

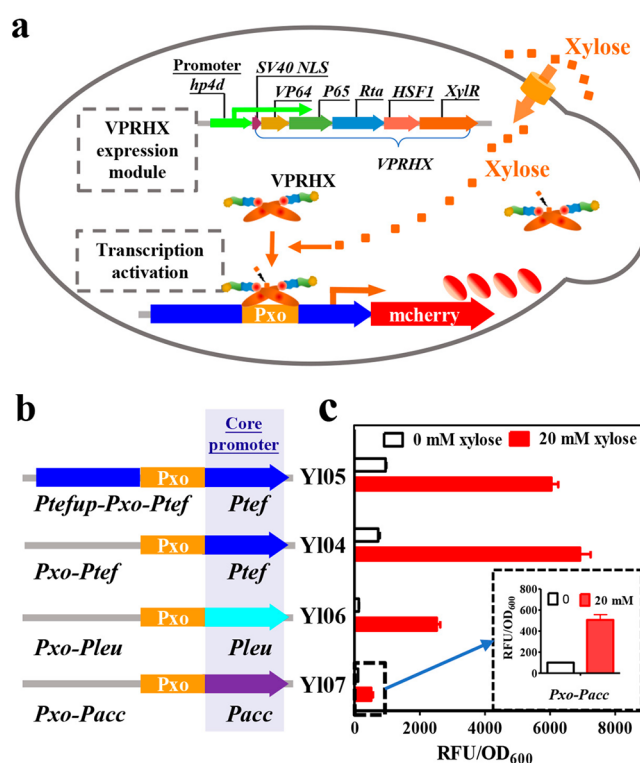


only exists in *E. coli*. The genes encoding enzymes involved in xylose utilization are controlled and activated by XylR, which can bind to the xylose responsive promoter of those genes only in the presence of xylose.<sup>13,14</sup> We hypothesized that *E. coli* XylR can be used to design xylose-inducible “turn-on” biosensors in yeast, as long as a complex with a universal ADs fused to the N-terminal of XylR is constructed. ADs that have been generally designed include VP64,<sup>15</sup> VPR,<sup>16</sup> and HSF1.<sup>17</sup> Once the ADs are fused to *E. coli* XylR to produce complex ADs-XylR, it is theoretically feasible that the ADs are recruited by XylR to generate reverse parallel dimers induced by xylose;<sup>13</sup> they will then bind to target hybrid promoter with *xylO* site and function as the transcriptional activator.

To investigate whether the *E. coli* XylR can be used to construct a “turn-on” xylbiosensor, we fused the *E. coli* XylR with VPR and HSF1 to form fusion protein VPRH-XylR (VPRHX), and designed a synthetic hybrid promoter with the *xylO* site. Lastly, we combined these components to complete the construction of the xylbiosensor. *Y. lipolytica* is widely used in chemical production processes and is an organism with “Generally Regarded as Safe” (GRAS) status.<sup>18</sup> It lacks a usable xylbiosensor; hence, it was selected as the first host to design the xylbiosensor. The xylbiosensor displayed an obvious response and good specificity to xylose and was then upgraded by designing a xylose-inducible bidirectional expression system (BDES) in *Y. lipolytica*. In addition, the pathway of xylose utilization was engineered through the inducible expression of *XDH* (YALI0E12463) and *XKS* (YALI0F10923) based on the xylbiosensor-mediated transcriptional activation. It is worth mentioning that the xylbiosensor derived from VPRHX also functioned well in *S. cerevisiae*. In yeast, this is the first report of a transcriptional activator biosensor responsive to the inexpensive and abundant biomass-derived carbon source xylose. The xylbiosensor is valuable in pathway engineering for yeast to utilize xylose and to produce xylose-derived value-added natural products.

## RESULTS AND DISCUSSION

**Design of Hybrid Promoter for Xylbiosensor.** In yeast, several biosensors are derived from prokaryotic TFs.<sup>2–4</sup> For biosensors, in addition to the core component of prokaryotic TFs, the promoter is another necessary element. Owing to the differences between prokaryotic and eukaryotic promoters with respect to the RBS, transcription start sites, and regulatory binding sites among others, exogenous prokaryotic promoters paired with prokaryotic TF may not play an effective role in eukaryotic cells for biosensor construction. Therefore, the common approach is to tailor suitable synthetic promoters for TFs based on the native yeast promoter.<sup>2–4,19</sup> Implement the specific TF binding site into a selected yeast core promoter could lead to generation of a new hybrid promoter containing the site for TF regulation and satisfactory functionality in yeast.<sup>1</sup> Four promoters, the TEF promoter, TEF core promoter, Leu core promoter, and ACC1 promoter (Figure 1a–b, Table S3), were screened to construct the specific synthetic hybrid promoter carrying the XylR binding site *XylO* (shortened to Pxo). The TEF promoter, as the strong promoter that can be widely used for gene expression or as a source to build hybrid synthetic promoters,<sup>20</sup> was used to build the hybrid synthetic promoter Ptefup-Pxo-Ptef through the insertion of the Pxo near the TATA box of the TEF promoter (Figure 1b, Table S3). Pxo-Ptef, the second hybrid synthetic promoter, contains only the Pxo and TEF core promoter. Similarly, the Pxo was inserted near



**Figure 1.** Refactoring the xylbiosensor based on *E. coli* XylR and VPRH in *Y. lipolytica*. (a) Designing the xylbiosensor in *Y. lipolytica*. The xylbiosensor was designed based on four core promoters. *mcherry* was cloned downstream of those promoters as a reporter gene. The transcriptional factor complex VPRHX includes the activation domain (i.e., VP64, P65, Rta, and HSF1 were selected and fused to form the new activation complex VPRH) and xylose-response transcriptional factor XylR from *E. coli*. It was constitutively expressed under the control of the *hp4d* promoter. (b) Design of the hybrid synthetic promoter. The individual Pxo sequence (XylR binding site *XylO* from *E. coli*) was fused upstream of core promoter of *Y. lipolytica*. The core promoter selected in this design from TEF, Leu, and ACC1 promoter. (c) *mcherry* expression response to xylose at 20.0 mM. The strains Y104–Y107 were cultivated in YPD for 72 h. The excitation wavelength was 580 nm and the emission wavelength was 608 nm.

the TATA box of the Pleu, the core promoter element of *hp4d*,<sup>18</sup> to generate a third hybrid promoter, Pxo-Pleu. The fourth hybrid promoter Pxo-Pacc1 was designed from Pacc1 (Figure 1b, Table S3), the core promoter of ACC1, which controls the expression of enzyme ACC1 to supply malonyl-CoA for lipid biosynthesis.<sup>21</sup> On the basis of these designs, four hybrid promoters were constructed (Table S3).

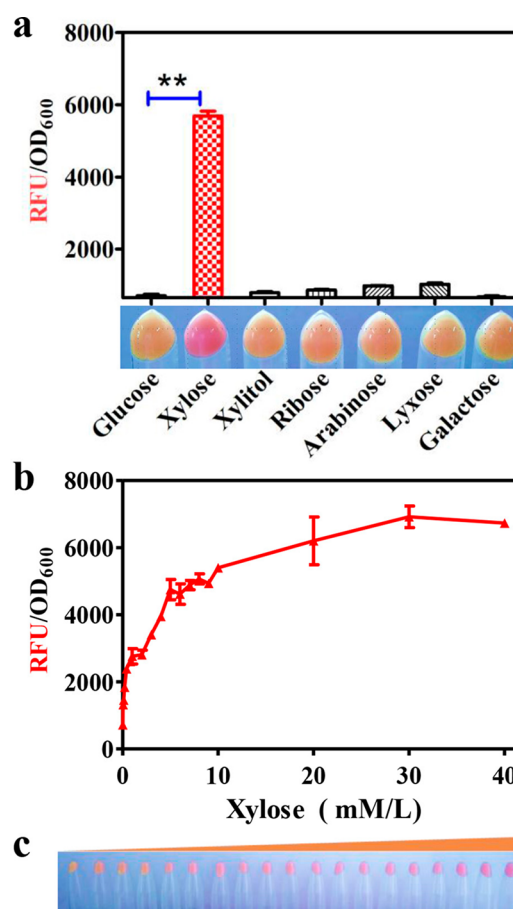
**Characterization of the Xylbiosensor System in *Y. lipolytica*.** Except for hybrid promoters containing the desired TF binding site, a biosensor requires a TF that is responsive to the specific chemical molecule. As previously stated, *E. coli* XylR was chosen as a xylose-sensitive TF. Many prokaryote-derived TFs (i.e., FdeR and BenM) are capable of responding to corresponding small molecules and functioning as a transcriptional activator when present alone in yeast.<sup>19</sup> For this reason, individual XylR and the hybrid promoter Pxo-Ptef were used to generate a biosensor and determine the transcriptional activation of XylR in *Y. lipolytica* Y101. *mcherry* expression of the xylose response module consisting of XylR and Pxo-Ptef indicated that XylR alone cannot function as a transcriptional activation factor in *Y. lipolytica* (Figure S1). Therefore, the transcriptional activation of XylR requires additional ADs. In

general, transcriptional activation requires ADs such as VPR<sup>16</sup> and HSF1<sup>17</sup> in traditional activation systems, as well as in CRISPRa. In *Y. lipolytica*, VPR-driven gene expression was slightly higher than gene expression driven by the strong promoter UAS1B8-TEF.<sup>12</sup> Here, we compared the xylose-responsive activation effect of the complex transcription factor formed by the fusion of different ADs (i.e., HSF, VPR, and VPRH) with XylR (Figure S2, Table S2). The activation effect of those ADs is characterized by the expression of the reporter gene *mcherry* (Figure S2). The results show that the complex VPRHX formed by VPR, HSF, and XylR has a better xylose-responsive activation effect than HSFX and VPRX. The VPRHX, comprising VPR, HSF, and XylR (Table S2), simultaneously plays a xylose-sensitive role in targeted promoter recognition and transcriptional activation (Figure 1a). The VPRHX contains the SV40-NLS sequence at the N-terminus, which ensures nuclear localization (Table S2). To evaluate the expression *in vivo*, VPRHX carrying the protein tag “Flag” was identified using Western blotting electrophoresis with a Flag-antibody (Figure S3). Results indicated the successful expression of VPRHX in *Y. lipolytica* Yl04.

Figure 1c shows that the RFU (relative fluorescent unit) signal increased by 6.4, 9.6, 20.9, and 5.1-fold when 20.0 mM xylose was added to the strains Yl05, Yl04, Yl06, and Yl07, carrying the hybrid promoter Ptefup-Pxo-Ptef, Pxo-Ptef, Pxo-Pleu, and Pxo-Pacc1, respectively. Generally, the short TEF promoter, only containing its core promoter sequence, has minimal expression in the absence of UAS.<sup>22</sup> Accordingly, the expression of *mcherry* could be enhanced by the hybrid synthetic promoter, specifically the Pxo-related activation effect. The addition of xylose results in the formation of antiparallel dimers of XylR, binding to operator sites of Pxo, and transcriptional activation in *E. coli*.<sup>13</sup> Here, the VPRHX presented the same xylose-inducible transcriptional activation in *Y. lipolytica*.

Comparison of the four hybrid synthetic promoters, each with different core promoter regions, revealed that the fluorescence intensity of *mcherry* derived by Pxo-Ptef was higher than that of the Ptefup-Pxo-Ptef and Pxo-Pleu in the presence of xylose (Figure 1c). Pxo-Ptef had a higher signal-to-noise ratio than Ptefup-Pxo-Ptef. In addition, Pxo-Pacc1 had a significant response after xylose was added ( $p < 0.05$ ), although its fluorescence intensity was lower than that of Pxo-Ptef and Pxo-Pleu. On the basis of these data, Pxo-Ptef was selected as the xylose-inducible promoter in subsequent experiments.

High selectivity of biosensors is necessary when they are widely used for detection and response of specific molecules.<sup>23,24</sup> The response to a set of xylose isomer monosaccharides and intermediate metabolites such as xylitol was investigated at the same concentration to determine the specificity of the xylbiosensor (Figure 2a). Xylose significantly induced *mcherry* expression (Figure 2a). Dynamic time-dependent response curves of *mcherry* fluorescence intensity from the strain Yl04 in the presence of 20.0 mM xylose further revealed a higher inducible effect throughout the cultivation (Figure S4). It is worth noting that xylose has a 14.8-fold induction for the xylbiosensor in the minimal medium YNB (Figure S5), which was higher than the fold induction in YPD (9.6-fold in Figure 1c). As mentioned above, the xylbiosensor showed a better response to xylose than other moleculars such as xylitol, ribose, arabinose, threose, and galactose. The development of a xylbiosensor in *Y. lipolytica* exhibits good prospects for utilization in industries. In an actual fermentation environment, the strain always grows using a mixed carbon source. Mixed



**Figure 2.** Fluorescence intensity of *mcherry* at different xylose concentrations from strain Yl04. (a) Ligand specificity of xylbiosensor in strain Yl04 carrying the pVPRHXbios1 plasmid. The ligands used were xylose, xylitol, ribose, arabinose, threose, and galactose, and all were used at 20.0 mM. The ligands were added at 24 h after inoculation, and this is the initial time to determine the fluorescence density. The data collection was performed at 48 h after inoculation. (b) Fluorescence density induced by different concentrations of xylose (0, 0.05, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0, 10.0, 20.0, 30.0, and 40.0 mM/L) at 48 h. The excitation wavelength was 580 nm and the emission wavelength was 608 nm. (c) The image was recorded using a VivoX7 phone at 48 h, the xylose concentration was 0, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 2.0, 3.0, 4.0, 5.0, 6.0, 7.0, 8.0, 9.0, 10.0, 20.0, 30.0, and 40.0 mM/L, respectively. The strain Yl04 was cultured and induced in YPD medium for 72 h.

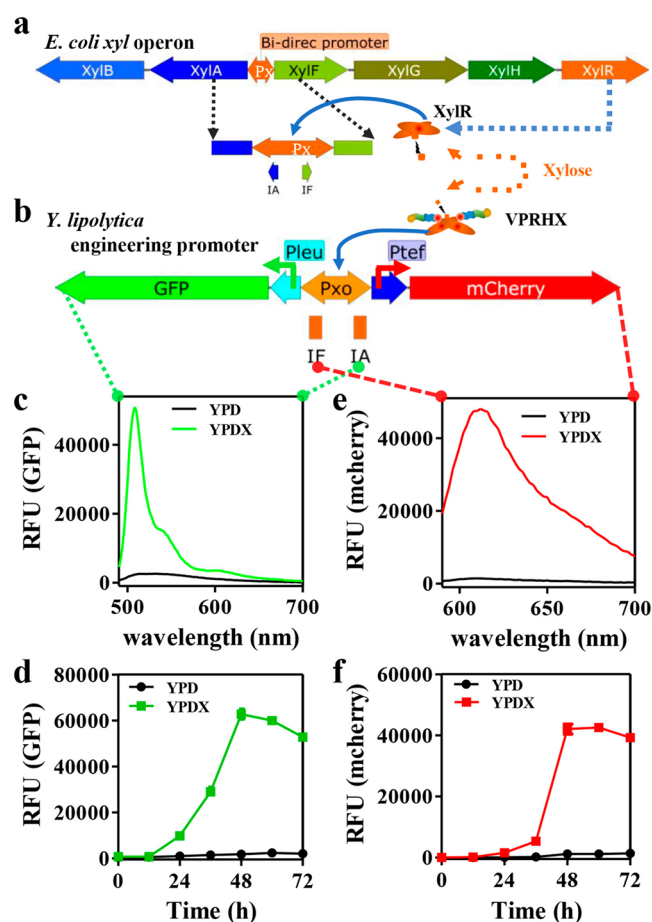
sugars derived from cereals and hydrolysates are generally used as a carbon source for microorganisms.<sup>25</sup> Specific responses to a single carbon source will contribute to spatiotemporal specific targeting to control transcription and subsequent gene expression.

Moreover, to investigate the response to the signal input relating to xylose concentration, we further studied the sensitivity and operational range of the xylbiosensor by measuring response curves *in vivo*. Strain Yl04 with Pxo-Ptef and VPRHX exhibited a dose-dependent increase in RFU when grown in YPD with gradually increasing xylose concentrations, which ranged from 0 to 40.0 mM. RFU sensitivity reached saturation between 20.0 and 40.0 mM at 48 h (Figure 2b). A higher output signal was observed and visualized with obvious *mcherry* expression (Figure 2c, Figure S6). High *mcherry* expression was induced by xylose. During the culture period, strains cultured in YPD medium with different concentrations



of xylose showed no significant difference in growth (Figure S7a). However, its mcherry expression was significantly affected by xylose addition, particularly from 48 to 72 h (Figure S7b). The signal output of xylose response has concentration and time-dependent characteristics that will make the xylobiosensor more suitable for precise regulation of gene expression in *Y. lipolytica*.

**Design of a Xylose-Inducible Bidirectional Transcriptional Activation System.** In *E. coli*, the xylose-induced specific promoter in the original *xyl* operon is bidirectional<sup>14</sup> (Figure 3a). The phenomenon of bidirectional distribution of



**Figure 3.** Construction of the xylose-inducible bidirectional expression system (BDES) in *Y. lipolytica*. (a) Native structure of *xyl* operon in *E. coli*. The *xyl* operon is involved in the reverse expression of *xylAB* and *xylFGH*. (b) Refactoring xylose-inducible BDES using Pxo, core promoter Pleu and Pterf in *Y. lipolytica*. Pleu and Pterf are distributed in opposite directions on both sides of Pxo, and the expression of GFP and mCherry indicated unilateral promoter activity. (c) RFU of GFP for the strain Y108. (d) Dynamic change in GFP expression BDES. (e) RFU of mCherry for the strain Y108. (f) Dynamic change in mCherry expression BDES. The strain Y108 carrying the pVPRHXBDES plasmid was cultivated in YPD containing 3.0 g/L xylose (YPDX).

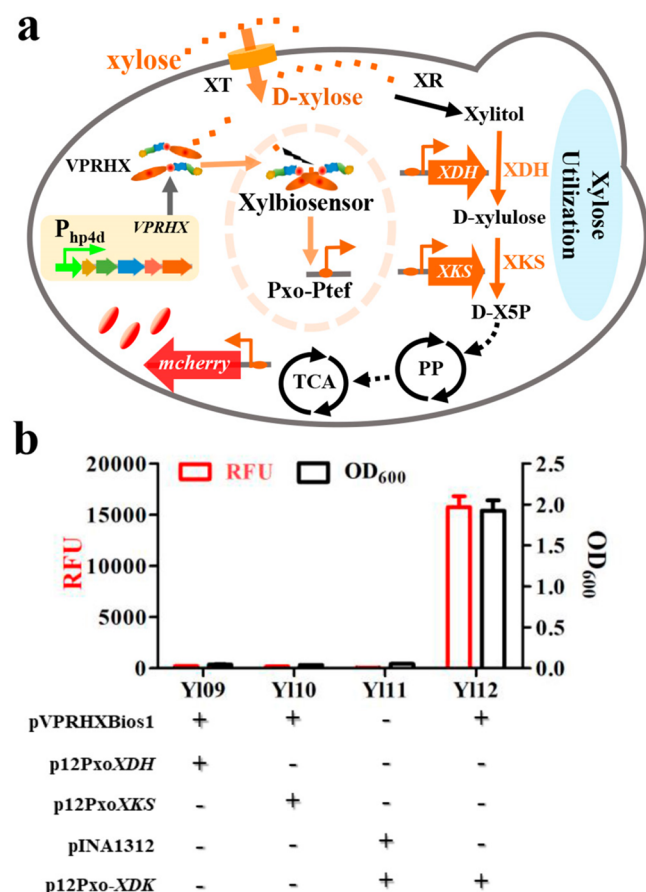
such operons is common in prokaryotes and eukaryotes.<sup>26</sup> To verify the possibility of refactoring of the xylose-inducible BDES in *Y. lipolytica*, we designed a transcriptional control model in which the core promoter sequence *Leu* and *TEF* share the same activation site *xylo* (as Pxo in Figure 3b).

It has been demonstrated that both Pxo-Pterf and Pxo-Pleu can successfully achieve xylose-responsive transcriptional activation (Figure 1). In theory, when a transcriptional activator binds to

the same TF binding site Pxo, the promoters on both sides share the change in transcriptional activity from the activator VPRHX (Figure 3b). Artificially constructed BDES, GFP, and mCherry were highly expressed in the presence of xylose compared with the expression in the blank control (Figure 3c–f). BDES produced an approximately 22.9-fold RFU increase in GFP expression (Figure 3c) and an approximately 33.4-fold RFU increase in mCherry expression (Figure 3e). The time nodes of the growth trend and fluorescence change were essentially identical for Pxo-Pterf and Pxo-Pleu (Figure 3e,f). The fold induction of gene expression in this system was higher than that of a single promoter (Figure 1). This difference may arise from the composition of the promoter and expressed gene sequences (Table S3), and shows that optimizing the adaptability between different exogenous operators, core promoters and target genes is particularly important for obtaining better fold induction in the later applied research of biosensor. Similar to this artificial BDES, generation of an artificial promoter by the addition of a cis-acting element is universal in eukaryotes.<sup>27,28</sup> As an exogenous cis-acting element, Pxo regulates the activity of BDES, which results in bidirectional transcription activation. As with yeast's native divergent transcription,<sup>29</sup> this artificial transcription control system may have a potential impact on targeted gene regulation. The application of BDES can activate the simultaneous expression of genes on both sides, particularly genes that are equally important for a synthesis process.

#### Inducible Utilization of Xylose Based on Xylobiosensor.

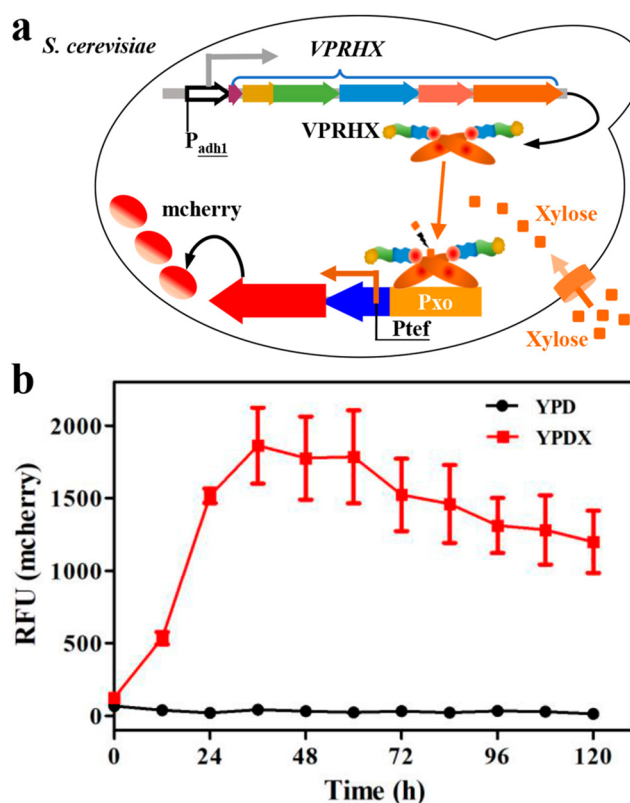
As a novel and effective transcriptional activation biosensor, the xylobiosensor should have the potential to simultaneously activate the expression of multiple genes. Excluding the high expression of mCherry, VPRHX would enable *Y. lipolytica* to utilize xylose by carrying related enzymes derived by the Pxo-Pterf promoter (Figure 4a). On the basis of the above assumptions, we overexpressed two native genes *XDH* and *XKS*, encoding the major enzymes in the xylose utilization pathway, by using the xylobiosensor. Specifically, *XDH* catalyzes the conversion of xylose to xylitol, and *XKS* can catalyze xylulose to xylulose-5-phosphate (Figure 4a), which enters the pentose phosphate pathway.<sup>8</sup> Growth of Y112 in the YNB–xylose medium was satisfactory only when *XDH* and *XKS* were simultaneously overexpressed (Figure 4b). This finding is consistent with prior results from other studies.<sup>8</sup> The OD<sub>600</sub> (biomass) of Y112 was approximately 2.0 at 72 h, which is higher than that of the engineered *Y. lipolytica* YISR02, in which *XDH* was overexpressed under the transcriptional control of the constitutive promoter Pterf (minimum medium, 10 g/L xylose as carbon source, OD<sub>600</sub> < 1.0 at 72 h).<sup>30</sup> From this point, xylose-inducible expression may offer greater advantages for enhancing the xylose metabolism capacity. However, the biomass in the xylose medium was still considerably less than that obtained in YPD (Figure S7, OD<sub>600</sub> > 10.0). This difference may be attributed to the available nitrogen sources in the minimum medium YNBX15 that were not abundant enough compared to that in YPD, and compared to glucose, xylose is far from being a carbon source that yeast cells prefer to utilize before systematic engineering. In addition, the intracellularly loaded reporter gene mCherry expression module also functioned normally (Figure 4b), indicating that the xylobiosensor has the potential to regulate multiple processes, not just xylose utilization. Only strain Y112 grew in the YNB–xylose medium, while Y111, which lacked plasmid pVPRHXBios1, lacked the capability to grow in this medium. These data indicated that the xylose-inducible utilization system of xylose can function well when the



**Figure 4.** Xylose utilization and mcherry expression mediated by xylbiosensor. (a) The xylose-inducible activator VPRHX mediates the utilization of xylose and the expression of targeted protein. (b) Strain growth and target protein expression by using the xylose as the sole carbon. Utilization of xylose by the xylose-inducible expression of XDH and XKS. The culture medium was YNB–xylose (6.7 g/L YNB, 15.0 g/L xylose). Growth conditions were 30 °C for 72 h. Abbreviation: XT, xylose transporter (YAL10B00396). XR, xylose reductase (YAL10D07634). X5P, xylulose-5-phosphate. PP, pentose phosphate pathway. TCA, tricarboxylic acid cycle.

VPRHX factor is present *in vivo*. Xylose was able to autoinduce its own utilization, allowing *Y. lipolytica* to initiate efficient expression of the xylose utilization gene in the presence of xylose, rather than the continuously constitutive expression independent of xylose. This feature may allow a more economical coordination of spatiotemporal specific expression of target genes and could promote the rational distribution of intracellular energy flow and metabolic flux according to the xylose concentration.

**Xylose-Inducible Transcription Activator Functions Well in *S. cerevisiae*.** Drawing on the successful construction of the xylbiosensor in *Y. lipolytica*, we applied it to *S. cerevisiae* (Figure 5a). The Padhl promoter drives the expression of VPRHX. The ability of VPRHX to target Pxo in synthetic promoters has been verified in *Y. lipolytica* (Figure 1 and Figure 3). The results of the xylose-induced expression of mcherry and the signal output (Figure 5b) indicated that the targeted binding of VPRHX to the newly constructed promoter PxoPtef in *S. cerevisiae* was also successful. Mcherry expression in YPDX was notably higher than that of YPD during culture (Figure 5b). The signal-to-noise ratio of the xylbiosensor in BY-Xbios reached 43.3 at 36 h, indicating the significance of xylose-induced



**Figure 5.** Xylbiosensor responsiveness in *S. cerevisiae*. (a) Schematic representation of xylose-inducible biosensor in *S. cerevisiae* BY-Xbios. The VPRHX expression module was controlled by the constitutive ADHI promoter. The synthetic promoter PxoPtef consists of the *E. coli* xylO and the *S. cerevisiae* TEF core promoter, with mcherry as the reporter gene. (b) The dynamic responsiveness of the xylbiosensor to xylose in strain BY-Xbios. The medium was YPD–His–Met–Leu (YPD medium with 0.5 g/L each of His, Met, and Leu). Xylose (3.0 g/L) was the inducer (as YPDX medium). For the mcherry fluorescence detection, the excitation and emission wavelengths were 580 and 608 nm, respectively.

activation ( $p < 0.01$ ). The transplantation of the xylbiosensor from *Y. lipolytica* to *S. cerevisiae* proved to be feasible after designing a synthetic promoter based on an effective combination of the yeast endogenous core promoter and the exogenous binding site Pxo. The realization of this activation effect is attributed to the versatility of activating factors such as VPR in yeast<sup>12,16</sup> and mammalian cells.<sup>15</sup> The re-emergence of transcriptional activation effects in *S. cerevisiae* indicated that the xylbiosensor developed in this study has the potential to be utilized in other eukaryotic cells.

## CONCLUSION

In this study, we constructed a xylose-responsive transcriptional activation biosensor termed the xylbiosensor, which shows a dynamic range of expression upon xylose induction and broadens the genetic tools available for engineering of yeast. The expanded development of xylbiosensor involved the creation of a BDES and refactoring the inducible xylose utilization pathway. On the basis of this xylbiosensor, the dual function of xylose as a carbon source and a molecular inducer was exploited to achieve a synchronized process, which combined utilization of substrates and inducible gene expression. The successful transplantation of the xylbiosensor

Table 1. Plasmids and Strains Used in the Current Study

| name                           | description                                                                                                                             | original plasmid | source         |
|--------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------|------------------|----------------|
|                                | plasmid                                                                                                                                 |                  |                |
| pINA1312                       | integration vector with <i>hp4d</i> promoter, XPR2 terminator, selection marker URA3, KmR                                               |                  | 18             |
| pINA1269                       | integration vector with <i>hp4d</i> promoter, XPR2 terminator, selection marker LEU2, AmpR                                              |                  | 18             |
| PUC57-VPRH                     | PUC57 with the codon-optimized VPR and HSF1                                                                                             | PUC57            | lab collection |
| PUC57-mCh                      | harboring <i>mcherry</i> fragment                                                                                                       | PUC57            | lab collection |
| pmCh                           | harboring <i>mcherry</i> fragment                                                                                                       | pINA1312         | this study     |
| pHSFX                          | harboring HSF1-XylR controlled by <i>hp4d</i> promoter                                                                                  | pINA1312         | this study     |
| pVPRX                          | harboring VPR-XylR controlled by <i>hp4d</i> promoter                                                                                   | pINA1312         | this study     |
| pVPRHX <sup>a</sup>            | harboring VPRHX controlled by <i>hp4d</i> promoter                                                                                      | pINA1312         | this study     |
| pHSFXbios                      | Pxo-Ptef and <i>mcherry</i> were inserted into <i>SalI</i> and <i>StuI</i> site                                                         | pHSFX            | this study     |
| pVPRXbios                      | Pxo-Ptef and <i>mcherry</i> were inserted into <i>SalI</i> and <i>StuI</i> site                                                         | pVPRX            | this study     |
| pVPRHXbios1 <sup>b</sup>       | Pxo-Ptef and <i>mcherry</i> inserted into <i>SalI</i> and <i>StuI</i> site                                                              | pVPRHX           | this study     |
| pVPRHXbios2                    | Ptefup-Pxo-Ptef and <i>mcherry</i> inserted into <i>SalI</i> and <i>StuI</i> site                                                       | pVPRHX           | this study     |
| pVPRHXbios3                    | Pxo-Pleu and <i>mcherry</i> inserted into <i>SalI</i> and <i>StuI</i> site                                                              | pVPRHX           | this study     |
| pVPRHXbios4                    | Pxo-Pacc1 and <i>mcherry</i> inserted into <i>SalI</i> and <i>StuI</i> site                                                             | pVPRHX           | this study     |
| pX                             | harboring <i>E. coli</i> XylR with the <i>Flag</i> and <i>SV40-NLS</i> sequence located at 5'-End                                       | pINA1312         | this study     |
| pXbios                         | pX with Pxo-Ptef and <i>mcherry</i> inserted into <i>SalI</i> and <i>StuI</i> site                                                      | pX               | this study     |
| pVPRHXBDES <sup>c</sup>        | xylose-responsive bidirectional promoter Pleu-Pxo-Ptef. The Pleu-Pxo to control <i>GFP</i> , and the Pxo-Ptef to control <i>mcherry</i> | pVPRHX           | this study     |
| pL1269                         | linearized plasmid amplified from pINA1269 without native <i>hp4d</i> promoter                                                          | pINA1269         | this study     |
| p12PxoXDH <sup>d</sup>         | with Pxo-Ptef and <i>XDH</i>                                                                                                            | pL1269           | this study     |
| p12PxoXKS <sup>e</sup>         | with Pxo-Ptef and <i>XKS</i>                                                                                                            | pL1269           | this study     |
| p12Pxo-XDK <sup>f</sup>        | with PxoXKS inserted into <i>KpnI</i> site                                                                                              | p12PxoXDH        |                |
| pYES2                          | with <i>GAL1</i> promoter and <i>CYC</i> terminator                                                                                     | -                | lab collection |
| pLYES                          | linearized pYES2 amplified by PCR, <i>GAL1</i> promoter was removed                                                                     | pYES2            | this study     |
| pYES2-mch                      | harboring <i>mcherry</i> fragment                                                                                                       | pYES2            | this study     |
| pLYES-Padh1-VPRHX-Pxo-Ptef-mch | with <i>Padh1</i> -VPRHX-Pxo-Ptef- <i>mcherry</i> fragment                                                                              | pLYES            | this study     |
|                                | Strains                                                                                                                                 |                  |                |
| Po1f                           | auxotrophic strain ( <i>Leu</i> -, <i>Ura</i> -). The derivatives <i>Y. lipolytica</i> strain W29 (CLIB89)                              |                  | 18             |
| Y101 <sup>g</sup>              | with pXbios                                                                                                                             | Po1f             | this study     |
| Y102                           | with pHSFXbios                                                                                                                          | Po1f             | this study     |
| Y103                           | with pVPRXbios                                                                                                                          | Po1f             | this study     |
| Y104                           | with pVPRHXbios1                                                                                                                        | Po1f             | this study     |
| Y105                           | with pVPRHXbios2                                                                                                                        | Po1f             | this study     |
| Y106                           | with pVPRHXbios3                                                                                                                        | Po1f             | this study     |
| Y107                           | with pVPRHXbios4                                                                                                                        | Po1f             | this study     |
| Y108                           | with pVPRHXBDES                                                                                                                         | Po1f             | this study     |
| Y109                           | p12PxoXDH                                                                                                                               | Y104             | this study     |
| Y110                           | p12PxoXKS                                                                                                                               | Y104             | this study     |
| Y111                           | pINA1312 and p12Pxo-XDK                                                                                                                 | Po1f             | this study     |
| Y112                           | p12Pxo-XDK                                                                                                                              | Y104             | this study     |
| BY4741                         | commonly used auxotrophic <i>S. cerevisiae</i> strain ( <i>his3</i> -, <i>leu2</i> -, <i>met</i> -, <i>ura3</i> -)                      |                  | lab collection |
| BY-Xbios                       | with pLYES-Padh1-VPRHX-Pxo-Ptef-mch plasmid                                                                                             | BY4741           | This study     |

<sup>a</sup>VPRHX is the fusion DNA fragment of VPRH and *E. coli* XylR. <sup>b</sup>Derived vector from pVPRHX, with the Pxo-Ptef to control *mcherry* and to form a biosensor plasmid ("bios"). <sup>c</sup>BDES, bidirectional expression system. <sup>d</sup>XDH gene (YALI0E12463). <sup>e</sup>XKS gene (YALI0F10923). <sup>f</sup>XDK, the abbreviation of XDH and XKS. <sup>g</sup>Y1, abbreviation of *Y. lipolytica*.

from *Y. lipolytica* to *S. cerevisiae*, based on the synthetic promoter and xylose-inducible transcription activator VPRHX, indicated that the xylbiosensor model developed in this study has the potential to be applied in other eukaryotic cells. This study successfully demonstrates the transformation of prokaryotic transcriptional activators into eukaryotic cells to construct a "turn-on" xylbiosensor induced by xylose addition, based on prokaryotic activator XylR and eukaryotic universal AD. In addition, the xylbiosensor displayed the potential to applied in engineering pathways involved in xylose utilization and xylose-derived chemical biosynthesis in yeast.

## MATERIALS AND METHODS

The original *Y. lipolytica* strain was po1f and the *S. cerevisiae* strain was BY4741. The strains and plasmids used in this study are summarized in Table 1. The complete "Materials and Methods" section is provided in the Supporting Information.

## ASSOCIATED CONTENT

### Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acssynbio.0c00122>.

Materials and methods: cultivation conditions; DNA manipulation; yeast transformation and construction of strains; determination of VPRHX expression; quantifica-



tion of biomass and fluorescence; cell imaging; primers used in this study; sequence of *HSFX*, *VPRX* and *VPRHX*; sequence of artificial hybrid promoter; biosensor construction based on *E. coli* xylose-responsive transcription factor XylR in *Y. lipolytica*; activation domains used for transcription activation in *Y. lipolytica*; determination of *VPRHX* expression *in vivo* by Western Blotting; response kinetics curves of strain Y104 in the YPD with different ligands; ligand specificity of xylbiosensor in minimal nutrient medium YNB; imaging of a single *Y. lipolytica* cell Y104 in the presence of xylose using laser scanning confocal microscopy; time-dependent change of mcherry expression response to xylose in YPD (PDF)

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### Author Contributions

W.W. was responsible for experimental design, data collection, and writing manuscript. Y.S. and P.Z. participated in plasmid construction. Y.L., D.Y., and B.Y. provided advice for experimental data analysis. B. Ye was responsible for experimental design, data analysis, and final approval of the manuscript.

### Notes

The authors declare no competing financial interest.

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## ABBREVIATIONS

xylbiosensor, xylose-inducible biosensor; *VPRHX*, VP64-P65-Rta-HSF1-XylR; TF, transcription factors; AD, activation domain; UAS, upstream activation sequence; NLS, nuclear localization signal; BDES, bidirectional expression system; YPD, yeast extract peptone dextrose; YPDX, Yeast extract peptone dextrose xylose; YNB, yeast nitrogen base; RFU, relative fluorescent unit.

## REFERENCES

- (1) Rantasalo, A.; Czeizler, E.; Virtanen, R.; Rousu, J.; Lähdesmäki, H.; Penttilä, M.; Jäntti, J.; and Mojzita, D. (2016) Synthetic Transcription Amplifier System for Orthogonal Control of Gene Expression in *Saccharomyces cerevisiae*. *PLoS One* 11, e0148320.
- (2) Dabirian, Y.; Gonçalves Teixeira, P.; Nielsen, J.; Siewers, V., and David, F. (2019) FadR-Based Biosensor-Assisted Screening for Genes Enhancing Fatty Acyl-CoA Pools in *Saccharomyces cerevisiae*. *ACS Synth. Biol.* 8, 1788–1800.
- (3) Wang, M., Li, S., and Zhao, H. (2016) Design and engineering of intracellular-metabolite-sensing/regulation gene circuits in *Saccharomyces cerevisiae*. *Biotechnol. Bioeng.* 113, 206–215.
- (4) Teo, W. S., and Chang, M. W. (2015) Bacterial XylRs and synthetic promoters function as genetically encoded xylose biosensors in *Saccharomyces cerevisiae*. *Biotechnol. J.* 10, 315–322.
- (5) Gärtner, D.; Degenkolb, J.; Ripperger, J. A.; Allmansberger, R., and Hillen, W. (1992) Regulation of the *Bacillus subtilis* W23 xylose utilization operon: interaction of the Xyl repressor with the xyl operator and the inducer xylose. *Mol. Gen. Genet.* 232, 415–422.
- (6) Sievert, C.; Nieves, L. M.; Panyon, L. A.; Loeffler, T.; Morris, C.; Cartwright, R. A., and Wang, X. (2017) Experimental evolution reveals an effective avenue to release catabolite repression via mutations in XylR. *Proc. Natl. Acad. Sci. U. S. A.* 114, 7349–7354.
- (7) Kwon, K. K.; Yeom, S. J.; Lee, D. H.; Jeong, K. J., and Lee, S. G. (2018) Development of a novel cellulase biosensor that detects crystalline cellulose hydrolysis using a transcriptional regulator. *Biochem. Biophys. Res. Commun.* 495, 1328–1334.
- (8) Rodriguez, G. M.; Hussain, M. S.; Gambill, L.; Gao, D.; Yaguchi, A., and Blenner, M. (2016) Engineering xylose utilization in *Yarrowia lipolytica* by understanding its cryptic xylose pathway. *Biotechnol. Biofuels* 9, 149.
- (9) Wang, X. J.; Deng, Z. X., and Liu, T. G. (2019) Marker-free system using ribosomal promoters enhanced xylose/glucose isomerase production in *Streptomyces rubiginosus*. *Biotechnol. J.* 14, 1900114.
- (10) David, F.; Nielsen, J., and Siewers, V. (2016) Flux Control at the Malonyl-CoA Node through Hierarchical Dynamic Pathway Regulation in *Saccharomyces cerevisiae*. *ACS Synth. Biol.* 5, 224.
- (11) Teo, W. S.; Hee, K. S., and Chang, M. W. (2013) Bacterial FadR and synthetic promoters function as modular fatty acid sensor-regulators in *Saccharomyces cerevisiae*. *Eng. Life Sci.* 13, 456–463.
- (12) Schwartz, C.; Curtis, N.; Lobs, A. K., and Wheeldon, I. (2018) Multiplexed CRISPR Activation of Cryptic Sugar Metabolism Enables *Yarrowia lipolytica* Growth on Cellobiose. *Biotechnol. J.* 13, 7.
- (13) Ni, L.; Tonthat, N. K.; Chinnam, N., and Schumacher, M. A. (2013) Structures of the *Escherichia coli* transcription activator and regulator of diauxie, XylR: an AraC DNA-binding family member with a LacI/GalR ligand-binding domain. *Nucleic Acids Res.* 41, 1998–2008.

- (14) Song, S., and Park, C. (1997) Organization and regulation of the D-xylose operons in *Escherichia coli* K-12: XylR acts as a transcriptional activator. *J. Bacteriol.* 179, 7025–7032.
- (15) Jusiak, B., Cleto, S., Perez-Piñera, P., and Lu, T. K. (2016) Engineering Synthetic Gene Circuits in Living Cells with CRISPR Technology. *Trends Biotechnol.* 34, 535–547.
- (16) Chavez, A., Scheiman, J., Vora, S., Pruitt, B. W., Tuttle, M., P R Iyer, E., Lin, S., Kiani, S., Guzman, C. D., Wiegand, D. J., Ter-Ovanesyan, D., Braff, J. L., Davidsohn, N., Housden, B. E., Perrimon, N., Weiss, R., Aach, J., Collins, J. J., and Church, G. M. (2015) Highly efficient Cas9-mediated transcriptional programming. *Nat. Methods* 12, 326–328.
- (17) Shao, J., Wang, M., Yu, G., Zhu, S., Yu, Y., Heng, B. C., Wu, J., and Ye, H. F. (2018) Synthetic far-red light-mediated CRISPR-dCas9 device for inducing functional neuronal differentiation. *Proc. Natl. Acad. Sci. U. S. A.* 115, 6722–6730.
- (18) Madzak, C., Gaillardin, C., and Beckerich, J. M. (2004) Heterologous protein expression and secretion in the non-conventional yeast *Yarrowia lipolytica*: a review. *J. Biotechnol.* 109, 63–81.
- (19) Skjoedt, M. L., Snoek, T., Kildegaard, K. R., Arsovska, D., Eichenberger, M., Goedecke, T. J., Rajkumar, A. S., Zhang, J., Kristensen, M., Lehka, B. J., Siedler, S., Borodina, I., Jensen, M. K., and Keasling, J. D. (2016) Engineering prokaryotic transcriptional activators as metabolite biosensors in yeast. *Nat. Chem. Biol.* 12, 951–958.
- (20) Dulerio, R., Brunel, F., Dulerio, T., Ledesmaamaro, R., Vion, J., Trassaert, M., Thomas, S., Nicaud, J. M., and Leplat, C. (2017) Using a vector pool containing variable-strength promoters to optimize protein production in *Yarrowia lipolytica*. *Microb. Cell Fact.* 16, 31.
- (21) Ledesmaamaro, R., and Nicaud, J. M. (2016) *Yarrowia lipolytica* as a biotechnological chassis to produce usual and unusual fatty acids. *Prog. Lipid Res.* 61, 40–50.
- (22) Shabbir Hussain, M., Gambill, L., Smith, S., and Blenner, M. A. (2016) Engineering Promoter Architecture in Oleaginous Yeast *Yarrowia lipolytica*. *ACS Synth. Biol.* 5, 213–223.
- (23) Zhang, J., Barajas, J. F., Burdu, M., Ruegg, T. L., Dias, B., and Keasling, J. D. (2017) Development of a Transcription Factor-Based Lactam Biosensor. *ACS Synth. Biol.* 6, 439–445.
- (24) Machado, L. F. M., and Dixon, N. (2016) Development and substrate specificity screening of an in vivo biosensor for the detection of biomass derived aromatic chemical building blocks. *Chem. Commun. (Cambridge, U. K.)* 52, 11402–11405.
- (25) Park, J., Hong, S.-K., and Chang, Y. K. (2015) Production of DagA and ethanol by sequential utilization of sugars in a mixed-sugar medium simulating microalgal hydrolysate. *Bioresour. Technol.* 191, 414–419.
- (26) Koyanagi, K. O., Hagiwara, M., Itoh, T., Gojobori, T., and Imanishi, T. (2005) Comparative genomics of bidirectional gene pairs and its implications for the evolution of a transcriptional regulation system. *Gene* 353, 0–176.
- (27) Hu, Q., Tong, H., Zhao, D., Cao, Y., Zhang, W., Chang, S., Yang, Y., and Yan, Y. (2015) Generation of an efficient artificial promoter of bovine skeletal muscle  $\alpha$ -actin gene (ACTA1) through addition of cis-acting element. *Cell. Mol. Biol. Lett.* 20, 160–176.
- (28) Strittmatter, G., and Chua, N. H. (1987) Artificial Combination of Two Cis-Regulatory Elements Generates a Unique Pattern of Expression in Transgenic Plants. *Proc. Natl. Acad. Sci. U. S. A.* 84, 8986–8990.
- (29) Seila, A. C., Core, L. J., Lis, J. T., and Sharp, P. A. (2009) Divergent transcription: a new feature of active promoters. *Cell Cycle* 8, 2557–2564.
- (30) Ryu, S., and Trinh, C. T. (2018) Understanding Functional Roles of Native Pentose-Specific Transporters for Activating Dormant Pentose Metabolism in *Yarrowia lipolytica*. *Appl. Environ. Microbiol.* 84, e02146–02117.