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Characterisation of the Effect of the Spatial Organisation of Hemicellulases on the Hydrolysis of Plant Biomass Polymer

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Abstract: Synergism between enzymes is of crucial importance in cell metabolism. This synergism occurs often through a spatial organisation favouring proximity and substrate channelling. In this context, we developed a strategy for evaluating the impact of the geometry between two enzymes involved in nature in the recycling of the carbon derived from plant cell wall polymers. By using an innovative covalent association process using two protein fragments, Jo and In, we produced two bi-modular chimeric complexes connecting a xylanase and a xylosidase, involved in the deconstruction of xylose-based plant cell wall polymer. We first show that the intrinsic activity of the individual enzymes was preserved. Small Angle X-rays Scattering (SAXS) analysis of the complexes highlighted two different spatial organisations in solution, affecting both the distance between the enzymes (53 Å and 28 Å) and the distance between the catalytic pockets (94 Å and 75 Å). Reducing sugar and HPAEC-PAD analysis revealed different behaviour regarding the hydrolysis of Beechwood xylan. After 24 h of hydrolysis, one complex was able to release a higher amount of reducing sugar compared to the free enzymes (i.e., 15,640 and 14,549 µM of equivalent xylose, respectively). However, more interestingly, the two complexes were able to release variable percentages of xylooligosaccharides compared to the free enzymes. The structure of the complexes revealed some putative steric hindrance, which impacted both enzymatic efficiency and the product profile. This report shows that controlling the spatial geometry between two enzymes would help to better investigate synergism effect within complex multi-enzymatic machinery and control the final product.

Keywords: xylanase; xylosidase; Bio Molecular Welding; spatial proximity; enzyme engineering; synergism

1. Introduction

Enzymes are biological catalysts that increase the rate of chemical reactions within cells without being consumed or permanently altered by the reaction [1]. They are involved in a large number of important functions such as metabolic pathways in cells. In many cases, they are part of complex organisations that involve several enzymes with distinct catalytic activities, embedded in a cascade of
reactions leading, for instance in the case of linear cascades, to the conversion of one substrate to one product [2–4]. However, a proper spatial organisation is required in order to provide suitable enzyme distance and active site orientation [5]. In nature, such parameters are encountered by (i) colocalising enzymes inside dedicated bacterial microcompartments [6], (ii) clustering enzymes in noncovalent dynamic complexes described as metabolon [7], and (iii) grafting enzymes on self-assembling scaffolding-based protein such as cellulosome [8].

Such protein organisations provide a beneficial effect to substrate channelling, mainly consisting of the transfer of reaction intermediates directly from one enzyme to another, thus decreasing the loss of reactants and intermediates with the bulk aqueous solvent [9]. However, recent studies suggest that the specific microenvironment created by enzyme proximity is a major determinant [10]. In the particular case of the plant cell wall carbohydrate-degrading cellulosome, the effect of the multienzyme cascade is slightly different, resulting also in an increase of synergistic effect rather than proper channelling [11]. Plant cell wall is a complex matrix of carbohydrate-based polymers such as cellulose, hemicelluloses, and pectins embedded with phenol-based lignin. The enzymes accomplishing the deconstruction of this matrix into single units of sugar are glycoside hydrolases (GHs), pectate lyases, carbohydrate esterases and other auxiliary enzymes [12,13]. The first description of the cellulosome, produced by the anaerobic bacterium Clostridium thermocellum, described an extracellular nanomachine of 2 MDa [14]. It is organised around a macro-molecular scaffold protein residing at the bacterial outer cell membrane and contains a Carbohydrate-Binding Module which binds to crystalline cellulose [15]. Nine receptor domains called the cohesins, connected by flexible linkers, interact with sub-nanomolar affinity with a complementary module fused to the GH called the dockerin [16]. The cellulosome composition is highly variable [17,18] and could also be organised in polycellulosomes at the surface of bacteria, hence displaying more than 100 catalytic domains. Previous work has also evidenced that the position of each GH docked to the scaffoldin is not random [19,20] and that spatial proximity is a key to the remarkable efficiency of the cellulosome [21,22]. The length itself of the linkers promotes spatial proximity and provides adaptation to the topology of complex polymers [23,24], bringing catalysts with complementary activity at specific site on the plant cell wall [25]. Therefore, it is challenging to assess the question of enzyme proximity at work in such context. Numerous publications investigated the spatial organisation in multi-enzyme cascades [26,27] and in our particular field involving GHs [28–32]. Nevertheless, the impact of the synergy on the chemical nature of the product [33,34] was rarely investigated, and to our knowledge, the spatial geometry between two GHs was never considered.

To shed light on the impact of the spatial organisation on enzyme synergy, we developed a new strategy to investigate the effect of the geometry between two GHs spatially close to each other. For this purpose, we used two engineered protein fragments, Jo and In, that spontaneously and covalently attach to form a complex [35]. The model enzymes of this study are two well-characterised GHs, the endo-β-1,4-xylanase GH11A from Neocallimastix patriciarum (NpXyn11A) [35] and the β-1,4-xylosidase GH43 from Bacillus halodurans (BhXyl43) [36,37]. While NpXyn11A released oligosaccharides from xylan, a linear polysaccharide consisting of β-1,4-linked xylose units with a large variety of side-chain substituents, BhXyl43 further hydrolyses the short oligomers of β-α-xylopyranosyl units that accumulate as a result of xylanase action. As Jo and In are covalently bound in a head to tail manner, by playing with the N- or C-terminal fusion of our enzymes, we produced chimeric bi-modular enzymes with two distinct spatial geometry, as revealed by SAXS analysis. Biochemical characterisation of the complexes on chromogenic substrates and polysaccharide from plants showed that subtle changes in the structure of the chimeric complex improve enzymatic efficiency and induce changes in product profiles compared to the free enzymes mixture in solution.
2. Results and Discussion

2.1. Production of the Recombinant Xylanase-Xylosidase Bi-Modular Complexes

The goal of this study was to engineer enzymes in a simple way in order to study the impact of the modulation of both geometry and spatial proximity between two catalysts to investigate their impact on synergism. For this purpose, the Bio Molecular Welding tool was used [35]. It consists of two small proteins Jo and In of 10 and 16 kDa respectively and able to bind to each other through a spontaneous and specific irreversible isopeptide bond involving the Lys191 from Jo and the Asn695 from In. The structure of this complex solved by crystallography (PDB: 5MKC) revealed an antiparallel organisation of about 5.5 nm long (Figure 1A). Hence, we made the assumption that expressing two enzymes of interest at both N-terminal of Jo and In or at the N-terminal of In and at C-terminal of Jo would contribute to modulate the orientation between the two proteins. Two well-characterised enzymes with complementary activity over xylan hydrolysis were elected: the endo-β-1,4-xylanase GH11A from *Neocalimastix patriciarum* (NpXyn11A) [38] and the β-1,4-xylosidase GH43 from *Bacillus halodurans* (BhXyl43) [37]. The xylanase NpXyn11A was expressed as a polyhistidine-tagged (His\(^6\)-Tag) protein with or without In at its N-terminal leading to previously described His-In-NpXyn11A or His-NpXyn11A, respectively [34] (Figure 1B). The xylosidase BhXyl43 was expressed without any His\(^6\)-Tag, in fusion with Jo at its N- or C-terminal, leading to soluble Jo-BhXyl43 and BhXyl43-Jo protein, respectively. This strategy was developed to allow in vitro formation following mixing of cell free extracts of complexes which could be recovered from the supernatant using the His\(^6\)-Tag displayed only by the xylanase. Although a molar ratio of 1:1 between Jo and In is efficient enough to lead to up to 95% of the covalent complex Jo-In within 1 h [34], the formation of complex between His-In-NpXyn11A and Jo-BhXyl43 or BhXyl43-Jo produced in the cell free extract was obtained with an optimised ratio of 1:5 as analysed on SDS-PAGE. This ratio can be explained by the possibility that the environment of few loops of Jo and In isolated from the originated multi-modular protein may be modified [35]. Actually, the intimate recognition process leading to the formation of the covalent bond involves flexible loops of Jo and In (N. Cox et al., manuscript in preparation) that participate to the formation of a hydrophobic pocket and thus promote a direct attack mechanism for isopeptide bond formation [39], in our case Lys191 of Jo and Asp600 and Asn695 for In [35]. A significant percentage of overexpressed chimeric proteins may display some distorted sub-structures which could explain the higher molar ratio of Jo containing enzymes, compare to His-In-NpXyn11A. Nevertheless, resulting complexes His-In-NpXyn11A-Jo-BhXyl43 and His-In-NpXyn11A-BhXyl43-Jo (Figure 1B) were purified by IMAC followed by size exclusion chromatography, leading to pure complexes close to the theoretical molecular weight of 111.99 kDa and 111.86 kDa for His-In-NpXyn11A-Jo-BhXyl43 and His-In-NpXyn11A-BhXyl43-Jo respectively (Figure 1C). Enzymes were pure at >95% as evaluated by SDS-PAGE.
Although previous work showed that In had no effect on the specific activity of 4-nitrophenyl-β-D-xylopyranoside (pNP-X₃), the effect of the fusion was evaluated on natural substrate in this study. NpXyn11A kinetic parameters were determined using Beechwood xylan (BWX), a natural polymer of β-(1,4) xylose units partially substituted with charged 4-O-methyl glucuronic acid units (MeGlcA) (Table 1). The affinity of the wild type xylanase against BWX is 2.4 fold higher than NpXyn11A, but the catalytic efficiency is very similar, with a $k_{cat}/K_M$ app value of $32.02 \times 10^3$ and $25.60 \times 10^3 \text{ min}^{-1} \cdot \text{mg}^{-1} \cdot \text{mL}$, respectively. Indeed, like GH11 xylanase, NpXyn11A is a globular protein of 24.7 kDa, displaying a large catalytic cleft within a head to tail orientation of the N- and C-termini (from PDB 5MKC).

2.2. Enzymatic Properties of the Xylanase and the Xylosidase Fused to Jo or In

Previous work has already demonstrated that introduction of In module at the N-terminal of NpXyn11A did not affect its enzymatic activity [34]. To evaluate the impact of Jo to the activity of NpXyn11A, an alternate of Jo-BhXyl43 was also expressed and purified with a His₆-Tag at its N-terminal (His-Jo-BhXyl43). The optimal pH for His-Jo-BhXyl43 was determined at 8 using 4-nitrophenyl-β-D-xylopyranoside (pNP-X), which is in agreement with the optimal pH published for His-BhXyl43 under the same experimental conditions [37]. As the pH-optimum of enzymatic activity and stability are correlated [40], this measurement is a good indicator of a non-deleterious effect of the Jo fusion to the xylanase. Both xylanase and xylosidase optimum pH curves displayed a characteristic bell curve shape. The xylanase His-In-NpXyn11A displayed an optimum pH = 6. Its residual activity at neutral pH was still consistent (68%), but was almost negligible at pH 8 (17%). However, the xylosidase displayed a high residual activity at pH 7 (92%) and to a lesser extent at pH 6 (66%) (Figure S1A). Although previous work showed that In had no effect on the specific activity of His-In-NpXyn11A on 4-nitrophenyl-β-D-xylopyranoside (pNP-X₃), the effect of the fusion was evaluated on natural substrate in this study. NpXyn11A kinetic parameters were determined using Beechwood xylan (BWX), a natural polymer of β-(1,4) xylose units partially substituted with charged 4-O-methyl glucuronic acid units (MeGlcA) (Table 1). The affinity of the wild type xylanase against BWX is 2.4 fold higher than His-In-NpXyn11A, but the catalytic efficiency is very similar, with a $k_{cat}/K_M$ app value of $32.02 \times 10^3$ and $25.60 \times 10^3 \text{ min}^{-1} \cdot \text{mg}^{-1} \cdot \text{mL}$, respectively. Indeed, like GH11 xylanase, NpXyn11A is a globular protein of 24.7 kDa, displaying a large catalytic cleft within a β-jelly roll domain with connected loops in a right-hand shape partially closed [41]. The catalytic site is located in the palm, and the thumb is a flexible loop overlapping the catalytic site [41]. The In protein was fused to the N-terminal β-sheet constituting the outer part of the palm of the xylanase. The presence of In might narrow the space in the prolongation of the active site, and could slightly reduce the affinity for the substrate. However, we considered that the In module did not affect dramatically the activity of NpXyn11A.
**Table 1.** Kinetic parameters of NpXyn11A, BhXyl43 and the Jo In derivate enzymes on Beechwood xylan (BWX) and 4-nitrophenyl-β-d-xyloside (pNP-X).

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>BWX K_cat (mg mL⁻¹ min⁻¹)</th>
<th>BWX k_{cat}/K_M (mg⁻¹ mL⁻¹)</th>
<th>BWX K_M (mM)</th>
<th>BWX k_cat (s⁻¹)</th>
<th>BWX k_cat/K_M (s⁻¹ M⁻¹)</th>
<th>pNP-X K_cat (mg mL⁻¹)</th>
<th>pNP-X k_{cat}/K_M (mg⁻¹ mL⁻¹)</th>
<th>pNP-X K_M (mM)</th>
<th>pNP-X k_cat (s⁻¹)</th>
<th>pNP-X k_cat/K_M (s⁻¹ M⁻¹)</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>His-NpXyn11A</td>
<td>0.75 ± 0.13</td>
<td>24.02 ± 1.51</td>
<td>32.02 ± 5.22</td>
<td>-</td>
<td>-</td>
<td>This work</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>His-In-NpXyn11A</td>
<td>1.8 ± 0.7</td>
<td>46.1 ± 8.8</td>
<td>25.6 ± 6.5</td>
<td>-</td>
<td>-</td>
<td>[37]</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>His-BhXyl43</td>
<td>-</td>
<td>-</td>
<td>4.40 ± 0.50</td>
<td>12.09 ± 0.93</td>
<td>2750 ± 520</td>
<td>This work</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>His-Jo-BhXyl43</td>
<td>-</td>
<td>-</td>
<td>6.01 ± 0.41</td>
<td>18.12 ± 1.17</td>
<td>3014.86 ± 10.88</td>
<td></td>
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</tbody>
</table>

The kinetic parameters of His-Jo-BhXyl43 were determined using pNP-X. The affinity against the substrate is almost not affected by the presence of the additional Jo domain compared to the wild type enzyme BhXyl43 (Table 1) [37]. The catalytic efficiency is comparable for both enzymes at 3014 and 2750 s⁻¹ M⁻¹, respectively. Thus, addition of the Jo domain fused at the N-terminal of BhXyl43 did not affect the catalytic parameters. We can reasonably assume that this is also the case for both Jo-BhXyl43 and BhXyl43-Jo. This is in accordance with the 3D structure of this 63 kDa enzyme (PDB:1YRZ, Fedorov et al., unpublished work), constituted by a five-bladed β-propeller fold for the catalytic domain, and an additional non-catalytic β-sandwich domain fused at its C-terminal. The active site possesses a pocket topology which is mainly constructed from residues of the β-propeller domain [42], located in the centre of the enzyme, without any obvious interaction with the N- or C-terminal of the protein.

### 2.3. SAXS Analysis Revealed Differences between the Structures of Each Complex in Solution

To investigate the spatial organisation of NpXyn11A and BhXyl43 in the complexes His-In-NpXyn11A-Jo-BhXyl43 and His-In-NpXyn11A-BhXyl43-Jo, Small Angle X-rays Scattering (SAXS) was used to determine the structure of each chimeric complex in solution. Most of the GH43 catalytic domains are extended with a C-terminal domain which is required for the catalytic activity [42], and present a dimeric structure [42]. This is also the case for BhXyl43, as revealed by its 3D structure (PDB: 1YRZ). At first, SAXS data were collected from His-BhXyl43. As shown in Figure S2 the SAXS data were fitted with the dimeric structure of the enzyme obtained by generating symmetry mates with Pymol software (Chi² = 1.22), confirming the dimer form of the xylanosidase in solution.

Regarding the chimeric complexes, Figure 2 displays the superimposition of the SAXS curves. The most important differences are observed at intermediate angles (0.01–0.07 Å⁻¹) and the calculation of the autocorrelation function clearly shows that the two constructs adopt different conformations in solution. According to biophysical parameters such as R_g, D_max, Porod’s volume and molecular weight (Table S1, His-In-NpXyn11A-Jo-BhXyl43 form appears more extended than the His-In-NpXyn11A-BhXyl43-Jo form with bigger R_g and D_max values (R_g: 56.4 > 50.5 Å and D_max: 230 > 200 Å, respectively). On the other hand, the p(r) function of the His-In-NpXyn11A-Jo-BhXyl43 form presents two distinct modulations correlated with the presence of two separated domains, not clearly visible on the p(r) of His-In-NpXyn11A-BhXyl43-Jo form.

The Porod’s volume and the molecular weight are close for both complexes and the calculated molecular weights are consistent with a dimeric form of the chimeric enzymes, but the values are less than expected. Although an HPLC online with size exclusion chromatography was used to isolate the fraction corresponding to the peak, an equilibrium dimer-monomer is quickly established and the measured SAXS curves contains finally a fraction of monomeric form. As the dissociation phenomenon is observed for His-In-NpXyn11A-Jo-BhXyl43 and His-In-NpXyn11A-BhXyl43-Jo but not for the His-BhXyl43 dimer, we can suppose that the addition of new domains at the N- or C-terminal of the xylanosidase could disturb slightly the association of the dimer.
Their respective catalytic pockets are one behind the other and separated by ~75 Å. The Jo-In association xylosidase in the middle, pointing outside the curvature, and the catalytic pocket of the xylanase facing the same side of Jo-In, which distanced the two GHs by ~53 Å. On the other hand, the complex Bh opposite direction at the extremity (Figure 4B).

The proposed models structurally mimic the SAXS data very well (Figure 3). The structural differences between the two complexes illustrate the differences observed in the measured biophysical parameters and in the pair distribution function p(r) calculation. The complex His-In-NpXyn11A-Jo-BhXyl43 presents an extended arc shaped structure with the catalytic pocket of the xylosidase in the middle, pointing outside the curvature, and the catalytic pocket of the xylanase facing one another at the extremity of the complex (Figure 4A). The chimer His-In-NpXyn11A-BhXyl43-Jo displays a much more compact structure, as an “M” shape. The catalytic site of the xylosidase points out from the middle of the structure, whereas the catalytic site of the xylanase faces down in the opposite direction at the extremity (Figure 4B).

This rigid body modelling approach allowed us to finally propose a low-resolution spatial organisation of the different catalytic domains and to measure the geometric influence of Jo fused at the N- or C-terminal BhXyl43. A closer view of the spatial organisation of each GH within a monomer is displayed in Figure 4. Each complex overlapped the Jo-In domain. In the complex His-In-NpXyn11A-Jo-BhXyl43 (Figure 4C), the two catalytic pockets are distanced by ~94 Å and faced the same side of Jo-In, which distanced the two GHs by ~53 Å. On the other hand, the complex His-In-NpXyn11A-BhXyl43-Jo (Figure 4D) presents the two GHs side by side, distanced by ~28 Å. Their respective catalytic pockets are one behind the other and separated by ~75 Å. The Jo-In association and its head to tail organisation therefore provide an original and efficient strategy for controlling the geometric organisation between two linked GH.
2.4. Impact of the Chimeric Enzyme Complexes on the Enzymatic Activity

Although the addition of In or Jo modules to the sequence of the xylanase and the xylosidase did not significantly affect their respective catalytic efficiency, we characterised the activity of each GH within their bi-modular association. For that purpose, the SA of the discrete xylanase and xylosidase was compared to each respective enzyme within the bi-modular complexes $\text{His-In-NpXyn11A-Jo-BhXyl43}$ and $\text{His-In-NpXyn11A-BhXyl43-Jo}$ (Table 2). By definition, a specific activity is defined as the number of $\mu$moles of product formed per minute and per milligram of protein (IU/mg). However, to properly compare the amount of catalytic site present during the reaction, a molar concentration of enzyme...
was considered instead of a mass concentration, resulting in a specific activity expressed as μmoles of product formed per minute and per μmoles of enzyme (IU/μmole). For clarity purposes, the term specific activity was conserved. Data demonstrated that the activity of \( \text{NpXyn11A} \) was preserved when it was covalently bound to \( \text{Jo-BhXyl43} \). Actually, the complex \( \text{His-In-NpXyn11A-Jo-BhXyl43} \) displays an increased xylanase activity (1404.7 IU/μmole) compared to \( \text{His-In-NpXyn11A} \) (1251.9 IU/μmole). This is probably due to the lesser extent of xyllosidase’s ability to recognise \( \text{NpNP-X} \) as a substrate (~100-fold less active on \( \text{NpNP-X} \) than \( \text{NpNP-X} \), Table 2). \( \text{NpNP-X} \) and \( \text{NpNP-X} \) are widely used to monitor xylanase and xyllosidase activity, respectively. However, previous publications have established that \( \text{BhXyl43} \) is active on xylodideose (X₂), xylotriose (X₃) and xylotetraose (X₄) [36,37], but also on \( \text{NpNP-X} \) and even xylohexaose (X₆) (Figure S4A,B respectively). The xyllosidase is not active on \( \text{XA}^3 \) (Figure 4C), confirming its ability to release xylose only from the non-reducing end sugar (following the oligosaccharide nomenclature of Fauré et al. [43]). Although the SA of \( \text{His-BhXyl43} \) was preserved when mixed with \( \text{His-In-NpXyn11A} \) (222.9 IU/μmole compared to 211.6 IU/μmole), the xyllosidase activity was reduced by 1.8 fold and 1.2 fold within the complexes \( \text{His-In-NpXyn11A-Jo-BhXyl43} \) and \( \text{His-In-NpXyn11A-BhXyl43-Jo} \), respectively, compared to the xyllosidase alone. Considering the relatively small size of the \( \text{NpNP-X} \), this result is surprising, as the substrate should diffuse easily in solution. An explanation may be provided by the structure of the complexes in solution solved from the SAXS data (Figure 4). Unlike for \( \text{His-In-NpXyn11A-BhXyl43-Jo} \), the catalytic pocket of the xyllosidase is buried in the middle of the complex \( \text{His-In-NpXyn11A-Jo-BhXyl43} \), where the branches of the arc constituted with Jo-In and \( \text{NpXyn11A} \) may induced some unspecific interactions with the substrate, reducing the efficiency of the catalyst.

Table 2. Specific activities of \( \text{NpXyn11A} \) and \( \text{BhXyl43} \), as single enzyme or in complex. The 4-nitrophenyl-β-β-xyloside (pNP-X) substrate was used to measure xyllosidase activity while 4-nitrophenyl-β-β-xyloptrioside (pNP-X) substrate was used to measure xylanase activity. Specific activity is defined as the μmoles of product formed per minute and per μmoles of enzyme. The value shown as ± mean standard deviation of replicate \( n = 3 \).

<table>
<thead>
<tr>
<th>Single Enzymes</th>
<th>Chimeric Enzymes</th>
<th>Specific Activity (IU/μmole)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>( \text{pNP-X} )</td>
</tr>
<tr>
<td>( \text{His-BhXyl43} )</td>
<td></td>
<td>211.6 ± 5.3</td>
</tr>
<tr>
<td>( \text{His-Jo-BhXyl43} )</td>
<td></td>
<td>-</td>
</tr>
<tr>
<td>( \text{His-In-NpXyn11A} )</td>
<td></td>
<td>0.4 ± 0.5</td>
</tr>
<tr>
<td>( \text{His-In-NpXyn11A +BH} )</td>
<td></td>
<td>222.9 ± 7.2</td>
</tr>
<tr>
<td>( \text{His-In-NpXyn11A-Jo-BhXyl43} )</td>
<td></td>
<td>118.0 ± 6.4</td>
</tr>
<tr>
<td>( \text{His-In-NpXyn11A-BhXyl43-Jo} )</td>
<td></td>
<td>177.3 ± 6.9</td>
</tr>
</tbody>
</table>

2.5. Characterisation of the Complexes on Plant Cell Wall Polysaccharide

\( \text{NpXyn11A} \) and \( \text{BhXyl43} \) displayed different pH optimum over aryl-β-xylosides, pH 6 and 8 respectively. Therefore, SA against BWX was determined at pH 6, 7 and 8 in order to compare the activity of the complexes to \( \text{NpNpXyn11A} \) or \( \text{BhXyl43} \) free in solution. To do so, we used an equimolar mixture of both GH and each bi-molecular enzymes \( \text{His-In-NpXyn11A-Jo-BhXyl43} \), and \( \text{His-In-NpXyn11A-BhXyl43-Jo} \) (Table 3). The equivalent amount of reducing xylose units released from BWX was measured by dinitrosalicylic acid assay (DNSA) [44]. Experiments were conducted at 37 °C, the optimal temperature of \( \text{NpXyn11A} \) [43], different to the optimal temperature of \( \text{BhXyl43} \) (45 °C) [37] at which the xylanase is not stable. As expected, \( \text{His-BhXyl43} \) was poorly active on BWX (0.36 × 10³ UI/μmole) and \( \text{His-In-NpXyn11A} \) displayed the best activity at pH 6 (47.11 × 10³ UI/μmole). However, unlike on \( \text{pNP-X} \) (Figure S1A), the xylanase activity on BWX remained high at pH 8 (39.98 × 10³ UI/μmole, 84% activity remaining). Adding 1% of BWX in the buffered solution did not affect the final pH. Therefore, the determination of the pH optimum for \( \text{His-In-NpXyn11A} \) in presence
of BWX was performed, revealing a better activity at pH 6 and 8, while activity at pH 7 was slightly diminished (Figure S1B). Actually, the modification of the acid dissociation constant $pK_a$ of the catalytic acid is a critical parameter for GH activity and the environment, such as mutation, changing in net charge of the catalytic residue or solvent accessibility could modulate the value of the $pK_a$ and cause a shift toward higher pH [45–49]. BWX is much larger and complex compared to pNP-X$_3$ and fit in both the glycone and aglycone part of the catalytic site, with two negatively charged MeGlcA side chains possibly accommodated by the −3 and/or +2 catalytic subsite [50,51], modifying the environment close to the active site [52]. The system of the buffer used might also modulate the value of the $pK_a$ of the catalytic residues. Altogether, these results suggest that NpXyn11A could be considered as an alkaline xylanase (Asn proximal to the catalytic Glu [52]) displaying a relatively large range of pH optimum activity as previously reported [53–55]. Compared to the activity of His-In-NpXyn11A alone, the reaction mixture supplemented with His-BhXyl43 displayed a very similar profile of SA at all considered pH value, while the complex His-In-NpXyn11A-Jo-BhXyl43 clearly displayed the lowest specific activity at all pH (around $33 \times 10^3$ UI/µmole) (Table 3). His-In-NpXyn11A-BhXyl43-Jo displayed the best overall specific activity at pH 7 ($48.21 \times 10^3$ UI/µmole). To evaluate the contribution of each enzymatic mixture, xylooligosaccharides released during the hydrolysis of BWX were monitored by HPAEC-PAD. It is clear that X$_3$ is produced at the very first step of the reaction, while X$_1$ started to be accumulated after 60 min of reaction (Figure S7). Accumulation of X$_3$ by a xylan GH11 degrading enzyme is a marker of a xylanase activity [56], just like X$_1$ is for GH43 [57]. This observation reflects the fact that enough small oligosaccharides have to be produced by the xylanase first before being hydrolysed by the xylosidase. As the SA were determined in the same experimental conditions, the initial rate of the reaction (within the 40 first minutes), we can reasonably assume that the SA measured (Table 3) reflect mainly the xylanase activity. Thus, differences in SA between the two complexes may be explained by spatial organisation, more or less impeding the access of the substrate to the catalytic site of NpXyn11A. As revealed by SAXS analysis, the structure of His-In-NpXyn11A-BhXyl43-Jo is more compact (Figure 4B), with the xylanase domains distanced by 105 Å, whereas the structure of His-In-NpXyn11A-Jo-BhXyl43 is more extended with the xylanase domains distanced by 175 Å. The closest proximity of the two xylanase domains may favour enzymatic hydrolysis events, resulting in a better SA.

Table 3. Comparison of the activity of the different enzyme at various pH. Activity is expressed as the amount of µmole of product formed per minute and per µmole of enzymes. Hydrolysis conditions: 1 nM of enzymes, 37 °C, 1% BWX. UI $= \mu$mol·min$^{-1}$. The value shown as ± mean standard deviation of replicate $n = 3$.

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>pH 6 Activity $10^3$ (UI/µmole)</th>
<th>pH 7 Activity $10^3$ (UI/µmole)</th>
<th>pH 8 Activity $10^3$ (UI/µmole)</th>
</tr>
</thead>
<tbody>
<tr>
<td>His-BhXyl43</td>
<td>0.36</td>
<td>0.36</td>
<td>0.24</td>
</tr>
<tr>
<td>His-In-NpXyn11A</td>
<td>47.11 ± 1.29</td>
<td>37.35 ± 2.05</td>
<td>39.98 ± 1.73</td>
</tr>
<tr>
<td>His-In-NpXyn11A + His-BhXyl43</td>
<td>41.76 ± 2.17</td>
<td>34.45 ± 0.71</td>
<td>36.03 ± 1.54</td>
</tr>
<tr>
<td>His-In-NpXyn11A-Jo-BhXyl43</td>
<td>35.36 ± 1.95</td>
<td>31.02 ± 1.97</td>
<td>33.08 ± 1.07</td>
</tr>
<tr>
<td>His-In-NpXyn11A-BhXyl43-Jo</td>
<td>41.81 ± 0.76</td>
<td>48.21 ± 1.16</td>
<td>36.79 ± 1.07</td>
</tr>
</tbody>
</table>

2.6. Analyses of Xylan Degradation Products by the Chimeric Bi-Modular Enzymes

To more deeply investigate the effect of the different spatial organisations in the chimeric complexes, analysis of the final product released during 24 h of hydrolysis of BWX at different pH was performed. Products were analysed by HPAEC-PAD (Figure 5) and DNS assay (Figure 6). HPAEC-PAD made it possible to accurately quantify the release of soluble xylooligosaccharides ranging from xylose (X$_1$) to xylohexaose (X$_6$). Meanwhile, the colorimetric assay quantified in a non-discriminatory manner soluble xylan-reducing ends, including both xylose and xylooligosaccharides, but also longer oligomers with various amounts of substitution, as previously determined by MALDI-ToF mass spectrometry under similar conditions [34]. Both NpXyn11A and BhXyl43 were stable, displaying a reduction of only 7% of
their respective activity after 24 h (Figure S5). As expected, the activity of BhXyl43 against BWX was almost indistinguishable (Figure S6) and almost no X₁ was produced by the activity of the xylanase alone (Figure 5). The contribution of the xylosidase to the xylanase activity was observed directly by the release of X₁, at first modestly during the 60 first minutes then more obviously after 240 min (Figure 5).

After 24 h at pH 7 (Figure 5B), X₁ represents 1.6% of the total amount of xylooligosaccharides released from BWX by His-In-NpXyn11A compared to 59% when the xylanase is supplemented with His-BhXyl43. A reduced amount of X₃, combined with an increase of X₂ was concomitant to the production of xylose by the BhXyl43. This accumulation of xylose revealed the specificity of the xylosidase, which is able to hydrolase small oligosaccharides produced by the xylanase [58]. Intermediate xylooligosaccharides ranging from X₄ to X₆ were not accumulated as they are substrate for both enzymes. The total amount of xylooligosaccharides reached its maximum at pH 7 after 24 h by the free xylanase and xylosidase mixture (9735 µM, Figure 5B). pH 8 had a dramatic effect on xylooligosaccharides production (6660 µM, Figure 5C), as did pH 6, although to a lesser extent (7213 µM, Figure 5A). This observation suggests that neutral pH preserved enough activity of both enzymes. Regarding the enzymatic activity of the complexes, both followed the same pH dependency as the mixture of the two GHs in solution. However, His-In-NpXyn11A-Jo-BhXyl43 released less total xylooligosaccharides compared to His-In-NpXyn11A-Jo-BhXyl43 after 24 h, as exemplified at pH 7, with 8694 µM and 9016 µM, respectively, but was able to generate at least 50% more xylose, whatever the pH value (Figure 5B). On the contrary, the amount of X₃ produced was higher for His-In-NpXyn11A-Jo-BhXyl43 than for His-In-NpXyn11A-Jo-BhXyl43 (1428 µM and 3191 µM, respectively, at pH 7).

**Figure 5.** Evolution of the concentration of xylooligosaccharides from X₁ to X₆ at (A) pH 6, (B) pH 7 and (C) pH 8 over time determined by HPAEC-PAD. Hydrolysis conditions: 1 nM of enzymes, 37 °C 1% BWX during 24 h. Representation of the average of triplicate experiments (see Figure S6 for details).
The main product was X1 (39.5% and 32.7%), to a lesser extent X2 (16.4% and 17.3%) and X3 (7.8% and 10.5%), and with only 3% of X4. On the contrary, His-In-Xyn11A-Jo-BhXyl43 presents a mid-way enzymatic mechanism. Actually, His-In-Xyn11A produced mostly X3 (29.8%), around 7% of X2 and X4 and no X1. When supplemented with the xylosidase, the proportion of xylooligosaccharides was very similar to those produced by the complex His-In-Xyn11A-BhXyl43-Jo. The main product was X1 (39.5% and 32.7%), to a lesser extent X2 (16.4% and 17.3%) and X3 (7.8% and 10.5%), and with only 3% of X4.

Total reducing end sugars were measured by DNSA, resulting in a concentration of equivalent xylose units expressed in µM. From these values, Figure 6 represents the total amount of xylose units, including the concentration of X1 and the sum of xylooligosaccharides from X2 to X6 as measured by HPAEC-PAD. The difference consists of polymers with a degree of polymerisation (DP) > 6. Considering the total amount of reducing end sugars after 24 h, the chimeric enzyme His-In-NpXyn11A-Jo-BhXyl43 was the most productive compared to the other enzymes, whatever the pH. At neutral pH after 24 h, His-In-NpXyn11A released 11,279 µM of equivalent xylose, compared to 14,549 µM when the reaction medium was supplemented with His-BhXyl43, 13,596 µM with His-In-NpXyn11A-BhXyl43-Jo, and 15,640 µM with His-In-NpXyn11A-Jo-BhXyl43 (Figure 6B). Considering the effect of the xylanase activity only with respect to the corresponding concentration of equivalent amount of reduced xylose of oligomers of DP > 6 (lower DP may be provided by xylosidase activity), the complex His-In-NpXyn11A-Jo-BhXyl43 was the most active, with 6623 µM of equivalent xylose at pH 7, whereas His-In-NpXyn11A released 5933 µM, His-In-NpXyn11A + His-BhXyl43 4757 µM, and His-In-NpXyn11A-BhXyl43-Jo 4858 µM.

Table 4 presents the percentage of xylooligomers as measured by HPAEC-PAD from the total amount of reducing sugar determined by DNSA, for the different enzymes at pH 7 after 24 h. Neither X5 nor X6 is accumulated under any of experimental conditions, reflecting the activity of both His-In-NpXyn11A and His-BhXyl43 on short xylooligosaccharides. However, this table highlights differences in enzymatic mechanism. Actually, His-In-NpXyn11A produced mostly X3 (29.8%), around 7% of X2 and X4 and no X1. When supplemented with the xylosidase, the proportion of xylooligosaccharides was very similar to those produced by the complex His-In-NpXyn11A-BhXyl43-Jo. The main product was X1 (39.5% and 32.7%), to a lesser extent X2 (16.4% and 17.3%) and X3 (7.8% and 10.5%), and with only 3% of X4.
profile with an equivalent percentage of both $X_1$ and $X_3$ (15.8% and 20.4%) and a similar percentage of $X_2$ and $X_4$ (11.8% and 8.4%).

**Table 4.** Amount of equivalent of reducing sugar as determined by DNS assay after 24 h of hydrolysis at pH 7 and percentage of xyloooligomers of DP ranging from 1 to 6 and oligomers of DP > 6. Hydrolysis conditions: 1 nM of enzymes, 37 °C 1% BWX after 24 h. Representation of the average of experiments in triplicate. The value shown as ± mean standard deviation of replicate $n = 3$.

<table>
<thead>
<tr>
<th>Enzyme</th>
<th>Total Reducing Sugar (µM)</th>
<th>$X_1$ (%)</th>
<th>$X_2$ (%)</th>
<th>$X_3$ (%)</th>
<th>$X_4$ (%)</th>
<th>$X_5$ (%)</th>
<th>$X_6$ (%)</th>
<th>$X_{&gt;6}$ (%)</th>
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</thead>
<tbody>
<tr>
<td>His$^+$-In-NpXyn11A</td>
<td>11,278</td>
<td>0.8 ± 1.1</td>
<td>7.6 ± 0.5</td>
<td>29.8 ± 1.6</td>
<td>7.8 ± 0.6</td>
<td>1.1 ± 0.08</td>
<td>0.2 ± 0.07</td>
<td>52.6 ± 2.4</td>
</tr>
<tr>
<td>His$^+$-In-NpXyn11A + His$^+$-BhXyl43</td>
<td>14,549</td>
<td>39.5 ± 1.5</td>
<td>16.4 ± 0.4</td>
<td>7.8 ± 0.2</td>
<td>2.9 ± 0.08</td>
<td>0.4 ± 0.01</td>
<td>0.1 ± 0.07</td>
<td>32.6 ± 1.6</td>
</tr>
<tr>
<td>His$^+$-In-NpXyn11A-Jo-BhXyl43</td>
<td>15,640</td>
<td>15.8 ± 2.8</td>
<td>11.8 ± 0.7</td>
<td>20.4 ± 0.6</td>
<td>8.4 ± 0.2</td>
<td>1.9 ± 0.1</td>
<td>0.3 ± 0.1</td>
<td>42.3 ± 4.6</td>
</tr>
<tr>
<td>His$^+$-In-NpXyn11A-BhXyl43-Jo</td>
<td>13,596</td>
<td>32.7 ± 1.7</td>
<td>17.3 ± 1.2</td>
<td>10.5 ± 0.6</td>
<td>3.2 ± 0.1</td>
<td>0.3 ± 0.1</td>
<td>0.2 ± 0.1</td>
<td>35.7 ± 3.2</td>
</tr>
</tbody>
</table>

### 3. Materials and Methods

#### 3.1. Gene Cloning

The xylanase 11A from *Neocallimastix patriciarum* (NpXyn11A) cloned into pET22b [38] was sub-cloned in pET28b in fusion with In as previously described [34]. The xylosidase 43 from *Bacillus halodurans* C-125 is cloned in pET28b (pET28b-BH3683, [37]). The resulting genes code for the C-terminal His-tagged His$^+$-NpXyn11A, the N-terminal His-tagged fusion proteins His$^+$-In-NpXyn11A and His$^+$-BhXyl43, respectively. The region of the *jo* gene was amplified by PCR from the plasmid pBMW2 [35] using the following primers: 5′ GGA GAT ATA CCA TGG GCA GCA GCC ATC ACC AT CATC 3′ and 5′ GAT TGA CCA TGC TAG CGC TGC CGC GCG GCA CCA GGT CGT CAT CAT ACA CTG TTT TCC C 3′, which introduce a Ncol and a Nhel site. The PCR product was introduced by homologous recombination (In-Fusion® HD cloning kit, Clonetech, Mountain View, CA, USA) into a pET28b-BH3683 linearized vector using Ncol and Nhel to produce pET28-Jo-BhXyl43-His. The resulting gene codes for the N-terminal His-tagged protein His$^+$-Jo-BhXyl43. The genes coding for Jo-BhXyl43 and BhXyl43-Jo were synthetized and subcloned in a pET28a linearized vector using Ncol and HindIII by GenScript HK Limited (Piscataway, NJ, USA), resulting in protein without a polyhistidine tag (Table S3).

#### 3.2. Production, Expression and Purification

To express NpXyn11A+His$^+$-BhXyl43 and derivate enzymes, *Escherichia coli* strain BL21 (DE3) harbouring the respective plasmids was cultured to mid-exponential phase ($A_{600 nm}$ 0.6) in Luria-Bertani broth at 37 °C. Expression of the recombinant enzyme was induced by the addition of isopropyl-β-D-thiogalactopyranoside to a final concentration of 1 mM and further incubation for 4 h at 37 °C. Harvested cells (10 min, 5000× g) were resuspended in 50 mM phosphate buffer, pH 7.2 containing 300 mM NaCl and a protease inhibitor cocktail (SigmaFAST protease inhibitor cocktail, Sigma-Aldrich, Darmstadt, Germany). The cells were lysed by sonication on ice for 1 min. The lysate was clarified by centrifugation (30 min at 74,000× g at 4 °C). Proteins harbouring a His$^+$-Tag were purified by immobilised metal ion affinity chromatography (IMAC) using Talon resin (TALON® Metal Affinity Resin, Clontech) and elution in 50 mM sodium phosphate buffer, pH 7.2 containing 300 mM NaCl and 150 mM imidazole. The eluted proteins were extensively dialyzed against 50 mM sodium phosphate buffer, pH 7.2. Purified proteins were adjudged homogenous by SDS-PAGE (Any kD™ Mini-PROTEAN® TGX Stain-Free™ Protein Gels, Bio-rad, Hercules, CA, USA). Protein concentrations were determined by measuring absorbance at 280 nm and applying the Lambert-Beer equation. Theoretical molar extinction coefficients and molecular weight were calculated using ProtParam online software (https://web.expasy.org/protparam/) [59] (Table S2).
3.3. Covalent Association of His-In-NpXyn11A and BhXyl43

The relative amount of His-In-NpXyn11A, Jo-BhXyl43 and BhXyl43-Jo present in cell free extracts (filtered at 0.45 µm) was evaluated by SDS-PAGE using Image Lab™ Software (version 6.0.1 build 34, Bio-rad). Usually, one volume of cell free extract of His-In-NpXyn11A was mixed to five volume of cell free extract of Jo-BhXyl43 or BhXyl43-Jo and incubated at room temperature for 90 min under constant agitation. Complexes were removed from the solution by immobilised metal ion affinity chromatography as described above and eluted with increasing concentrations of imidazole (5 mM, 200 mM and 300 mM). Traces of non-complexed His-In-NpXyn11A were removed by a final round of purification carried out using a XK16 HiLoad 16/600 Superdex HiLoad S200 prep-grade gel filtration column (GE Healthcare Life Sciences, Chicago, IL, USA) connected to an Äkta Pure system. Typically, 3 mL of protein were loaded onto the column at 1 mL/min and finally eluted from the column using 50 mM sodium phosphate buffer, pH 7 containing 150 mM NaCl. Purified proteins were adjudged homogenous by SDS-PAGE.

3.4. Enzymatic Activity

The kinetics parameters \( K_M, V_{\text{max}}, k_{\text{cat}}, \) and \( k_{\text{cat}}/K_M \) of His-Jo-BhXyl43 were calculated from initial velocities at substrate concentration of 4-nitrophenyl-\( \beta \)-n-d-xylopyranoside (pNP-X, Carbosynth Ltd., Compton, UK) varying from 0.1 to 18 mM. Assays were conducted in 50 mM Tris-HCl pH 8 supplemented with 1 mg/mL BSA, at 45 °C for 10 min as previously described (10.1007/s00253-006-0512-5). Specific activities of xylodidase (50 nM) were determined using 5 mM of pNP-X for 15 min at 37 °C, in 50 mM Tris-HCl pH 8 supplemented with 1 mg/mL BSA. Specific activities of xylanase (100 nM) were determined using 5 mM of 4-nitrophenyl-\( \beta \)-n-d-xylotrioside (pNP-X₃, LLC “Institute of road surfaces”) for 15 min at 37 °C, in 50 mM phosphate pH 7.2 supplemented with 1 mg/mL BSA [38]. Absorbance at 401 nm of the released 4-nitrophenolate \((\varepsilon = 12,578 \text{ M}^{-1}\text{·cm}^{-1})\) was measured in quartz cuvettes with a chamber volume of 500 µL (cuvettes Hellma Analytics), using a spectrophotometer Cary 100 Bio (Agilent Technology, Santa Clara, CA, USA). One unit of \( \beta \)-xylosidase activity or endo-xylanase activity was defined as the amount of enzyme releasing 1 µmol of pNP per minute using the defined conditions. To determine the optimum pH of His-Jo-BhXyl43, 5 mM of pNP-X was used and reactions were performed at 45 °C for 15 min under constant agitation at 1400 rpm (ThermoMixer® C, Eppendorf, Hamburg, Germany) in 2 mL centrifuge tube, in presence of 1 mg/mL BSA. An aliquot of 50 µL was withdrawn and instantly mixed with 200 µL of 1 M Na₂CO₃. To vary pH from 4 to 5, 50 mM citrate was used, from 6 to 7, 50 mM phosphate buffer was used, from pH 8 to 9, 50 mM bicine was used and at pH 10, glycine/NaOH buffer was used. Absorbance at 401 nm \((\varepsilon = 22,209 \text{ M}^{-1}\text{·cm}^{-1})\) was measured using a microplate spectrophotometer (Eon Microplate Spectrophotometer, Biotek Instruments, Winoski, VT, USA).

Dinitrosalicylic acid assay (DNSA) was performed to estimate the concentration of reducing sugar equivalent to xylose when beechwood xylan (BWX, Megazyme, Bray, Ireland) was the substrate. BWX solution was prepared by mixing the dry powder with water during at least 30 min at 90 °C. The enzymatic reactions were performed at 37 °C under constant agitation at 1400 rpm (ThermoMixer® C, Eppendorf) in 2 mL centrifuge tube. At the regular time, an aliquot of 100 µL was mixed with 100 µL of DNS and incubated for 10 min at 95 °C. After cooling down on ice, 1 mL of deionised water was added and absorbance at 540 nm was measured (microplate reader Tecan Infinite M200 PRO). The apparent kinetics parameters \( K_{\text{Mapp}}, V_{\text{max}}, k_{\text{cat}}, \) and \( k_{\text{cat}}/K_{\text{Mapp}} \) of NpXyn11A were calculated from initial velocities at substrate concentration of BWX varying from 0.3 to 15 mg/mL as previously described [38] in 12 mM sodium citrate, 50 mM sodium phosphate buffer pH 6 supplemented with 1 mg/mL of BSA. Specific activities were determined using BWX at 1% and 1 nM of enzymes in 50 mM phosphate buffer supplemented with 1 mg/mL BSA, during 1 h at 37 °C. The pH of the reaction mixtures was adjusted to 6, 7 or 8 after adding the substrate using orthophosphoric acid or NaOH. For the kinetics over 24 h, aliquots of 150 µL were pipetted out at regular times and inactivated by heating at 95 °C for 5 min. Samples were split in two and stored at
−20 °C until further analysis by HPAEC-PAD (see below). A sample volume of 25 µL was added to 25 µL of DNS and incubated for 10 min at 95 °C. A volume of 250 µL of deionised water was added before absorbance at 540 nm was measured (microplate reader Tecan Infinite M200 PRO). A standard curve was prepared accordingly. All experiments were performed in triplicate, and the reported values are the means of three experiments. Mathematical calculations and kinetic parameters derived from Michaelis-Menten representations were performed using the software SigmaPlot 11.0 (Systat Software, San Jose, CA, USA).

3.5. HPAEC-PAD

Quantification of short xylooligosaccharides released over the time from BWX by complexes and free enzymes were determined using aliquots removed at regular time intervals and heated at 95 °C for 5 min to terminate the reaction. Each sample (5 to 50 µL, depending on the progress of the reaction) was centrifuged at 20,000× g for 5 min and quantified by HPAEC-PAD using a Dionex ICS 3000 dual chromatography system. Xylooligosaccharides were separated on a Carbo-Pac PA-100 guard and analytical column PA-100 (2 × 50 mm and 2 × 250 mm). Separation of oligosaccharides was achieved by isocratic elution with 100 mM NaOH at a flow rate of 1 mL/min from 0 to 10 min, a gradient of 0 to 75 mM sodium acetate in 100 mM NaOH from 10 min to 25 min, and isocratic elution with 500 mM sodium acetate in 100 mM NaOH from 25 min to 35 min, then the column was re-equilibrated with 100 mM NaOH for another 10 min. Calibration was achieved using xylose and xylooligosaccharides (X, X₂, X₃, X₄, X₅ and X₆) at concentrations from 5 µg/mL to 40 µg/mL. All experiments were performed in triplicate, and reported values are the means of three experiments (Dionex™ Chromeleon™ 7.2, ThermoFisher, Waltham, MA, USA).

3.6. Small Angle X-ray Scattering

Before analysis, samples were buffer exchanged using PD-10 column (GE Healthcare) in 50 mM phosphate pH 7. Proteins were concentrated to around 10 mg/mL using centrifugal filter devices (Amicon® Ultra 30 or 50K, Merck KGaA, Darmstadt, Germany) and final concentration values were measured (NanoDrop™ 2000, ThermoFischer). SAXS measurements were performed at Laboratoire de Genie Chimique, Toulouse, on the XEUSS 2.0 bench with a copper internal source (Genix3D) that produces an X-ray beam with an energy of 8 keV and a flow of 30.10⁶ ph·s⁻¹ with a beam size resolution close to 500 × 500 µm. Samples were pipetted (volume of 50 µL) from the sample holder maintained at a constant temperature using a circulating water bath, to the measurement cell placed under vacuum to limit air absorption. Alternatively, an HPLC with a size exclusion column online is coupled to the SAXS to remove the aggregate and obtain a SAXS curve from monodisperse solution. Data were collected on 150 × 150 mm area DECTRIS detector (Pilatus 1M) at a sample to detector distance of 1.216 m, giving a range comprised from 0.005 to 0.5 Å⁻¹. Then each scattering curve obtained for every sample is an average of at least 6 measurements with a data collection time of 1800 s. The averaged curves obtained with direct injection and SEC-HPLC are merged to obtain a composite curve with no aggregation contribution at small angles and a low noise at high angles. Finally, to obtain the absolute scattering intensity I(q) for the solutes, the background with the buffer solution contribution was subtracted from the total SAXS profile. The data integration and reduction were performed with FOXTROT. The biophysical parameters such as gyration radius Rg, maximal distance Dmax and Porod volume were calculated by using PRIMUS [60] from ATSAS suite, and the rigid bodies molecular modelling against SAXS was performed with SASREF [61].

4. Conclusions

This work demonstrated the possibility of using the Jo-In modules to create chimeric enzyme with modulated spatial organisation as demonstrated by SAXS analysis. Introduction of Jo or In as fusion to the xylanase NpXyn11A or the xylosidase BtXyl43 did not alter their respective kinetic parameters. However, these Jo and In modules were of major interest in covalently associating the
enzymes and creating chimeric complexes, the structures of which were solved in solution by SAXS. The arc shape or the “M” shape of the complexes resulting in a different positioning of the Jo module fused to BhXyl43 impacted the activity of each chimeric enzyme. Of course, a xylanase supplemented with a xylosidase increases the total activity, as measured by total reducing end sugar compared to xylanase alone [58]. However, by covalently associating the two GHs, we were able to modulate the SA or to increase the amount of hydrolytic events, as measured by DNSA. The arc shape probably presents a more solvent-exposed catalytic pocket of the xylanase, whereas the “M” shape presents a more compact structure, with the catalytic pocket of the GH one behind the other. Beyond the kinetic parameters, the two chimeric structures display some differences in product profile. Indeed, His-In-NpXyn11A-Jo-BhXyl43 presents the lowest SA on pNP-X and BWX. However, this complex generated the highest amount of total reducing end sugar, with a high percentage of X₃ and X₄. On the other hand, His-In-NpXyn11A-BhXyl43-Jo maintained a relatively stable SA on pNP-X and BWX compared to the two GHs free in solution. However, after 24 h, its activity measured by DNSA on BWX was low, releasing an equivalent amount of X₁ and X₃ compared to NpXyn11A and BhXyl43 in free solution. However, the structure of the two complexes revealed some putative steric hindrance that impacted both enzymatic efficiency and product profile, and which still needs to be elucidated. This intimate correlation between the enzymatic activity and the structure of the complexes in solution provides some evidence that controlling the distance, but also the spatial geometry, between two GHs is of importance in controlling enzymatic processes.

Supplementary Materials: Supplementary Materials can be found at http://www.mdpi.com/1422-0067/21/12/4360/s1.

Author Contributions: T.E. performed protein purification, enzymatic experiments, DNSA and HPAEC-PAD analysis. M.D.L.M. performed protein purification and HPAEC-PAD analysis. P.R. performed and analysed SAXS experiment and provide expertise in SAXS. L.B. performed enzymatic experiments. T.V. provided expertise about Jo and In. C.D. provided expertise in enzymology. C.Y.M. conceived the initial project, designed the experiments, performed protein purification and enzymatic experiments, analysed the data and wrote the manuscript. All authors have read and agreed to the published version of the manuscript.

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Conflicts of Interest: The authors declare no conflict of interest.

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