

MS07-P09 | ACTIVE SITE EVOLUTION IN BIOMASS DEGRADING ENZYMES

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Plant polysaccharides are important resources for energy and biomaterials production, but many applications rely on breaking down the biomass to monosaccharides, thus the recalcitrance of *eg* lignocellulose is an obstacle to its full utilization.

Lytic polysaccharide monooxygenases (LPMOs) and glucuronoyl esterases (GEs) are enzymes characterized within the last ten years and can boost the action of longer-known polysaccharide- degrading enzymes, which are primarily glycoside hydrolases.

LPMOs have a characteristic histidine brace motif binding the active site copper, which activates oxygen leading to oxidative breakage of the glycosidic bond [1]. LPMOs have relatively flat binding surfaces, allowing them to attack regions on the surface of crystalline polysaccharides inaccessible to most glycoside hydrolases.

GEs act through a classic Ser, His, Asp/Glu catalytic triad [2]. GEs are believed to attack ester bonds between hemicellulose and lignin, thus making the polysaccharides in lignocellulose more accessible to other enzymes.

Focus of this presentation will be our recent results showing how the active sites of LPMOs and GEs have diversified to tune/change their function, providing fascinating examples of enzyme evolution. In particular:

- The active site carboxylate in GEs can be positioned differently on the structure, and sometimes two carboxylate residues are present
- A newly discovered family of LPMOs has a carboxylate as additional copper ligand and has taken roles in copper homeostasis
- Some LPMO homologues have lost their copper site, yet still play roles in biomass degradation

[1] Tandrup et al, BST, 2018

[2] Baath et al, JBC, 2019