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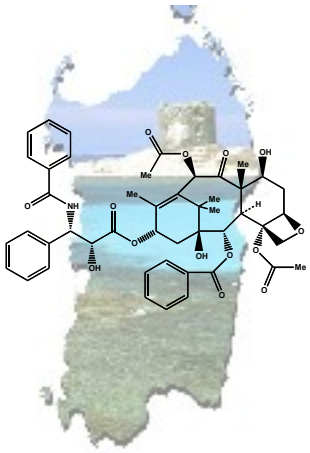

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GLYCOSAMINOGLYCAN DIVERSITY IN MARINE SPONGE EXTRACELLULAR MATRIX

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The composition in sulphated polysaccharides from the sponge extracellular matrix (ECM) is almost unknown with few exceptions, although pharmacological activities tested as anti-inflammatory and anti-viral drugs, have been recently discovered (Cimino et al., 2001). In the evolutive history of the kingdom Animalia the extracellular matrix (ECM) appeared firstly in the phylum Porifera, being Protista unable to produce the fundamental matrices to support the existence of a pluricellular organism (Morris, 1993). Sponges are the lowest eukaryotic multicellular organisms and their body plan architecture can be described as a glycoproteic jelly containing independent and mobile cells in a network of fibrous protein honeycombed by canals (mesohyl) (Garrone, 1978, 1985). The extracellular matrix of these primitive metazoans resembles that of higher taxa, being composed of collagen, proteoglycans (PGs), and minor amounts of structural proteins and glycosaminoglycans (GAGs) (Garrone, 1978, 1985; Simpson, 1984; Morris, 1993; Müller, 1995). Moreover, structure and function of extracellular matrices depend on interactions between anionic glycosaminoglycans (Scott, 2001). Proteoglycan-like molecules are involved in cell-cell interaction and species-specific cell re-aggregation (MacLennan, 1970; Müller et al., 1982; Junqua et al., 1981; Spillmann et al., 1995; Misevic et al., 1982). The structural features and biological roles of sulphated glycans in the ECM of sponges are however poorly known. About twenty years ago it was discovered that sponges are able to produce hyaluronic acid (HA), dermatan sulfate (DS), chondroitin 4-sulfate (C4S), chondroitin 6-sulfate (C6S) and heparin (Evans and Bergquist, 1977; Cassaro and Dietrich, 1977).
Aim of this paper is to report on a screening on sponge ECM glycosaminoglycan (GAG) diversity. To investigate the heterogeneity of sponge extracellular sulphated glycans, we determined their content and distribution in some Mediterranean and Caribbean species. To focus on biological and morpho-functional roles of these molecules in the sponge ECM some selected species were considered as models to investigate the topographic distribution of GAGs in sponge body according with the different architecture of specialized regions. Sulphated polysaccharides were extracted by proteolitic treatment from specimens preserved in absolute ethanol and subjected to both quantitative and qualitative analyses by standard methods. Most samples displayed a notable amount in sulphated polysaccharides, with an extremely wide range in their content at different taxonomic levels confirming that species-specific variations in both GAG chemical composition and molecular masses occur in different species (Zierer and Mourao, 2000). From the qualitative point of view, we detected that sponge GAGs do not fit the standards used for vertebrates, therefore they are not suitable substrata for specific enzymatic reactions able to degrade GAGs from vertebrates as reported by different authors (Katzman and Jeanloz, 1970; Katzman et al.,

1970; Misevic et al., 1990) and as confirmed by their resistance to specific eliminase degradation (chondroitin-lyases and hyaluronidase). These findings strongly suggest a lower sulphation degree associated with a different sugar composition, substitution and sequential arrangement compared with classical GAGs. The astonishing diversity of sulphated polysaccharides could be related to a wide adaptive radiation in the structural and functional organization of sponge ECM. Some taxa display sulphated polysaccharides with peculiar electrophoretic patterns, however this trait appears to be not exclusive of each taxon. Sponge GAGs need a deeper structural characterisation in order to test their potential as molecular markers. Our aim for the future is to investigate their role in the applicative field for pharmacological activities and as sources of biomaterials.

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