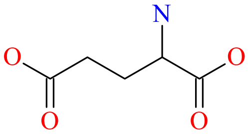
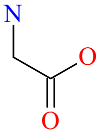
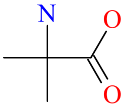
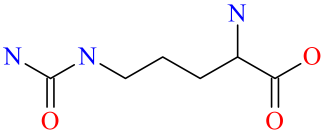
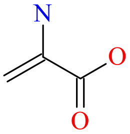
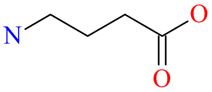
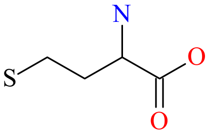
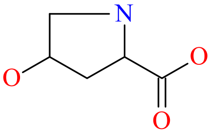
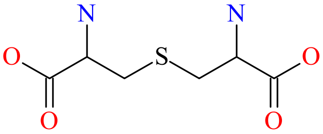
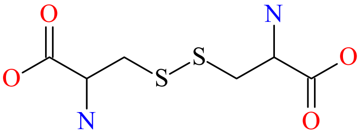
Hydrophobic interactions in cellular processes support the idea that the thermodynamic potential arising from an incompatibility of organic compounds with water is likely to be the driving force of evolution (Black 1973[13]). Thus, the hydrophobicity is responsible for a multitude of biological facts. The pK_a of Cytosine is 12.2 (primary one) and 4.5 (secondary one), for Guanine is 12.3 (primary), 9.2 (secondary), and 3.3 (amide), for Adenine is 9.80 (primary), 4.15 (secondary), for Thymine is 9.70 and for Uracil is 10.0.

A list of 32 amino acids is given in the next table (see Table 2). For further details including the hydrophobicity scales please see Bolboacă & Jäntschi 2008[14].

Table 2. A list of 32 amino acids

Name/3l/mol/use/no	2D structural formula	Remarks
Histidine His $C_6H_9N_3O_2$ E/1		Responsible for histamine biosynthesis
Isoleucine Ile $C_6H_{13}NO_2$ E/2		Almost exclusively in proteins and enzymes
Leucine Leu $C_6H_{13}NO_2$ E/3		Almost exclusively in proteins and enzymes Supplementary ref: [15]
Lysine Lys $C_6H_{14}N_2O_2$ E/4		Positive charge on the aliphatic side chain
Methionine Met $C_5H_{11}NO_2S$ E/5		Initiate protein synthesis
Phenylalanine Phe $C_9H_{11}NO_2$ E/6		Aromatic amino acid from proteins
Threonine The $C_4H_9NO_3$ E/7		Involved in porphyrin metabolism
Tryptophan Trp $C_{11}H_{12}N_2O_2$ E/8		Must be obtained from the diet (1.1%)
Valine Val $C_5H_{11}NO_2$ E/9		Hold proteins together
Arginine Arg $C_6H_{14}N_4O_2$ C/10		Present in active sites of enzymes

Name/3l/mol/use/no	2D structural formula	Remarks
Cysteine Cys $C_3H_7NO_2S$ C/11		Present in active sites and protein tertiary structure Supplementary ref: [16]
Glutamine Gln $C_5H_{10}N_2O_3$ C/12		Easily cross the blood brain barrier
Pyrrolysine Pyl $C_{12}H_{21}N_3O_3$ C/13		Biosynthesis of proteins in some methanogenic archaea and bacterium
Ornithine Orn $C_5H_{12}N_2O_2$ C/14		Role in the urea cycle
Proline Pro $C_5H_9NO_2$ C/15		Role in synthesis of collagen
Selenocysteine Sec $C_3H_7NO_2Se$ C/16		Building block of selenoproteins
Serine Ser $C_3H_7NO_3$ C/17		Present in active site of serine proteases
Taurine Tau $C_2H_7NO_3S$ C/18		Involved in bile acid biochemistry Is not a amino-acid by the definition of amino-acids Supplementary ref: [17]
Tyrosine Tyr $C_9H_{11}NO_3$ C/19		Used to build neurotransmitters and hormones
Alanine Ala $C_3H_7NO_2$ N/20		Used in the biosynthesis of proteins
Asparagine Asn $C_4H_8N_2O_3$ N/21		Used at the active sites of enzymes Supplementary ref: [18]

Name/3l/mol/use/no	2D structural formula	Remarks
Aspartic acid Asp $C_4H_7NO_4$ N/22		Intermediate in the citric acid cycle Supplementary ref: [19]
Glutamic acid Glu $C_5H_9NO_4$ N/23		Found on the surface of proteins
Glycine Gly $C_2H_5NO_2$ N/24		Acts as a neurotransmitter antagonist Supplementary ref: [15]
2-Aminoisobutyric acid Aib $C_4H_9NO_2$ O/25		Found in some antibiotics of fungal origin Supplementary ref: [20]
Citrulline Cit $C_6H_{13}N_3O_3$ O/26		Works to detoxify and eliminate unwanted ammonia Supplementary ref: [21]
Dehydroalanine Dha $C_3H_5NO_2$ O/27		Found in peptides of microbial origin Supplementary ref: [22]
γ-Aminobutyric acid Gaba $C_4H_9NO_2$ O/28		Is inhibitory neurotransmitter in the mammalian central nervous system Supplementary ref: [23]
Homocysteine Hcy $C_4H_9NO_2S$ O/29		Biosynthesized from methionine Supplementary ref: [24]
Hydroxyproline Hyp $C_5H_9NO_3$ O/30		Used in structural proteins like collagen Supplementary ref: [19]
Lanthionine Lth $C_6H_{12}N_2O_4S$ O/31		Found in bacterial cell walls Supplementary ref: [25]
Cystine - $C_6H_{12}N_2O_4S_2$ -/32		It is a site of redox reactions and a mechanical linkage allowing proteins to retain their 3D structure Supplementary ref: [26]

Legend. 3l: three letters acronym [27]; mol: molecular formula; E: essential amino acids [28]; C: essential amino acids only in certain cases [29,30]; N: nonessential amino-acids but occurs in living organisms [31]; O: other amino acids.

NANO-CHEMICAL APPLICATION(S)

A chain of the **nucleic acids** (see Figure 1 and Figure 4) alternates the Pho and the Glu units, being from this point of view a copolymer of these monomers.

Proteins (with more than 50 amino acids) and peptides (with less than 51 amino acids) have a primary structure linearly chaining the amino acids (mmdb_id 106025, pdb_id 1JXW from NCBI-protein databank depicted in Figure 7), a secondary structure stabilized by hydrogen bonds, a tertiary structure stabilized by a hydrophobic core (but also through salt bridges, hydrogen bonds, and disulfide bonds) and a quaternary structure when several protein molecules becomes subunits of a single protein complex.

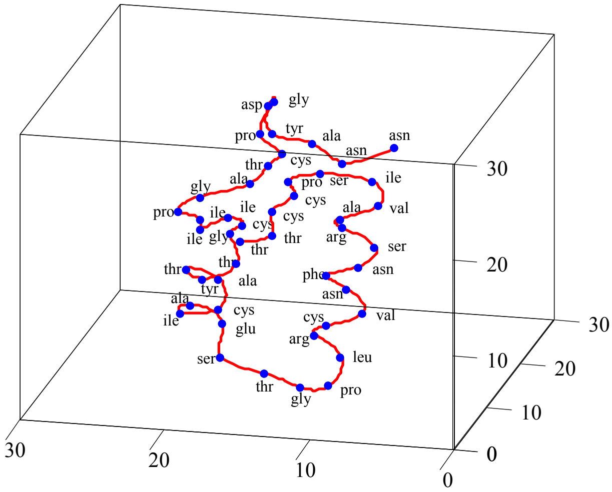
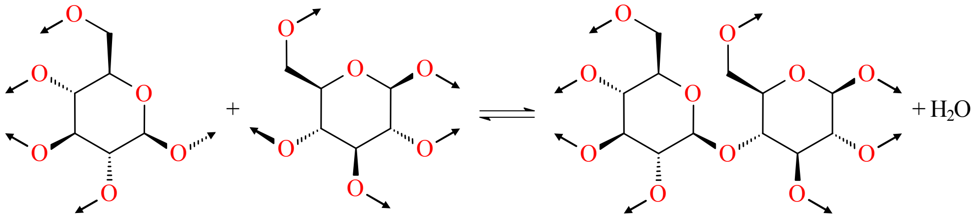


Figure 7. Protein with 47 amino acids (to scale, in Å) with ends depicted

Polysaccharides are polymers of carbohydrates in which monosaccharide units are bound from linear to highly branched, through glycosidic linkages (see Figure 8). Hydrolysis gives the constituent monosaccharides or oligosaccharides.



Legend: ⟶, ▬►, ·······► are bonds to H or to other carbohydrate (glycosidic bond)

Figure 8. Formation of the polysaccharides

With few exceptions (such as is deoxyribose, H-(C=O)-(CH_2)-($CHOH$)$_3$-H, $C_3O_4H_{10}$) monosaccharides have the molecular formula $(CH_2O)_n$, where n ranges from 2 (only one with n = 2, diose, H-(C=O)-(CH_2)-OH, $C_2O_2H_4$) to usually 7 (n = 3 triose, n = 4 tetrose, n = 5 pentose, n = 6 hexose, n = 7 heptose). The molecular structure of a monosaccharide can be written as $H(CHOH)_x(C{=}O)(CHOH)_yH$, where $x + y + 1 = n$ to have $(CH_2O)_n$ as molecular formula. The most important monosaccharide, glucose (depicted as monomeric unit in Figure 8), is a hexose. Examples of heptoses include the ketoses mannoheptulose and sedoheptulose. Monosaccharides with eight or more carbons are rarely observed as they are quite unstable. In the next table are given the monosaccharides for n from 3 to 6 (see Table 3). From n = 5 the monosaccharides are stable also in their cyclic tautomeric form (see Figure 9), the lactol being prevalent in nature against aldose, while smaller ones (e.g. n = 3 and n = 4) may cyclize by dimerization (when resulted cyclic monosaccharides have n = 6 and n = 8 respectively, see Figure 10).

Table 3. Monosaccharides from trioses to hexoses

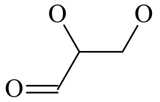
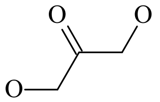
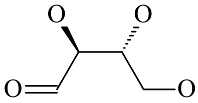
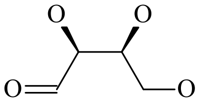
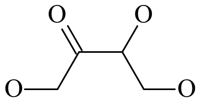
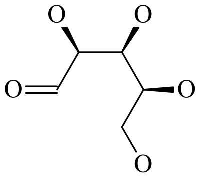
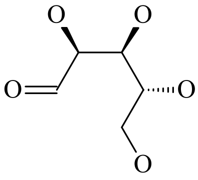
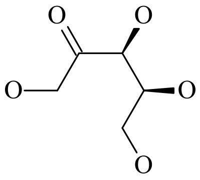
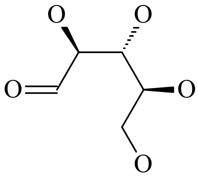
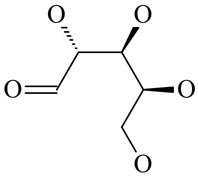
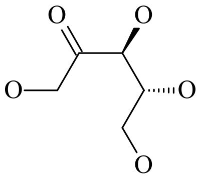
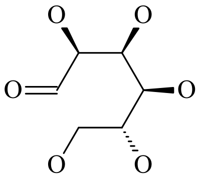
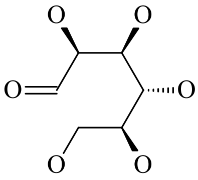
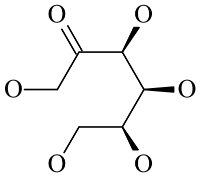
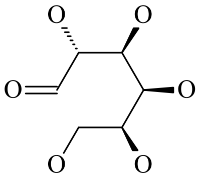
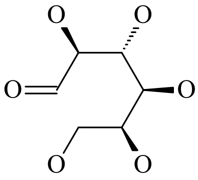
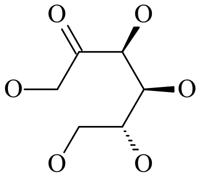
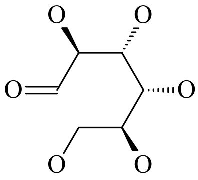
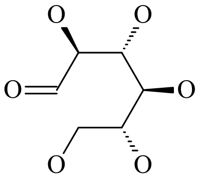
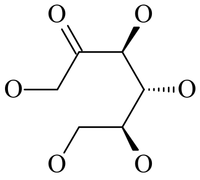
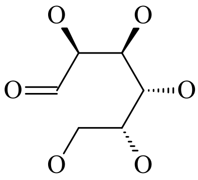
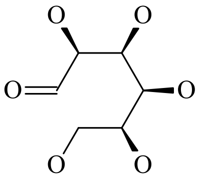
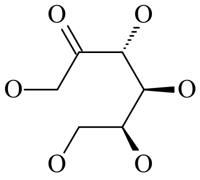
n=	Aldoses		Ketoses
3	 D-glyceraldehyde		 D-dihydroxyacetone
4	 D-erythose	 D-threose	 D-erythrulose
5	 D-ribose	 D-arabinose	 D-xylulose
	 D-xylose	 D-lyxose	 D-ribulose
6	 D-talose	 D-gulose	 D-psicose
	 D-altrose	 D-glucose	 D-tagatose
	 D-galactose	 D-idose	 D-sorbose
	 D-mannose	 D-allose	 D-fructose

Figure 9. Transition states in tautomerization of a monosaccharide (e.g. D-glucose here)

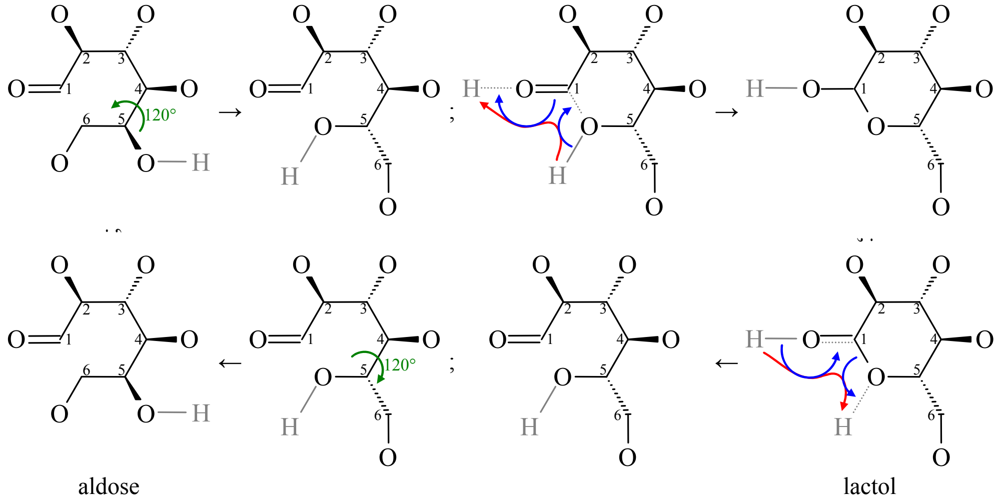
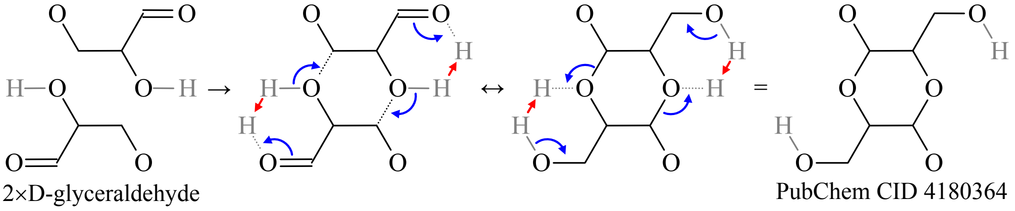
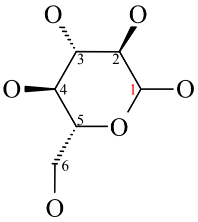
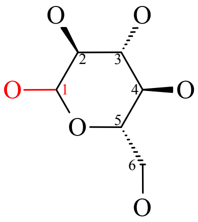
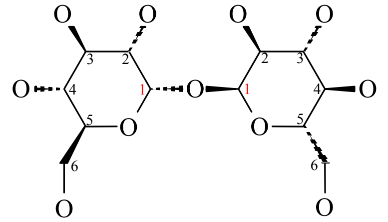
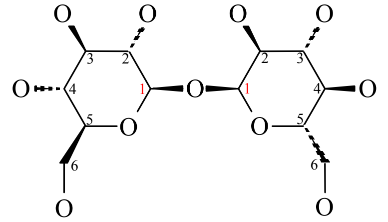
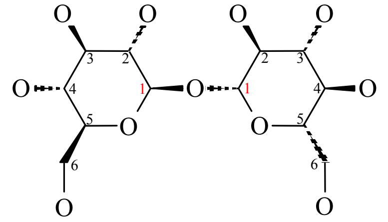


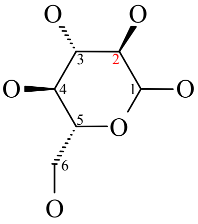
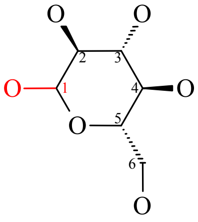
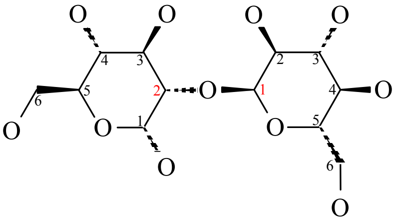
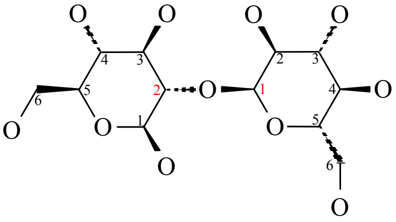
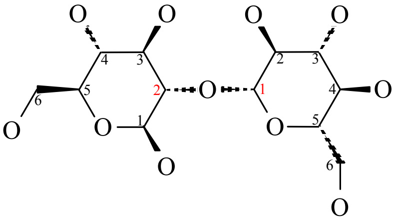
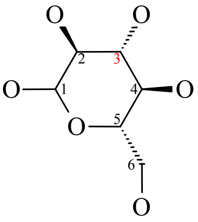
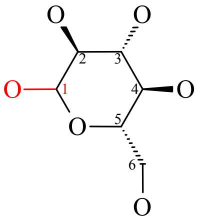
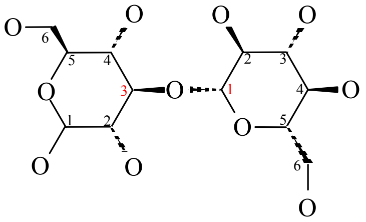
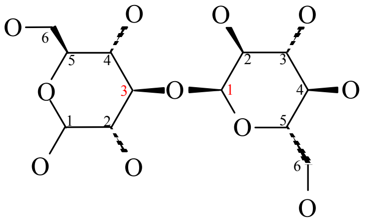
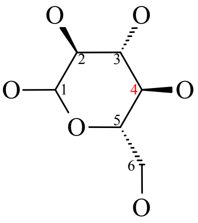
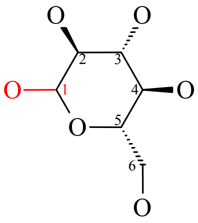
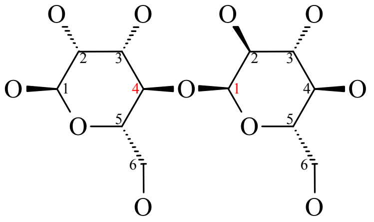
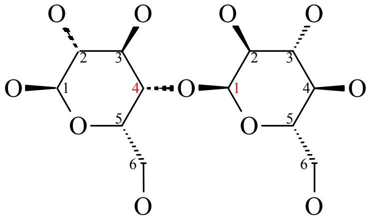
Figure 10. Dimerization & tautomerization D-glyceraldehyde

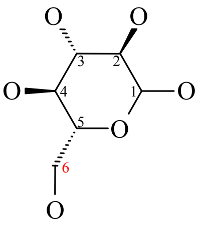
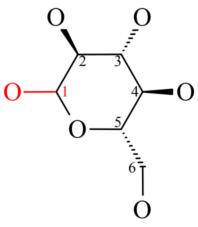
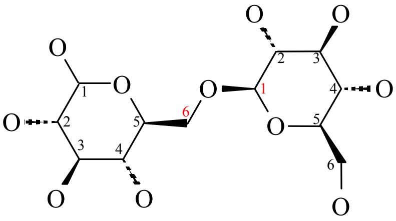
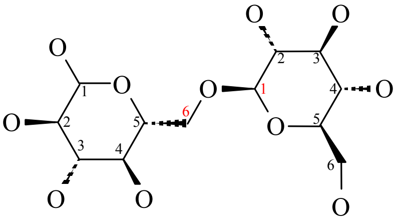


Dimers as two units of monosaccharides are the first level of polymerization in carbohydrates (monosaccharides, disaccharides, oligosaccharides, and polysaccharides). The next table gives some common encountered representatives (see Table 4; the carbons of the chain are conventionally numbered from 1 to n, starting from the end which is closest to >C=O group).

Table 4. Disaccharides condensation from units of monosaccharides (e.g. D-glucose here)

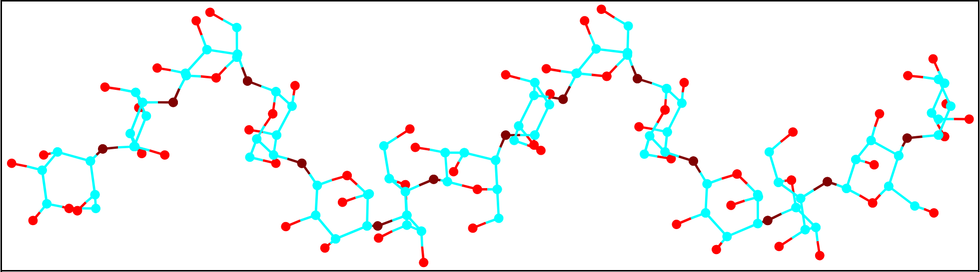
Monosaccharide 1		Monosaccharide 2		Disaccharides	Remarks
	+		→ H_2O +		2×Glucose in alpha-alpha 1-1 linkage. α,α-Trehalose
					2×Glucose in alpha-beta 1-1 linkage. α,β-Trehalose
					2×Glucose in beta-beta 1-1 linkage. β,β-Trehalose

Monosaccharide 1		Monosaccharide 2		Disaccharides	Remarks
	+		→ H_2O +		2×Glucose in alpha 1-2 linkage. α-Kojibiose
					2×Glucose in alpha 1-2 linkage. β-Kojibiose
					2×Glucose in alpha 1-2 linkage. α-Sophorose
	+		→ H_2O +		2×Glucose in beta (α,β) 1-3 linkage. Laminarabiose
					2×Glucose in alpha (α,β) 1-3 linkage. Nigerose
	+		→ H_2O +		2×Glucose in alpha 1-4 linkage. D-Maltobiose Obtained from hydrolysis of malt & starch
					2×Glucose in beta 1-4 linkage. D-Cellobiose Obtained from hydrolysis of cellulose

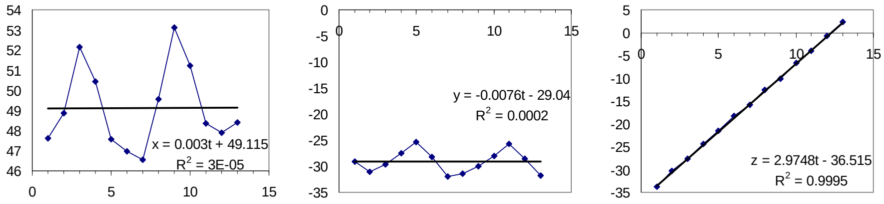
Monosaccharide 1		Monosaccharide 2		Disaccharides	Remarks
	+		→ H_2O +		2×Glucose in alpha (α,β) 1-6 linkage. Isomaltose
					2×Glucose in beta (α,β) 1-6 linkage. Gentiobiose

In the next figure (see Figure 11) a polysaccharide made from 14 units of glucose is given. The glucose units are connected together through positions 1-4 (1 to 4, see Figure 9 or Table 4) in a helix geometrical arrangement.

Figure 11. Polysaccharide of 14 units of glucose in a helix arrangement



Helix alignment (for oxygen atoms bridging the glucose units, marked in brown):
$(x'_i,y'_i) \leftarrow \text{rotate}(a_0,x_i,y_i)$; $(z1_i,x2_i) \leftarrow \text{rotate}(a_1,z_i,x'_i)$;
where: $\text{rotate}(\alpha,u,v) \leftarrow (u\cdot\cos(\alpha)-v\cdot\sin(\alpha),u\cdot\sin(\alpha)+y\cdot\cos(\alpha))$ should maximize variance on Oz' axis.
The plots of the (new) coordinates (x,y,z) vs. iteration (t) after the two rotations is given below:

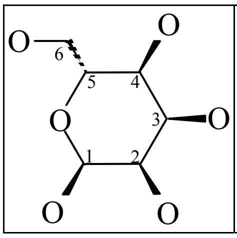


With this arrangement of the molecule, after maximization of the agreement, helix equations are:
$z \sim c_2\cdot t + c_6$; $c_2 = 2.975$ Å; $c_6 = -36.885$ Å; $t = 0..13$
$x \sim c_3\cdot\cos(2\cdot\pi\cdot c_7\cdot t + c_8\cdot 2\cdot\pi) + c_4$; $c_7 = -1.324$; $c_8 = 0.436$;
$y \sim c_3\cdot\sin(2\cdot\pi\cdot c_7\cdot t + c_8\cdot 2\cdot\pi) + c_5$; $c_3 = -0.833$ Å; $c_4 = 49.124$ Å; $c_5 = -28.910$ Å;

It should be noted that in a polymeric arrangement of the monosaccharides, the geometrical arrangement of the oxygen atoms relative to the plane of the glycosidic cycle determines the geometry of the polymer. By taking as example the glucose molecule, the topology determines four different arrangements of two glucose units, while the geometrical arrangement increases the number of isomers to twelve (see Table 4).

By taking even a simpler case, with only one glucose unit, there are 5 different positions susceptible to provide different geometrical arrangements, but not all of them equivalent, because the 5th is connected with a carbon. Calculating for four positions, $2^4 = 16$ gives each geometrical isomer twice (are 8 isomers by keeping position 5 fixed), and letting now the position 5 to be placed on one or another side of the cycle formal plane, it is arrived back to 16 geometrical isomers (see Table 5). From these ones, only half of them (8, the "D-" type ones) are listed in Table 3.

Table 5. Enumerating the isomers of glucose

	From 1 to 4 can be "a" or "b", but being "a" or being "b" is irrelevant (e.g. is the same with the one having everywhere "b" in place of "a" and vice-versa).	all 16: aaaa, aaab, aaba, aabb, abaa, abab, abba, abbb, baaa, baab, baba, babb, bbaa, bbab, bbba, bbbb.	only 8: aaaa, aaab, aaba, aabb, abaa, abab, abba, abbb.	again 16: aaaac, aaabc, aabac, aabbc, abaac, ababc, abbac, abbbc, aaaad, aaabd, aabad, aabbd, abaad, ababd, abbad, abbbd.

It should be noted that in a polymeric arrangement of the monosaccharides, the geometrical arrangement of the oxygen atoms relative to the plane of the glycosidic cycle determines the geometry of the polymer. By taking as example the glucose molecule, the topology determines four different arrangements of two glucose units, while the geometrical arrangement increases the number of isomers to twelve (see Table 4).

Polymers of monosaccharides are therefore many. The most important ones are:

- Glycogen - a branched polysaccharide of glucose serving as the main energy storage in animals and fungi (Tebb 1898[32]).
- Cellulose - a linear chain polysaccharide of glucose with the molecular formula $(C_6(H_2O)_5)_n$ from several hundred to many thousands of repeated units (Updegraff 1969[33]) is structural component of the primary cell wall of green plants, many forms of algae and the oomycetes, being the most abundant biopolymer on Earth (Klemm et al. 2005[34]).
- Starch - a part linear (amylose) part branched (amylopectin) polysaccharide of glucose serving as the main energy storage in most green plants (Payen 1839[35]).

Peptidoglycan (also known as murein) is a co-polymer of N-acetylglucosamine and N-acetylmuramic acid as alternating monosaccharides (see Figure 12). To the N-acetylmuramic acid a chain of three to five amino acids is attached (conjugation not depicted on Figure 1). Taking a mesh-like layer form outside of the plasma membrane of most bacteria, it forms a part of the cell wall (see Figure 13). Peptidoglycan is about 90% of the dry weight of Gram-positive bacteria and only 10% of Gram-negative ones, serving thus as primary determinant of the characterisation of bacteria type (Gram 1884[36]).

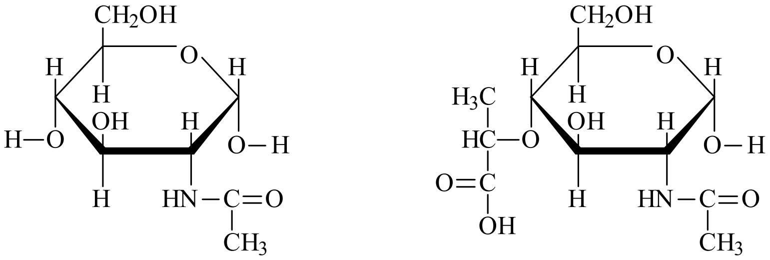


Figure 12. N-acetylglucosamine (left) and N-acetylmuramic acid (right)

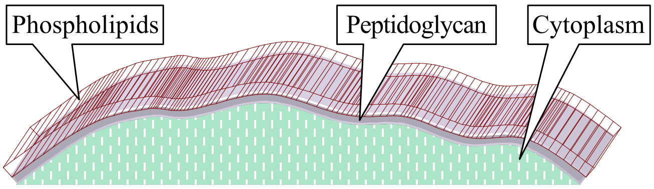


Figure 13. Two biopolymers (phospholipids and peptidoglican) creates the cells wall

The structure of a phospholipid molecule generally consists of a (hydrophilic) phosphate head and hydrophobic fatty acid (R-COO) tails (see Figure 14).

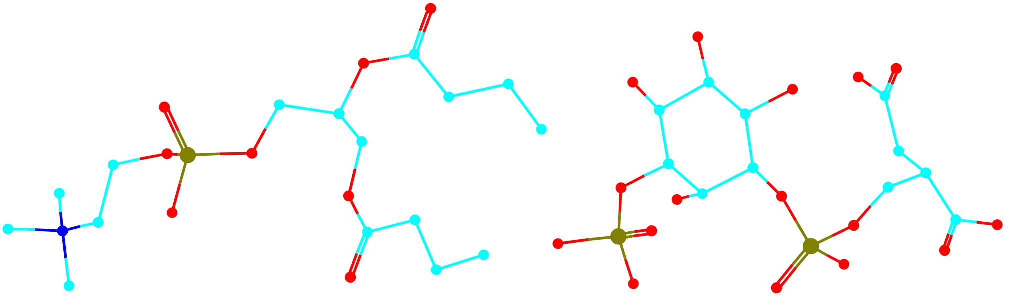


Figure 14. Dibutanoyllecithin (left) and Phosphatidylinositol 3-phosphate (right)

MULTI-/TRANS- DISCIPLINARY CONNECTION(S)

A series of biopolymers based bio-composites are synthesized by the living organisms and are currently used as is or with minimal chemical treatment, the following list including only the most common ones:

÷ Latex, as stable water based emulsion of 30-45% (see Jacob et al. 1993[37]) isoprene polymers with minor impurities of other organic compounds is found mostly in *Magnoliopsida* class of land plants (see Metcalfe 1967[38]). Rubbers, as its thermal treatment with sulfur (or vulcanization) were patented in 1839 (Hayward 1838[39]).

÷ Guncotton, obtained nitrating cellulose through exposure to nitric acid were discovered in 1833 (see Braconnot 1833[40]), later plasticized with camphor as celluloid (see Parkes 1855[41]).

÷ Casein which is about 80% of the proteins in cow milk simply treated with caustic-alkali solution (Spitteler 1899[42]), and later plasticized with formaldehyde as galalith (Siegfeld 1904[43]).

÷ Polylactide is derived from corn starch, tapioca roots, chips, starch or sugarcane, the polymerization of the lactide being favored by the presence of potassium carbonate (Carothers et al. 1932[44]).

÷ Wool contains up to 90% keratin (Cardamone et al. 2005[45]), a member of scleroprotein group shaped like rods or wires. Silk contains two main proteins, sericin and fibroin (Hakimi et al. 2007[46]).

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Sun passes the sky from east to west, and it is possibly responsible for the selectivity of the bio-synthesizers among chiral molecules. Thus, the D-isomer (D-glucose), also known as dextrose, occurs widely in nature, but the L-isomer (L-glucose) does not.

The appearance of the biological organisms is at conjunction of a series of coincidences from at least are the earth's mass, its position in the biologically suitable region and possibly to the presence of the moon, involved in tides, a natural way of producing cyclic movements of a chemical equilibrium.

The worlds of prebiotic chemistry and primitive biology lie on opposite sides of the defining moment for life, when darwinian evolution first began to operate (Fig. 1). Before that time, chemical processes may have led to a substantial level of complexity. Depending on the nature of the prebiotic environment, available building blocks may have included amino acids, hydroxy acids, sugars, purines, pyrimidines and fatty acids. These could have combined to form polymers of largely random sequence and mixed stereochemistry (handedness). Some of the polymers may have had special properties, such as adherence to a particular mineral surface, unusual resistance to degradation, or the propensity to form supramolecular aggregates. Eventually every polymer, no matter how stable, would have succumbed to degradation.

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