DISCOVERING NOVEL CARBOHYDRATE-ACTIVE ENZYMES

Bernard Henrissat, Centre National de la Recherche Scientifique, Marseille, France
Bernard.Henrissat@afmb.univ-mrs.fr

Carbohydrate-active enzymes (CAZymes) mediate the assembly and breakdown of the multitude of complex carbohydrate structures that are found in nature. Because CAZymes find numerous applications in health and in industry, the discovery of novel enzymes is of wide interest. A sequence-based family classification of these enzymes was initiated over 25 years ago, and is continuously updated in the CAZy database (www.cazy.org). While the number of sequences of CAZymes continues to grow exponentially, the number of experimentally characterized enzymes grows at a much lower pace. Strikingly, the number of families keeps on growing at a steady rate, suggesting that many more CAZyme families are to be discovered. Traditionally CAZymes were identified (i) by serendipity, (ii) by screening against a particular substrate or (iii) by direct similarity to a previously characterized CAZyme. We will present various alternative methods that we have used recently to discover novel CAZymes and novel CAZyme families, including the module walk, the exploitation of genetic context and the systematic exploration of sequence space.
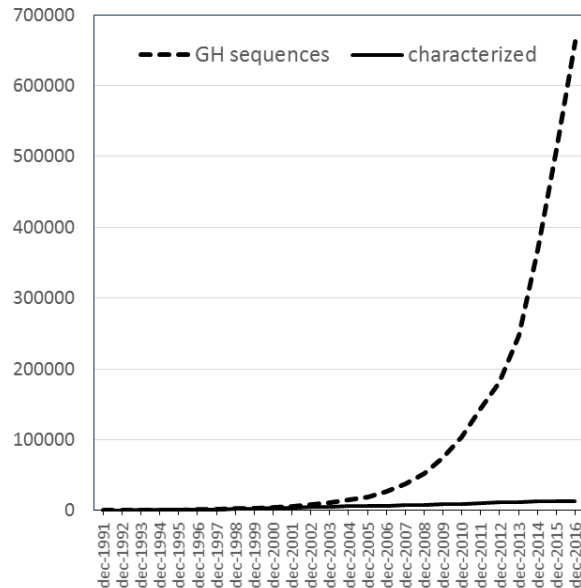

Figure 1 – Comparative growth of sequence and functional data for glycoside hydrolases