Comparisons of N-glycans across invertebrate phyla

Katharina Paschinger and Iain B. H. Wilson

Department für Chemie, Universität für Bodenkultur, 1190 Wien, Austria

Abstract

Many invertebrates are either parasites themselves or vectors involved in parasite transmission; thereby, the interactions of parasites with final or intermediate hosts are often mediated by glycans. Therefore, it is of interest to compare the glycan structures or motifs present across invertebrate species. While a typical vertebrate modification such as sialic acid is rare in lower animals, antennal and core modifications of N-glycans are highly varied and range from core fucose, galactosylated fucose, fucosylated galactose, methyl groups, glucuronic acid and sulphate through to addition of zwitterionic moieties (phosphorylcholine, phosphoethanolamine and aminoethylphosphonate). Only in some cases are the enzymatic bases and the biological function of these modifications known. We are indeed still in the phase of discovering invertebrate glycomes primarily using mass spectrometry, but molecular biology and microarraying techniques are complementary to the determination of novel glycan structures and their functions.

Introduction

The co- or post-translational addition of glycans to proteins takes various forms in all kingdoms of life (Varki, 2011); amongst the most common is N-glycosylation, by which asparagine residues are modified. In eukaryotes, most commonly a Glc3Man9GlcNAc2 precursor is transferred from dolichol to proteins in the endoplasmic reticulum (Aebi, 2013); however, some protists utilise shorter precursors or even do not N-glycosylate at all (Samuelson et al., 2005). The fates of protein-linked N-glycans are varied and depend on the types of glycosidases and glycosyltransferases expressed in the Golgi apparatus. It is this variability that makes glycan analysis a challenge, as so many possibilities occur by which N-glycans are trimmed and then built up again.

Other than the first steps in the endoplasmic reticulum, the final size and form of N-glycans differ between protists, fungi, plants and animals (whether invertebrate or vertebrate), although some modifications are found in more than one of these groups of organisms. Unlike plants whose N-glycomes are similar from mosses through to Arabidopsis, there is high variability between non-vertebrate eukaryotes (Schiller et al., 2012). Here, we will concentrate on primarily structural aspects of invertebrate N-glycans, not only due to the parasitological relevance (as many invertebrates are either hosts, vectors or themselves parasites), but also because only recently have mass spectrometric analyses revealed a previously unrealised range of modifications, some of which are shared with O- and lipid-linked glycans. A few years ago, one would probably have read that invertebrates only produce oligomannosidic (Manα1,2GlcNAc2) and paucimannosidic (Manα1,4GlcNAc2Fucα2,3) N-glycans (Williams et al., 1991); this may be due to insensitive methods and low expectations, but it is now known that even complete glycomes of some mammalian cell types are dominated by oligomannosidic forms present within the secretory pathway (Hamouda et al., 2014).

Oligomannosidic N-glycans

Even within the glycans containing primarily mannose residues (hence oligomannosidic or high mannose), there is variation arising from the different orders of processing by so-called class I α1,2-mannosidases, also in parasitic metazoa. Most eukaryotes have multiple forms of these α1,2-mannosidases (Wilson, 2012), which also include enzymes known as EDEMs (ER degradation-enhancing α-mannosidases) acting as part of the quality control pathway in the endoplasmic reticulum. The result is that there are multiple isomers of oligomannosidic structures (e.g. three isomers of glycans with the composition Manα1GlcNAc2β, Fig. 1) just depending on which mannosidase acts first on particular terminal mannose residues; the final product is the ‘Golgi’ isomer of Manα1GlcNAc2β. These structures can be differentiated by, e.g. RP-HPLC in combination with MS/MS and thus it is only appropriate to annotate specific isomers based on such information; for instance, a Hexα1HexNAc2 structure could also be Glcα1Manα1GlcNAc2β and not necessarily one of three typical forms of Manα1GlcNAc2β. Oligomannosidic glycans may also be the ‘final’ processed forms in the cases where protein folding prevents a specific glycosylation site from being accessible to enzymes in the Golgi apparatus (Thaysen-Andersen and Packer, 2012). On the basis of the universality of oligomannosidic glycans in metazoa,
it is not surprising that these glycans have been observed in a wide range of invertebrates including trematodes, nematodes, molluscs and insects.

Hybrid and pseudohybrid N-glycans

The classical 'hybrid' structure is a 'Golgi-type' Man₅GlcNAc₂ modified on the 'lower' α1,3-mannose by β1,2-specific N-acetylgalactosaminyltransferase I (GlcNAc-TI) which generates a 'hybrid' structure which can be further modified by the action of Golgi mannosidase II, GlcNAc-TII and Golgi hexosaminidase. The maximum number of antennae (three or four) depends on the presence of GlcNAc-TIV and GlcNAc-TV; example hybrid, pseudohybrid, paucimannosidic and tri-/tetra-antennary glycans are shown as known from various model, host, vector or parasitic invertebrates. For simplicity, fucosylation and other modifications are not included. Glycans are depicted according to the Standard Nomenclature for Glycans (see also box).

Fig. 1. Simplified biosynthetic scheme for N-linked glycans in animals. Starting with the Glc₃Man₉GlcNAc₂ precursor, various glycosidases result in different isomers of oligomannosidic glycans with the maximal degree of processing by class I mannosidases yielding Man₅GlcNAc₂. This is the substrate for N-acetylgalactosaminyltransferase I (GlcNAc-TI) which generates a 'hybrid' structure which can be further modified by the action of Golgi mannosidase II, GlcNAc-TII and Golgi hexosaminidase. The maximum number of antennae (three or four) depends on the presence of GlcNAc-TIV and GlcNAc-TV; example hybrid, pseudohybrid, paucimannosidic and tri-/tetra-antennary glycans are shown as known from various model, host, vector or parasitic invertebrates. For simplicity, fucosylation and other modifications are not included. Glycans are depicted according to the Standard Nomenclature for Glycans (see also box).
The lower arm β1,2- and β1,4-GlcNAc residues on hybrid glycans can be modified in different ways; elongation by β1,4-N-acetylglactosamine and β1,3- or β1,4-galactose are known in insects, molluscs, nematodes and trematodes, whether these be host or parasitic organisms (Nyame et al., 1989; Kurz et al., 2013, 2015; Martini et al., 2019; Smit et al., 2015). If however, GlcNAc-TII acts and then the ‘lower’ arm β1,2-GlcNAc, transferred by GlcNAc-TI, is removed by a Golgi hexosaminidase such as fdl (fused lobes) in insects or HEX-2 in nematodes (Gutternigg et al., 2007b; Geisler and Jarvis, 2012), then the resulting glycans can be referred to as ‘pseudo hybrid’. Such structures are also found in protist parasites lacking GlcNAc-TI, but having GlcNAc-TII-like enzyme activities (Paschinger et al., 2012b; Damerow et al., 2014). The core of hybrid glycans in animals can also be modified, most commonly by α1,6-fucose.

### Paucimannosidic N-glycans

The term ‘paucimannosidic’ glycans was introduced to cover those glycans which have been processed sequentially by GlcNAc-TI, Golgi mannosidase II and a Golgi hexosaminidase to result in Man$_{a}$,GlcNAc$_{b}$ (Gutternigg et al., 2007b). Such structures are well known in invertebrates and plants, but also occur due to the action of acidic glycosidases on glycoproteins in the secretory granules in some mammalian cells (Loke et al., 2017). A significant portion of paucimannosidic glycans are core fucosylated and carry the ‘mammalian-like’ α1,6-fucosyl and the ‘plant-like’ α1,3-fucosyl either alone or in combination on the reducing-terminal (proximal) GlcNAc of the core region of the N-glycan as found first on bee venom glycoproteins (Kubelka et al., 1993). In nematodes, the second (distal) GlcNAc can also be modified (Haslam et al., 1996; Hanneman et al., 2006).

Both proximal core α1,3-fucose and substitution of the β-mannose by β1,2-xylose (see Fig. 2 for example structures) are immunogenic in mammals and antibodies raised against plant and invertebrate glycoproteins often recognise these epitopes, the best known example of which is anti-horseradish peroxidase (anti-HRP); both structural elements are epitopes for IgE or IgG and invertebrate glycoproteins often recognise these epitopes, the best known example of which is anti-horseradish peroxidase (anti-HRP).

### Modified N-glycan cores

In addition to fucosylation and xylosylation, some invertebrates attach further monosaccharide units to the basic paucimannosidic core. Recently joining the list of core modifications alongside galactosylation of core α1,6-fucose (‘GalFuc’), first detected in squid and then in keyhole limpet, planaria and nematodes (Takahashi et al., 2004; Wuhrer et al., 2004; Titz et al., 2009; Paschinger et al., 2011; Subramanian et al., 2018), are α-galactosylation of the proximal and distal core α1,3-fucose residues (Yan et al., 2018a), elongation of the GalFuc unit by galactose (Wuhrer et al., 2004; Subramanian et al., 2018), fucose (Yan et al., 2015b), phosphorylcholine or methylaminophosphonate (Eckmair et al., 2016), β-mannosylation of the proximal GlcNAc (Eckmair et al., 2016; Hykollari et al., 2018) and the galactosylation of the core β-mannose to form a bisected structure, which can also be modified by methylated or nonmethylated fucose (Yan et al., 2015a) (Fig. 2). While the latter bisecting modifications have only been found in the non-parasitic nematode Caenorhabditis elegans, the zwitterionic modifications of the GalFuc have been detected uniquely in a marine gastropod; however, galactosylation of the proximal α1,6-fucose and distal α1,3-fucose residues has also been found in the parasitic nematodes Oesophagostomum dentatum and Haemonchus contortus (Paschinger and Wilson, 2015; Sutov, 2016; Jiménez-Castells et al., 2017).

Some of the reason for the apparent restriction in what is found might be methodological. For instance, the presence of α-galactose on the proximal α1,3-fucose was only detected in C. elegans when using hydrazine or the newly-developed PNGase A enzyme to release the N-glycans, whereby the maximal degree of core fucosylation in this worm (five fucoses) was only found after hydrazinolysis (Yan et al., 2018a). Only in the case of O. dentatum can we say that these modifications are absent, since hydrazinolysis was also performed with samples from this organism and MS/MS did not reveal any glycan with the relevant fragmentation pattern (Jiménez-Castells et al., 2017). On the other hand, H. contortus glycans were only ever analysed after ‘classical’ PNGase F and A digestion and so it can only be speculated as to whether it shares more complex cores with C. elegans.

The enzymatic basis for only some of these modifications is known. Three core-modifying α-fucosyltransferases (FUT-1, FUT-6 and FUT-8) are known from C. elegans as is the α1,6-fucose-modifying GALT-1 galactosyltransferase from the same organism (Paschinger et al., 2004, 2005; Titz et al., 2009; Yan et al., 2013). The in vitro activity data is complemented by glycomic studies on mutants showing the absence of the relevant epitopes (Butschi et al., 2010; Yan et al., 2015b). Some of these glyco-mutants have altered susceptibility to nematotoxic fungal lectins (Butschi et al., 2010; Schubert et al., 2012), which are also toxic to H. contortus (Heim et al., 2015). For all the other modifications around the core, e.g. the addition of various α-galactose residues or of bisecting β-galactose in C. elegans we have no clues as to which enzymes may be responsible. The same lack of knowledge applies to β-mannosylation of the proximal core GlcNAc in molluscs and insects.

### Complex N-glycans

The definition ‘complex N-glycan’ is based on the knowledge of mammalian glycosylation and refers to glycans with at least one GlcNAc modifying both α-mannose residues of the trimannosyl core. Thus, both GlcNAc-TI and -TII (MGAT1 and MGAT2) have acted and these can be supplemented by GlcNAc-TIV, GlcNAc-TV and in some species ‘GlcNAc-TV’ (Schächter, 1986). The other common N-acetylgalactosaminyltransferase, GlcNAc-TIII, is a bisecting enzyme found in vertebrates. The result of the action of these various enzymes (see Fig. 1) is the various b1-, tri- and tetrantennary glycans (even penta-antennary in birds and fish), which are well known from the serum glycories of mammals.

It may come as a surprise that even relatively primitive animals have tri- or tetra-antennary N-glycans as found in Hydra, molluscs, insects and nematodes (Kang et al., 1993; Morelle et al., 2000; Kurz et al., 2013, 2015; Sahadevan et al., 2014; Eckmair et al., 2016). The exact nature of the tri-antennary glycans varies, as GlcNAc-TIV products occur in molluscs and insects (Kurz et al., 2013, 2015), but GlcNAc-TV acts in glycan biosynthesis in a number of nematodes such as C. elegans and Pristionchus pacificus (Yan et al., 2015c). Other nematodes, though, do have

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both GlcNAc-TIV and -TV homologues and so can have up to four branches on their N-glycans as found in filarial species or in *Trichinella* (Haslam et al., 1999; Kang et al., 1993; Morelle et al., 2000; Martini et al., 2019). Amongst trematodes, triantennary glycans have been long established to exist in *S. mansoni* males (Nyame et al., 1989); it has also been suggested that up to four branches may also be on N-glycans of *S. mansoni* eggs or in *Opisthorchis viverrini* (Talabnin et al., 2013; Smit et al., 2015); however, as in another trematode *Fasciola hepatica* (McVeigh et al., 2018), BLAST searching of the available genomes only shows an obvious GlcNAc-TV homologue and none of GlcNAc-TIV (unpublished data).

Subsequent to the initial transfer of up to four non-reducing terminal GlcNAc residues, further elongation events can occur and these are extremely variable and, in non-vertebrates, include substitutions with \(\beta_1,3\)-galactose, \(\beta_1,4\)-N-acetylgalactosamine, \(\alpha_1,4\)-N-acetylgalactosamine or fucose as well as anionic, zwitterionic or methyl groups (Fig. 2). The typical mammalian form \(\beta_1,4\)-galactosylation is not so widespread in lower animals in general, but it can, e.g. be found in *Schistosoma* spp. (Khoo et al., 1997; Smit et al., 2015); it can only be distinguished from \(\beta_1,3\)-galactosylation by use of specific galactosidases and, if amounts allow, by NMR spectroscopy or GC-MS methods.

Fig. 2. Example N-glycans from invertebrates. Structures are depicted from either parasitic or free-living organisms, whereby some of the latter are hosts or vectors for parasites. Some types of structures are species- or class-specific, but others are found in more than one phylum. Only a non-exhaustive selection of core and antennal epitopes is shown in the inset: core difucosylation, core 'GalFuc', Lewis X (LeX), fucosylated and non-fucosylated LacdiNAc (LDN) and blood group A (BGA). (A) The bisecting and distal core modifications found in the free-living *C. elegans* are indicated by pink boxes; (B) free-living *C. elegans*, the necromenic *P. pacificus* and the parasites *H. contortus*, *H. polygyrus* and *O. dentatum* express di- and/or tri-fucosylated cores with species-specific galactosylation and methylation; (C) varying antennal modifications are found in all nematodes as well as the cestodes *E. granulosus* and *T. crassiceps*, (D) while filarial species have up to four long antennae including *D. immitis*, which has in addition glucuronoylated structures; (E) galactosylated core fucose ('GalFuc') is found in many invertebrates, sometimes in substituted form; (F, G and H) selected complex glycans from larval of different insect phyla; (I) selected *S. mansoni* N-glycan modifications which are partly stage-specific; (J, K and L) selected gastropod and bivalve glycans, including those of *Crassostrea virginica*, *B. glabrata*, *Volvarina rubella* and *Mytilus edulis*. Note that some modifications, such as core \(\beta\)-mannosylation, are at low abundance in the relevant glycomes. Glycans are depicted according to the Standard Nomenclature for Glycans; undefined hexoses/N-acetylhexosamines are shown as white circles/squares. Me, methyl; MAEP, N-methyl-aminoethylphosphonate; PC, phosphorylcholine; PE, phosphoethanolamine (2-aminoethylphosphate); S, sulphate. Broken lines, bars or brackets indicate structure-, species- or stage-dependent variations in these elements.

1736 Katharina Paschinger and Iain B. H. Wilson

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mosquitoes acting as intermediate hosts for parasites and viruses (Kurz et al., 2015) and β1,3-Gal is also found in the oyster Crassostrea virginica, which is a host for the Perkinsus marinus protist parasite (Kurz et al., 2013). On the other hand, GalNACβ1,4GlcNAc (LacdiNac) is a known motif from various insects and nematodes (see also the section on fucosylated antennae below) and a stage-specific bias in its expression is known from trematode parasites (Talabni et al., 2013; Smit et al., 2015). Longer chito-based (GlcNAcβ1,4GlcNAc) antennae are a feature of filarial nematodes as well as of H. contortus and O. dentatum (Haslam et al., 1999; Sutov, 2016; Jiménez-Castells et al., 2017; Martini et al., 2019).

For some of these terminal modifications, the relevant enzymes have been identified and characterised in recombinant form, such as β1,4-N-acetylgalactosaminyltransferases from C. elegans and Trichoplusia ni, a β1,3-galactosyltransferase from the honeybee and an α1,4-N-acetylgalactosaminyltransferase from Drosophila (Kawar et al., 2002; Mucha et al., 2004; Vadaie and Jarvis, 2004; Ichimiya et al., 2015). However, although some relevant enzyme activities have been detected in crude extracts, the identities of relevant genes in parasites are yet to be established.

### Antennally fucosylated N-glycans

Fucose as a deoxysaccharide rather than a standard hexose may well, due to its chemical properties, be pre-destined to act as a recognition element. Indeed, fucose is the basis for mammalian histoblood group antigens such as ABO and Lewis motifs (Fig. 2). Fucosylated LacNAc (Leβ) and LacdiNac (LDNF) epitopes are well known from S. mansoni (Kho et al., 1997; Wuhrer et al., 2006; Smit et al., 2015) and may contribute to the lectin-dependent immunomodulatory activity of secreted schistosome proteins (Willers et al., 2017). Also, some nematodes (e.g. Dictyocaulus viviparus, Trichuris suis or H. contortus) and insects (e.g. the honeybee) express these epitopes (Kubelka et al., 1993; Haslam et al., 2000; Pasching and Wilson, 2015; Wilson and Pasching, 2016), while fucosylated chito-oligomers are a feature of the antennae of some N-glycans from Diofilaria immitis (Martini et al., 2019) and Fucol1,3GlcNAc as a terminal motif is also known from the cestode Taenia crassiceps (Lee et al., 2005). Less familiar may be the occurrence of blood group A on oyster glycans (Kurz et al., 2013), which are probable ligands for noroviruses in the marine environment, but which are also recognised by the oyster’s own galectins (Feng et al., 2013). Interestingly, though, these galectins also mediate entry of P. marinus into oyster haemocytes, despite the apparent lack of blood group antigens on the parasite.

Generally, fucose on glycan antennae is unsubstituted, but branched fucose (i.e. disubstituted) is known in some molluscs (Zhou et al., 2013; Eckmair et al., 2016) and fucosylated fucose (Fucol2,Fucol3) occurs in S. mansoni (Jang-Lee et al., 2007; Smit et al., 2015) (Fig. 2). Interestingly, the various fucosylated antennal modifications of S. mansoni are epitopes for various natural and monoclonal antibodies (van Remoortere et al., 2000; van Diepen et al., 2012) and may mediate interactions of parasitic proteins with cells of the host immune system (Meevissen et al., 2012). The schistosome genome encodes a number of fucosyltransferases, but only one has proven enzymatic activity in recombinant form, specifically as a Leα synthase (Mickum et al., 2016b).

Other defined invertebrate Lewis-type fucosyltransferases include the FucTC from the honeybee and a mosquito (Kurz et al., 2016; Rendić et al., 2007).

### Methylated N-glycans

Substitution of glycans by methyl groups is known in bacteria, plants and invertebrates. In the case of N-glycans from mollusc, planaria and free-living or parasitic nematodes, examples include methylation of mannose, fucose, galactose and N-acetylgalactosamine residues (van Kuik et al., 1986, 1987b; Gutternigg et al., 2007a; Paschingher et al., 2011; Kurz et al., 2013; Hewitson et al., 2016; Jiménez-Castells et al., 2017; Yan et al., 2018a) (Fig. 2). If analysing the glycans using standard permethylation conditions, such natural methyl groups are lost; thus, perdeuteromethylation has to be employed (Wohlshlager et al., 2014). For standard exoglycosidase sequencing, methylation normally prevents removal of a residue, but the methylated GalNAC on oyster glycans could be removed with chicken α-N-acetylgalactosaminidase (Kurz et al., 2013), while methylated α1,2- or α1,3-fucose residues on nematode glycans can be partially or fully released by hydrofluoric acid treatment (Yan et al., 2018a). The type of methylation can also vary within a species, as methylation of mannose was more common in male O. dentatum parasites as opposed to the methylfucose residues found in the female (Jiménez-Castells et al., 2017).

### Glucuronylated and sialylated N-glycans

By separating neutral from anionic glycans early in the analyses, we have been able to find glucuronic acid on the termini of N-glycans from a number of species, including mosquitoes, moths and the honeybee, as well as a marine snail (Kurz et al., 2013, 2015; Eckmair et al., 2016; Stanton et al., 2017; Hykollari et al., 2018) (Fig. 2). Like methylated hexose residues, the presence of glucuronic acid results in a mass increment of 176 Da, but GlcA-containing glycans can be detected by negative mode mass spectrometry (Hykollari et al., 2017). Using permethylation, others also detected glucuronic acid on N-glycans of Drosophila (Aoki and Tiemeyer, 2010), whereas we have also used glucuronidases to help prove its occurrence on oligosaccharide structures from other insects (Stanton et al., 2017; Hykollari et al., 2018). Except for Dirofilaria immitis (Martini et al., 2019), there are no reports to date of GlcA on N-glycans of nematodes or trematodes, but glycosaminoglycan chains and O-glycans from these species do contain this residue (Palaima et al., 2010; Vanbeselaere et al., 2018), including the circulating anodic antigen of S. mansoni (Bergwerff et al., 1994).

As glucuronic acid is a major component of glycosaminoglycans and these are known to play roles in host-pathogen interactions (Pinzon-Ortiz et al., 2001; Armistead et al., 2011), one can speculate that glucuronic acid on N-glycans may be another ligand and involved in, e.g. Plasmodium transmission by mosquitoes. The role of glucuronolysis of Dirofilaria N-glycans is also unclear. The actual transfer of glucuronic acid to N-glycans has not been proven for any invertebrate glucuronyltransferase, other than for two enzymes of broad specificity from Drosophila (Kim et al., 2003).

In terms of sialylation, for which there is no hint in most invertebrates, its occurrence in insects has been controversial. Other than mass spectrometric studies on N-glycans from Drosophila embryos (Aoki et al., 2007; Frappasio et al., 2017), there is no firm proof to date for sialylation in any other insect; this is despite genome sequencing typically indicating the presence of one sialyltransferase homologue per insect species, some of which have proven in vitro activities (Koles et al., 2004; Kajura et al., 2015). Higher up the evolutionary tree, however, there is good evidence for sialic acids on the O-glycans of Echinodermata (Miyata et al., 2006). Lectin binding data, although suggestive, is too ambiguous to be considered proof of the presence of sialic acid in unknown glycans, as the ‘summarised’ specificities of many lectins are probably a simplification, but also contamination must be considered if detecting sialylation in glycans of a parasite derived from a mammalian host.
Sulphated and phosphorylated N-glycans

Another surprisingly widespread anionic modification is sulphate, which results in signals in negative mode mass MS and a Δm/z of 80 mass units. Thereby, for many instruments, sulphate cannot be differentiated from phosphate; however, some very high resolution mass spectrometers can be used to distinguish these. Other proofs include the ionisation of phosphate in both positive and negative mode or the susceptibility of phosphate (and not of sulphate) to hydrofluoric acid or phosphatase treatments (Hykollari et al., 2017). By pre-separating neutral and anionic glycans prior to off-line LC-MS, we have detected sulphate in marine molluscs (including oyster) and in insects (including mosquitoes). On the other hand, standard permethylation procedures will result in loss of sulphated glycans, but modified solid phase extraction methods are compatible with subsequent detection of permethylated sulphated glycans as performed with mosquito or royal jelly N-glycans (Kurz et al., 2015; Hykollari et al., 2018).

Sulphation of invertebrate N-glycans may occur at different positions, e.g. of mannose or core fucose in arthropods or of galactose as in oyster (van Kuik et al., 1987a; Kurz et al., 2013, 2015) (Fig. 2), but we have yet to definitely prove sulphation in a parasite. Others have detected phosphorylation of mannose residues in F. hepatica (Ravida et al., 2016). The mannose-6-phosphorylation system known for trafficking of lysosomal enzymes in vertebrates is not proven in any invertebrate; strangely, though, a mannose phosphorylation mediated by a homologue of the relevant GlcNAc-1-phosphotransferase enzyme is found in an amoeba (Qian et al., 2010). There is no information regarding any N-glycan-modifying sulpho- or phosphotransferase from any invertebrate.

Zwitterionic N-glycans

Phosphodiester and phosphate modifications such as phosphorylcholine, phosphoethanolamine and aminoethylphosphonate may be familiar to many from bacterial lipopolysaccharides and glycosylphosphatidylinositol anchors or related molecules, but have been reported on a number of invertebrate N-, O- and lipid-linked glycans. While detection of these modifications is incompatible with permethylation procedures, they can all be released with hydrofluoric acid (HF) and so some earlier reports for their presence were based partly on detection of permethylated structures without HF treatment (Haslam et al., 1999; Morelle et al., 2000). However, when conducting more ‘native’ mass spectrometric analyses, phosphorylcholine (PC; Δm/z 165 mass units) ionises very well in positive mode and is a widespread modification of nematode N-glycans (Hanneman et al., 2006; Pöltl et al., 2007; Paschinger and Wilson, 2015; Hewitson et al., 2016; Wilson and Paschinger, 2016; Jiménez-Castells et al., 2017; Martini et al., 2019), but has also been found in a cestode (Echinococcus granulosus) and more recently on moth N-glycans (Paschinger et al., 2012a; Stanton et al., 2017) (Fig. 2).

Phosphoethanolamine (PE; Δm/z 123), aminoethylphosphonate (AEP; Δm/z 107) and methylaminophosphonate (MEAP; Δm/z 121) are detected in both positive and negative modes (Paschinger and Wilson, 2016). PE is found on N-glycans of royal jelly, AEP on those of a locust glycoprotein and MEAP on their antennae and core regions of N-glycans from a marine snail (Hård et al., 1993; Eckmair et al., 2016) (Fig. 2); other reports have shown PC, PE and MEAP on glycolipids or O-glycans of various invertebrates, including Ascaris suum (Hayashi and Matsubara, 1989; Sugita et al., 1992; Lochnit et al., 1998; Seppo et al., 2000; Maes et al., 2005; Urai et al., 2009).

PC and PE are ligands for pentraxins and so binding of Echinococcus Ag5 or of Dirofilaria glycans to C-reactive protein or of royal jelly N-glycans to serum amyloid P have been shown (Paschinger et al., 2012a; Hykollari et al., 2018; Martini et al., 2019). On the other hand, PC modifications of glycoconjugates are associated with immunomodulation; a well-known example of this being the ES-62 excretory-secretory protein from the filarial worm Acanthocheilonema vitae (Pineda et al., 2014). The biosynthesis of zwitterionic N-glycans remains unresolved, other than a requirement for the prior action of GlcNAc-TI in C. elegans (Houston et al., 2008), but comparisons with pathways in bacteria and fungi may help in the future to decipher the molecular basis for these reactions.

N-glycan arrays

Glycans mediate function when they can be recognised and glycan arrays have become an established method for determining which proteins can bind them. However, other than S. mansoni (van Diepen et al., 2012; Mickum et al., 2016a), studies using natural structures are in their relative infancy for invertebrates, but pools or fractions of natural N-glycans from royal jelly, Dirofilaria and C. elegans have been tested recently in an immobilised format with pentraxins, selected antibodies or standard lectins (Hykollari et al., 2018; Jankowska et al., 2018; Martini et al., 2019). The bias in the literature towards schistosome arrays is probably due to a number of factors, such as availability of the various stages of the life-cycle and of monoclonal antibodies as well as three decades of relevant glycomic research. Thus, it has been possible to construct arrays of N-, O- and lipid-linked glycans derived from different stages of the schistosome life-cycle and screen them, e.g. with antibodies or antisera (van Diepen et al., 2012, 2015; Yang et al., 2017, 2018). Otherwise, some anti-helminth antibody responses have been tested against the primarily mammalian array of the Consortium for Functional Glycomics, remodelled glycans or conjugates with shorter saccharides to identify potential protective or diagnostic epitopes (van Stijn et al., 2009; Aranzamendi et al., 2011; Luyai et al., 2014).

Another option is to use chemoenzymatic synthesis to replicate natural glycostructural motifs and so some structures akin or identical to those of schistosomes or nematodes have been prepared, in part with our defined C. elegans FUT-1, FUT-6 and FUT-8 core fucosyltransferases (Yan et al., 2013). The resulting synthetic arrays, which can also be studied in parallel to natural arrays, have been probed with, e.g. human lectins, anti-Schistosoma monoclonal antibodies or with the sera of Schistosoma-infected humans or macaques (Brzezicka et al., 2015; Yang et al., 2017, 2018; Eccheverria et al., 2018). Thereby, some detailed insights into recognised structures can be obtained; for instance, antibodies recognising fucosylated antennae may correlate with the stage of parasite infection, while the presence of xylose or the exact antennal N-glycan configuration may have a negative role on lectin binding or be associated with skewed IgG subtype reactivity.

Conclusion

With this brief summary of the different categories of N-glycan modifications in invertebrates, we hope the reader will appreciate the great glycomic variety. Comparing parasitic, non-parasitic and host species is still far from complete; thus, it is still difficult to state whether certain N-glycans or epitopes are themselves hallmark for parasitism or tropism. It may well be that each parasite has adopted aspects of its ancestors’ or its hosts’ glycomic capacity in order to fill a specific patho-ecological niche. On the other hand, knowledge about the glycomic status of hosts for
recombinant protein production (e.g. insect cell lines) is important before, or may even aid, their use as factories for production of vaccines against parasites. In any case, only carefully performed glycomics can yield the deepest knowledge about invertebrate glycans, including exclusion of host glycans from the analyses, and is a pre-requisite for binding and other functional studies. Here, one challenge is to isolate sufficient natural glycans from parasites or related species or to recreate the structures in vitro. Another is to identify relevant ‘glycozyme’ genes, which will allow more recombinant glycosyltransferases to be used in chemoenzymatic synthesis and, as CRISPR/Cas9-based genetic engineering is beginning to be used in metazoan parasites (Gang et al., 2017; McVeigh and Maule, 2019), enable the switching on/off of certain glycosylation pathways. Indeed, a mix of analytical, biological and chemical tools will certainly prove valuable in the future to not only define the binding partners of specific glycans, but to predict their wider evolutionary occurrence and determine their function in host-parasite interactions.

Author ORCIDs. Katharina Paschinger, 0000-0002-3594-7136; Iain B. H. Wilson, 0000-0001-8996-1518.

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