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Novel IF1 mechanism preventing ATP hydrolysis by the ATP synthase subcomplex in *Saccharomyces cerevisiae*.

Orane Lerouley[1], Isabelle Larrieu[1], Benoît Pinson[1,2], Marie-France Giraud[3] and Arnaud Mourier[1]*

[1] University of Bordeaux, CNRS, IBGC, UMR 5095, 33000 Bordeaux, France.
[2] Metabolic Analyses Service, TBMCore-Université de Bordeaux-CNRS UAR 3427-INSERM US005, Bordeaux, France.
[3] Univ. Bordeaux, CNRS, Bordeaux INP, CBMN, UMR 5248, F-33600 Pessac, France

* For correspondence

Arnaud Mourier
1, rue Camille Saint-Saëns
33077 Bordeaux
arnaud.mourier@ibgc.cnrs.fr

Abstract

The mitochondrial F_1F_0-ATP synthase is crucial for maintaining the ATP/ADP balance which is critical for cell metabolism, ionic homeostasis, cell division, proliferation and motility. This enzyme, conserved across evolution, is found in the mitochondria or chloroplasts of eukaryotic cells and the plasma membrane of bacteria. *In vitro* studies have shown that the mitochondrial F_1F_0-ATP synthase is reversible, capable of hydrolyzing instead of synthesizing ATP. In vivo, its reversibility is inhibited by the endogenous peptide IF1 (Inhibitory Factor 1), which specifically prevents ATP hydrolysis in a pH dependent manner. Despite its presumed importance, the loss of IF1 in various model organisms does not cause severe phenotypes, suggesting its role may be confined to specific stress or metabolic conditions yet to be discovered. In this study, we explored the structural and physiological importances of IF1 inhibitory peptides in *Saccharomyces cerevisiae*. Our analyses indicate that inhibitory peptides are crucial to mitigating metabolic adverse outcomes caused by mitochondrial depolarizing stress under glyco-oxidative metabolic conditions. Under glyco-oxidative metabolic state, the energy maintenance relies both on glycolysis and oxidative phosphorylation. Additionally, we found that the absence of IF1 destabilizes the nuclear-encoded free F_1 subcomplex. This novel mechanism of action highlights the role of IF1 in preventing harmful ATP wastage, offering new insights into its function under physiological and pathological conditions.

Introduction

The mitochondrial F_1F_0-ATP synthase is among the most advanced molecular enzymatic nanomachines in the living word. This enzyme is highly evolutionary conserved (Sinha and Wideman, 2023), and ubiquitous in the mitochondria or chloroplasts of eukaryotic cells, as well as in the plasma membrane of bacteria (Lau et al., 2008; Hahn et al., 2018; Gu et al., 2019; Pinke et al., 2020; Yang et al., 2020; Courbon and Rubinstein, 2022). This multisubunit enzyme is a cornerstone of the oxidative phosphorylation system (OXPHOS) as it transduces the proton electrochemical gradient (ΔμH+) generated by the respiratory chain, to synthesize ATP from ADP and inorganic phosphate (Mitchell, 1961; Boyer et al., 1973; Stock et al., 1999; Watt et al., 2010). In *Saccharomyces cerevisiae*, this 600 kDa enzyme comprises a catalytic domain F_1 ($\alpha_3\beta_3\gamma\delta\varepsilon$) and a F_0 region, divided in a membranous rotor (Su 9_{10}-ring) and a peripheral stalk (su 4, su 6, su 8, su f, OSCP, su d, su h, su i/j) that connects the catalytic head to the rotor ring. Three additional subunits, Su e, su g and su k are involved in enzyme dimerization. Proton translocation across two hemi-channels at the interface of su6 and the membranous ring induces the ring rotation, that triggers the rotation of a central stalk (γ,δ,ε) inside the two catalytic subunits (α and β), enabling conformational changes required for ATP-synthesis. The eukaryotic F_1F_0-ATP synthase are composed of 17 different subunits, which are encoded by the nuclear (nDNA) or mitochondrial genome (mtDNA) (Senior, 1988; Kühlbrandt, 2019). The dual genetic origin of the F_1F_0-ATP synthase implies that gene expressions from both genomes must be tightly coordinated to ensure proper biogenesis and assembly of the enzyme. Nevertheless, in cells presenting defectives mitochondrial genome levels and expression or impaired ATP synthase assembly, F_1 is commonly found assembled as a stable subcomplex capable of ATP hydrolysis (Tzagoloff, 1969; Carrozzo et al., 2006; Wittig et al., 2010). The F_1F_0-ATP synthase, along with glycolysis and other pathways that allow substrate-level phosphorylation, is critical in maintaining the ATP/ADP balance, which is required for cell metabolism, ionic homeostasis, cell division, proliferation and motility. In multicellular organisms, the mitochondrial ATP synthesis is finely adjusted to sustain specialized function of differentiated cells, and in human defective OXPHOS-driven ATP synthesis causes multiple and severe diseases frequently affecting high-energy demanding tissues such as cardiac and skeletal muscles, as well as nervous system (Galber et al., 2021).

Interestingly, the mitochondrial F_1F_0-ATP synthase is fully reversible and *in vitro* experiment performed on purified enzymes or functional mitochondria demonstrated that the ATP hydrolysis could be coupled to protons translocation, generating protons

electrochemical potential across the inner mitochondrial membrane (Boyer et al., 1973; Pietrobon et al., 1983; Mourier et al., 2010). However, the reversibility of the F_1F_0-ATP synthase is, under physiological conditions, prevented by the membrane potential generated by the respiratory chain and is only observed when the respiratory chain is blocked (chemical inhibitor or anoxia), or when the proton electrochemical membrane potential is abolished. The reversibility of the F_1F_0-ATP synthase is also regulated by a nuclear encoded inhibitory peptide, so called inhibitory factor 1 (IF1), which can physically interact and inhibit the F1 catalytic domain (Pullman and Monroy, 1963). Since its discovery, homologs of IF1 were found and characterized in other species (Cintrón and Pedersen, 1979; Hashimoto et al., 1981; Matsubara et al., 1981; Norling et al., 1990; Ichikawa and Ogura, 2003). The IF1 amino acid sequences are well conserved across evolution, and for yet unclear reason, two homologous inhibitory peptides, namely IF1 and STF1 (STabilizing Factor 1), presenting redundant activity were identified in *S. cerevisiae* (Hashimoto et al., 1987; Cabezon et al., 2002; Venard et al., 2003). An important wealth of experiments on independent eukaryote models have contributed to characterize the mechanism of action (Pullman and Monroy, 1963; Hashimoto et al., 1981, 1984; Cabezon et al., 2000, 2002; Venard et al., 2003), as well as the structural interaction of these peptide inhibitor with the F_1F_0-ATP synthase (Cabezón et al., 2001; Robinson et al., 2013; Boreikaite et al., 2019; Gu et al., 2019; Mühleip et al., 2021; Romero-Carramiñana et al., 2023). One of the most remarkable and evolutionary conserved features of the IF1 inhibition is its regulation by pH conditions, being optimal under neutral or slightly acidic pH conditions and inactive at pH 8 (Pullman and Monroy, 1963; Hashimoto et al., 1987). The pH-dependent IF1 inhibition of F_1F_0-ATP synthase strikingly aligns and supports its function, potentiating its capacity to prevent ATP hydrolysis under depolarization when the delta pH is abolished. Interestingly, the importance of IF1 under genetic or chemical stress preventing the maintenance of membrane potential by the respiratory chain has been confirmed in various model organisms (Buchet and Godinot, 1998; Rouslin and Broge, 1996; Sgarbi et al., 2018; Venard et al., 2003).

The Cryo-EM structures of oligomeric F_1F_0-ATP synthases demonstrated that IF1 dimers, could bridge adjacent F_1F_0-ATP synthase dimers, suggesting that IF1 could stabilize oligomers (Cabezón et al., 2000; Pinke et al., 2020; Gu et al., 2019). Functional investigations in mammalians cells and mouse models supported the idea that IF1 regulates the F_1F_0-ATP synthase oligomerization (Domínguez-Zorita et al., 2023) and even suggested that the IF1 could also regulate ATP synthesis (García-Bermúdez et al., 2015; Sánchez-Cenizo et al., 2010). However, the role of IF1 in controlling the F_1F_0-ATP synthase oligomerization and ATP synthesis activity remains debated and needs to be

confirmed in other model organisms (Dienhart et al., 2002; Lucero et al., 2021; Gatto et al., 2022). The current controversy over the role of IF1 in energy metabolism partly arises from the lack of methods to monitor, *in vivo*, the ATP hydrolysis by the mitochondrial ATP synthase operating in reverse. Furthermore, the absence of major phenotypes associated with IF1 loss in many organisms suggests that its action may be limited to specific stress or metabolic conditions that remain to be discovered (Ichikawa et al., 1990; Nakamura et al., 2013; Fernández-Cárdenas et al., 2017).

The goal of our study was to clarify the structural and physiological roles of inhibitory peptide IF1/STF1 in the yeast *S.cerevisiae*. Our analyses demonstrate that the IF1/STF1 activity is dispensable to sustain the growth of yeast under 'respiro-fermentative' or 'respiratory strict' carbon sources. However, we observed that inhibitory peptides are key to sustain growth of yeast subjected to mitochondrial depolarizing stress under glyco-oxidative metabolic conditions. We also hereby demonstrate that loss of inhibitory peptides does not impact high supramolecular organization of the F_1F_0-ATP synthase but surprisingly destabilize the free F_1 subcomplex. This discovery prompted us to revisit the role of the free F_1 subcomplex to sustain the ability for *S. cerevisiae* to lose and to grow in total or partial absence of mitochondrial genome ($\rho^{-/\circ}$).

Results

IF1/STF1 inhibitors are required to maintain the ATP synthase free F_1 subcomplex.

Independent works have previously established that *S. cerevisiae* expresses two F_1F_0-ATP synthase inhibitory peptides named IF1 and STF1 respectively encoded by the genes *INH1* and *STF1* (Ichikawa et al., 1990; Hashimoto et al., 1990). Therefore, to investigate the role of F_1F_0-ATP synthase endogenous inhibitory peptides on yeast energy producing system and metabolism, we generated an *inh1*Δ *stf1*Δ double knockout strain. The complete loss of IF1 and STF1 was validated by Western blot analyses performed on total protein extracted from yeast harvested during the exponential growth on non-fermentable carbon source (glycerol 2%) (Figure 1A). We observed that the loss of both peptide inhibitors did not affect the growth on respiratory strict carbon sources such as lactate (2%) (Figure 1B). This unaltered growth on lactate carbon source, which depends on mitochondrial OXPHOS content and activity (Devin et al., 2006), suggested that the loss of IF1 and STF1 did not strongly affect OXPHOS capacities under physiological conditions. We then performed classical native polyacrylamide gel electrophoresis to characterize the supramolecular assembly of the F_1F_0-ATP synthase in *inh1*Δ *stf1*Δ purified mitochondria (Figure 1C). The in-gel ATPase activity staining demonstrated that, in line with previous reports (Dienhart et al., 2002), the F_1F_0-ATP synthase monomers and dimers were

unchanged in *inh1*Δ *stf1*Δ. Interestingly, our native PAGE experiments demonstrates that levels of higher F_1F_0-ATP synthase oligomers were not impacted either by the loss of IF1 and STF1 (Figure 1C). However, in contrast to the F_1F_0-ATP synthase oligomers, we noticed that the free F_1 subcomplex level was almost undetectable in *inh1*Δ *stf1*Δ. The free F_1 subcomplex used to be frequently interpreted as a degradation or destabilization by products of the F_1F_0-ATP synthase potentially occurring during mitochondrial isolation or detergent solubilization. To minimize the risk of degradation, we decided to characterize the F_1F_0-ATP synthase supramolecular organization on total soluble protein extract bypassing potential mitochondrial degradations inherent to the fastidious mitochondrial isolation procedure. Despite dampening the resolution and characterization of high molecular weight complexes, the BN-PAGE performed on total cell extracts confirmed that free F_1 subcomplex was present in control yeast but lost in *inh1*Δ *stf1*Δ (Figure 1D). Intriguingly, in contrast to the F_1F_0-ATP synthase monomers and oligomers levels, the free F_1 subcomplex was clearly detected in WT under blue native and hardly visible under clear native PAGE conditions. This observation prompted us to determine if the free F_1 subcomplex observed in BN-PAGE could result from (i) the potential impact of the Coomassie brilliant blue on destabilization of the fully assembled complexes (V and oligomers) or (ii) the fact that migration of the free F_1 would rely on the binding of the charged Coomassie dye. To this end we performed CN or BN-PAGE to characterize the F_1F_0-ATP synthase assemblies present in digitonin solubilized proteins present in (i) total cell extracts, (ii) total cell membrane extracts and (iii) total cell soluble fraction (Figure 1E). As expected, the membrane and soluble fractionation could efficiently separate the membrane-anchored fully assembled ATP synthase from the membrane-free F_1 subcomplex, confirming that the free F_1 subcomplex is a soluble entity. Moreover, the absence of the free F_1 subcomplex in the solubilized membrane extract demonstrated that this subcomplex is not a destabilization by products of the fully assembled ATP synthase post solubilization. Our conclusion supporting that the free F_1 subcomplex is not a destabilization by product was strengthened by the titration of the ratio between digitonin and mitochondrial protein (Figure S1A). We observed that the progressive increase in digitonin to protein ratio gradually destabilized oligomers, but did not impact the levels of free F_1 subcomplex detected in WT or in *inh1*Δ *stf1*Δ. Consequently, the faint level of free F_1 observed in all extracts subjected to CN-PAGE suggested that the migration of the soluble free F_1 subcomplex is heavily conditioned by the Coomassie-conferred charge (Figure 1E). Altogether, our analyses clearly indicate that the amounts of free soluble F_1 subcomplex rely on IF1/STF1 inhibitors.

IF1 binds and inhibits ATP synthase oligomers, monomers and free F_1 subcomplex.

The intriguing interdependency between IF1/STF1 and the free F_1 subcomplex prompted us to further investigate the interplay between these actors. First, to gain structural insights in the interaction between IF1 and the mitochondrial F_1F_0-ATP synthase, we performed two-dimensional electrophoresis *i.e* BN-PAGE followed by a SDS-PAGE denaturing second dimension (Figure 2A). The Western blot experiments confirmed that the entities identified so far through their in-gel ATPase activities (Figure 1C-E), were indeed the mitochondrial F_1F_0-ATP synthase complexes and subcomplexes (Figure 2A) and confirmed the drastic loss of free F_1 in *inh1*Δ *stf1*Δ. Beyond some specific subunits of the F_1F_0-ATP synthase, we also managed to localize IF1 proteins and confirmed that IF1 physically interacts with the different F_1F_0-ATP synthase assemblies (Figure 2A and B). Interestingly, the densitometric signal quantification demonstrated that IF1 exhibit an even binding capacity toward the different F_1F_0-ATP synthase assemblies (Figure 2B). However, we could not detect or visualize STF1 in the second dimension. The previously reported lower binding efficiency and affinity of STF1 for the F_1F_0-ATP synthase compared to IF1 (Venard et al., 2003), could likely explain the undetectable level of STF1 following the digitonin extraction and BN-PAGE procedures. Then we functionally characterize the interplay between IF1/STF1 and F_1F_0-ATP synthase assemblies on non-solubilized samples (Figure 2 C-E). The ATP hydrolysis flux measurement performed on yeast total protein extract confirmed that the pH dependent inhibition of the ATPase activity was completely abolished in *inh1*Δ *stf1*Δ (Figure 2C). Furthermore, our analyses demonstrated that the oligomycin-sensitive ATPase activity, associated with fully assembled F_1F_0-ATP synthases, assessed in WT and *inh1*Δ *stf1*Δ samples were identical (Figure 2D). In contrast, the oligomycin-insensitive ATPase activity, mainly related to free F_1 subcomplex, was drastically reduced in the *inh1*Δ *stf1*Δ strain (Figure 2D). The complete oligomycin insensitivity of the ATP hydrolysis activity assessed in the soluble fraction, containing exclusively free F_1 subcomplexes (Figure 1E), confirmed that the oligomycin-resistance was inherent to free F_1 subcomplexes (Figure 2E). Interestingly, the oligomycin-resistant ATPase activity of free F_1 subcomplexes was fully inhibited by IF1/STF1 through its characteristic pH dependent inhibition (Figure 2E), confirming their capacity to physically and functionally interact (Figure 2 A-B). This functional characterization nicely corroborates the structural observation showing that *inh1*Δ *stf1*Δ and WT present similar levels of F_1F_0-ATP synthases monomers and oligomers (Figure 1C-E). Altogether, native PAGE (Figure 1C-E) and functional analyses demonstrate that the oligomycin-insensitive free F_1 subcomplex is almost completely lost in *inh1*Δ *stf1*Δ (Figure 2D and E).

IF1/STF1 are specifically involved in free F_1 subcomplex stabilization

To further investigate the interplay between the inhibitory peptides IF1/STF1 and the free F_1 subcomplex, we decided to evaluate the stability of the different F_1F_0-ATP synthase assemblies in *inh1*Δ *stf1*Δ strain. To this end, we characterized the fate of the different ATP synthase assemblies in WT and *inh1*Δ *stf1*Δ strain grown in complete medium containing glycerol (2%) and subjected to a cycloheximide treatment inhibiting the cytosolic translation (Buchanan et al., 2016). This experiment clearly showed that a 90 minutes treatment did not affect the steady state levels of the inhibitory peptide IF1/STF1 but severely affected, with distinct kinetics, the levels of F_1F_0-ATP synthase assemblies (Figure 3A and B). Interestingly, the destabilization profile of F_1F_0-ATP synthase monomers and oligomers in *inh1*Δ *stf1*Δ was comparable to WT, and the loss of these different entities was not followed by any detectable increase in the free F_1 subcomplex level. To further investigate the importance of IF1/STF1 and free F_1 subcomplex interplay, we decided to investigate how loss of IF1 impacts the phenotype of the *atp18*Δ strain lacking the F_1F_0-ATP synthase subunit i/j. This strain was previously characterized and presents a perturbed assembly and fragilized supramolecular organization of the F_1F_0-ATP synthase associated with a profound deficiency in enzyme activity. Loss of subunit i/j was also associated with an increased free F_1 subcomplex and oligomycin-insensitive activity (Vaillier et al., 1999; Wagner et al., 2010). The CN and BN-PAGE performed on the solubilized ATP synthase from total protein cell extract confirmed previous observations demonstrating that the levels of F_1F_0-ATP synthase oligomers were severely reduced whereas the levels of free F_1 subcomplex were strongly increased (Figure 3C). Interestingly, the isolated loss of IF1, in the *atp18*Δ *inh1*Δ strain we engineered, drastically reduced the level of the free F_1 subcomplex without affecting the levels of the monomeric F_1F_0-ATP synthase present in the *atp18*Δ strain (Figure 3C). The predominant role of IF1 on F_1F_0-ATP synthase stability compared to STF1 was also observed on purified mitochondria where we confirmed that the isolated loss of IF1 was sufficient to almost completely abolish the pH dependent inhibition of the F_1F_0-ATP synthase (Figure S3A). As expected, the F_1F_0-ATP synthase deficiency drastically impaired the growth of the *atp18*Δ on medium containing glycerol (2%) a non-fermentable carbon source (Figure 3D). Intriguingly, the combined loss of IF1 and free F_1 subcomplex in this *atp18*Δ strain did not worsen nor rescue its growth deficiency (Figure 3D).

IF1/STF1 mitigate the impact of mitochondrial depolarizing stress on glycerol medium.

To further evaluate the metabolic importance of IF1/STF1, we took advantage of the great metabolic flexibility of *S. cerevisiae* and characterized the phenotype of *inh1*Δ *stf1*Δ strain grown under various carbon sources. To this end, we compared different carbon sources promoting respiro-fermentative (glucose 0.5% and galactose 2%) and non-fermentable conditions (glycerol 2% and lactate 2%). The respective capacity to metabolize these carbon sources and produce biomass were assessed using drop tests and growth curves (Figures 4A and B). In parallel, the cell respirations of yeast grown on different carbon sources were recorded using high-resolution respirometer O2K oxygraph under endogenous conditions, or in presence of ethanol alleviating potential kinetic controls under endogenous, non-phosphorylating (triethyltin) and uncoupled (CCCP titration) states (Figure 4C). These combined approaches assessing the growth of the *inh1*Δ *stf1*Δ strain in various metabolic conditions demonstrated that the loss of the inhibitory peptides did not affect the growth (Figure 4 A and B). The cell respiration assessed during exponential phase demonstrated that OXPHOS capacities are strongly adjusted in response to the carbon sources. As expected, the overall respiration rates as well as the part of the respiration devoted to ATP synthesis (respiration loss in response to triethyltin), were both gradually increased from the highly glycolytic glucose medium to the highly oxidative lactate medium. Interestingly, the *inh1*Δ *stf1*Δ strain grown under galactose, glycerol and lactate, consistently exhibited a significantly higher respiration compared to WT strain. These results indicate that the combined loss of IF1/STF1 is linked to an increased OXPHOS activity (Figure 4C).

The enhanced OXPHOS activity of the *inh1*Δ *stf1*Δ strain prompted us to evaluate its capacity to respond to OXPHOS uncoupling stress induced by the mitochondrial depolarizing agent CCCP. To this end, yeast cultures were supplemented with the minimal CCCP concentration abolishing cell respiration's responses to triethyltin or CCCP validating that mitochondria are fully uncoupled (Figure 4C). The CCCP treatment did not affect the growth of the *inh1*Δ *stf1*Δ and WT strains under fermentable carbon sources as glucose (0.5%) and galactose (2%) (Figure 4A and B). However, the CCCP treatment differentially impacted the growth of the two strains under non fermentable carbon sources *i.e.* glycerol (2%) and lactate (2%) (Figure 4A and B). The mitochondrial uncoupling stress, under lactate (2%) medium, almost completely prevented the growth of both strains (Figure 4A and B) causing severe deficiency of cell respiration (Figure 4C). In contrast, the *inh1*Δ *stf1*Δ and WT strains cultivated under glycerol (2%) strongly differ in their ability to tolerate the uncoupling stress (Figure 4A and B). Our analyses clearly demonstrate that the IF1/STF1 inhibitors are essential to mitigate the impact of OXPHOS uncoupling stress on cell growth (Figure 4A and B) and respiration (Figure 4C).

Glycerol is a glyco-oxidative metabolic condition where the energy balance relies on ATP production from both glycolysis and OXPHOS.

To further investigate the IF1/STF1 mediated mechanism involved in the OXPHOS uncoupling stress response, we first quantified the IF1 and STF1 levels in the different growth conditions. The western blot analyses performed on total proteins extract from WT yeast grown under various carbon sources demonstrated that the levels of both IF1 and STF1 normalized to the F_1F_0-ATP synthase subunit β, were almost doubled under the different non-fermentable conditions compared to glucose and galactose conditions (Figure 5A and B). Our results also showed that the levels of both inhibitors were not impacted during the OXPHOS uncoupling stress (Figure S5A). The uniform expression of IF1 and STF1 under lactate and glycerol conditions indicated that the WT strain's resistance toward uncoupling stress in glycerol media was not merely due to changes in IF1/STF1 expression levels (Figure 5A-B). We then decided to challenge the assumed metabolic homogeneity between glycerol and lactate conditions, commonly defined as non-fermentable carbon sources relying on OXPHOS activity. To determine the dependency of energy metabolic toward the OXPHOS or glycolytic produced ATP, we followed the growth of genetically engineered yeast mutants presenting altered glycolysis or OXPHOS driven ATP production (Figure 5C). The previously generated and characterized mutant yeast strains *pyk1*Δ and *atp18*Δ (Sprague, 1977; Vaillier et al., 1999), were selected to decipher the growth dependency toward these different energy producing pathways. The drop test analyses, nicely confirmed that the growth on glucose and galactose media almost exclusively relied on the glycolysis-driven ATP production (insensitive to OXPHOS ATP production defects). Conversely, the growth on lactate medium almost exclusively relied on the OXPHOS-driven ATP production (insensitive to defective glycolytic ATP production) (Figure 5C). However, the drop test experiment unexpectedly demonstrated that the growth on glycerol medium is either hindered by defects in OXPHOS or glycolysis driven ATP production (Figure 5C). This strongly confirms the ability of glycerol metabolic by-products as glycerol-3-phosphate (G3P) and dihydroxyacetone phosphate (DHAP) can fuel both the OXPHOS from Gut2p and the glycolysis from the triose phosphate intermediates (Figure 5D).

To further investigate the metabolic importance of the alternative glycolytic-driven ATP production in response to uncoupling stress, we measured, using HPIC method, the adenylic energy charge of *inh1*Δ *stf1*Δ and WT strains cultivated under glycerol medium (Figure 5E). The adenylic energy charge measurement demonstrated that the glycolytic driven ATP production pathway could preserve the cell energy status of WT from

OXPHOS uncoupling stress. The fact that adverse energetic outcomes associated with the loss of IF1/STF1 only appeared under depolarization stress strongly suggest that the drop of adenylic energy charge is caused by the non-prevented ATP hydrolysis from the reversed mitochondrial F_1F_0-ATP synthase. Further analyses demonstrated that this acute energy crisis occurring within the first hour of treatment (Figure 5E), affected the cell respiration in later time points (Figure 4C). Interestingly, the respiration defects were associated with decreased levels and activity of the complex III, IV and V (Figure 5F and G), but the OXPHOS deficiencies were not linked to mitochondrial genome deficiency (Figure 5H) or loss of complex IV subunits (Figure 5I). Altogether, our analyses demonstrate that the canonical role of IF1/STF1 in preventing ATP hydrolysis and safeguarding energy metabolism under mitochondrial depolarization stress is unmasked under the very specific glyco-oxidative metabolic condition *i.e.* where yeast energy metabolism relies both on glycolysis and OXPHOS activities.

The IF1/STF1 inhibitors as well as F_1F_0-ATP synthase free F_1 subcomplex are both dispensable for the viability of $\rho^{-/\circ}$ yeasts

According to several reports, the ATPase activity of the free F_1 subcomplex coupled to the electrogenic activity of the adenylic nucleotides translocator (ANT), is crucial to support mitochondrial membrane potential and growth of yeast lacking their mitochondrial genome ($\rho^{-/\circ}$ cells) (Clark-Walker, 2007; Giraud and Velours, 1997; Kominsky et al., 2002). The improved growth capacity of $\rho^{-/\circ}$ cells lacking IF1 also strongly supported the importance of the free F_1 subcomplex ATPase activity in supporting the growth of mtDNA deprived cells (Liu et al., 2021). These previous works supporting that free F_1 subcomplexes could be more active in the absence of IF1 in the context of $\rho^{-/\circ}$, would contrast with the interdependence between IF1/STF1 and free F_1 subcomplex we observed (Figure 1 and 2). Therefore, we decided to characterize the interplay between IF1/STF1 and free F1 subcomplex in the context of $\rho^{-/\circ}$ cells. First, we analyzed during the stationary growth phase of WT and *inh1*Δ *stf1*Δ, the proportion of cells undergoing $\rho^{-/\circ}$conversion. In line with previous works, we observed that the loss of IF1/STF1 activity was in fact favoring the loss of mitochondrial genome and the conversion of yeast into $\rho^{-/\circ}$cells (Figure 6A). Then, we generated stable WT and *inh1*Δ *stf1*Δ $\rho^{-/\circ}$ cells and observed that the IF1/β ratio was unchanged in WT $\rho^{-/\circ}$ whereas the STF1/β ratio, while not significant, tended to be reduced (Figure 6B). While favoring the conversion into $\rho^{-/\circ}$ cells (Figure 6A), the loss of IF1/STF1 did not impact the $\rho^{-/\circ}$ cells growth rate under fermentative conditions (Figure 6C). Moreover, our data demonstrated that the overall ATP hydrolysis activity (Figure 6D)

as well as the free F_1 subcomplex (Figure 6E) were barely detected in total extract from WT and *inh1*Δ *stf1*Δ $\rho^{-/\circ}$ cells. Interestingly, BN-PAGE experiments performed on highly concentrated extracts from $\rho^{-/\circ}$ cells confirmed that the free F_1 subcomplex levels were, like in the ρ^{+} context (Figure 1D and E), severely reduced in the *inh1*Δ *stf1*Δ $\rho^{-/\circ}$ compared to the WT $\rho^{-/\circ}$cells. Collectively, our findings suggest that the deletion of IF1/STF1 is beneficial for ρ-/° cells, but they also refute hypotheses supporting that this effect could be tightly linked to an activation of the F_1 subcomplex driven ATP hydrolysis. Instead, our results demonstrated that the loss of IF1/STF1 together with the free F_1 subcomplex favored the conversion into $\rho^{-/\circ}$, and did not affect the growth of $\rho^{-/\circ}$ cells on fermentable carbon source (Figure 6).

Discussion

The present work confirmed that, in contrast to their mammalian homologs IF1, the yeast IF1/STF1 inhibitors are dispensable for the biogenesis and stability of F_1F_0-ATP synthase dimers and provides first evidence that IF1/STF1 are not required for the stability of F_1F_0-ATP synthase oligomers. The resolution of the F_1F_0-ATP synthases tetramers' structures by Cryo-EM, demonstrating that IF1 dimers could bridge and likely stabilize adjacent dimers (Gu et al., 2019; Pinke et al., 2020; Mühleip et al., 2021), has supported the previously proposed role of IF1 in the supramolecular structuration of the mammalian F_1F_0-ATP synthase (Cabezón et al., 2000). The role of mammalian IF1 in F_1F_0-ATP synthase supramolecular organization was recently comforted, by single molecule tracking microscopy and native electrophoresis performed on IF1 knock-in and knock-out cell lines (Romero-Carramiñana et al., 2023; Weissert et al., 2021). In contrast, the lack of cryo-EM structure of yeast F_1F_0-ATP synthase oligomers larger than dimers (Hahn et al., 2016), along with previously characterized differences in IF1 dimerization and function, has cast doubts on the potential implication of IF1/STF1 inhibitors in the F_1F_0-ATP synthase supramolecular organization in yeast (Cabezon et al., 2002; Hong and Pedersen, 2002; Le Breton et al., 2016). Our work confirms previous findings showing that the levels of F_1F_0-ATP synthase dimers remained unchanged in *inh1*Δ *stf1*Δ (Dienhart et al., 2002), but also demonstrated that loss of these inhibitory peptides does not preclude the assembly and levels of higher molecular weight F_1F_0-ATP synthase oligomers (Figure 1C). Instead, structural and functional investigations consistently demonstrated that IF1 is required to maintain the levels of the free F_1 subcomplex, which is functionally characterized by its oligomycin insensitivity (Figure 1 and 2)(Wittig et al., 2007).

The free F_1 subcomplex observed under native PAGE or density gradients used to be considered as an artifact resulting from the destabilization of the F_1F_0-ATP synthase holoenzyme by the action of detergent or improper sample preparation and storage (Ackerman and Tzagoloff, 1990; Jänsch et al., 1996; Wittig et al., 2007). The native PAGE and solubilization techniques development combined with the use of milder detergent as digitonin have then convincingly demonstrated that the free F_1 subcomplexes were stable assembly intermediates formed independently from the ATP synthase F_0 sectors (Li et al., 2012; Nijtmans et al., 1995). The native PAGE and oligomycin sensitive enzymatic analyses, have independently demonstrated that the ratio between the free F_1 subcomplex and the fully assembled F_1F_0-ATP synthase were not impacted by the use of mild detergent or by the BN-PAGE approach. Our findings support that the free F_1 subcomplex is not a degradation by-product resulting from the digitonin treatment since no F_1 subcomplex could be detected in the digitonin-solubilized membrane fraction containing fully assembled F_1F_0-ATP synthases (Figure 1C-E). Instead, our work strongly supports previous reports claiming that the free F_1 subcomplex is a stable intermediate assembly. This hypothesis is also strengthened by the enhanced levels of free F_1 we observed in yeast presenting aberrant ATP synthase assembly as the *atp18*Δ (Figure 3C), and $\rho^{-/\circ}$ (Figure 6E and F), comforting also independent observations obtained in different model organisms (Carrozzo et al., 2006; Wittig et al., 2006, 2007; Mourier et al., 2014; He et al., 2018). Our quantitative analyses comforted independent reports demonstrating that IF1 binding and inhibitory capacities prevailed on STF1(Cabezon et al., 2002; Venard et al., 2003). Interestingly, we demonstrated that IF1 evenly binds the various ATP synthase assemblies (Figure 2A and B), and can very efficiently inhibit their ATP hydrolysis activity in a characteristic pH dependent manner (Figure 2C-E).

Several independent studies have previously demonstrated that the maintenance of mitochondrial membrane potential and the ADP/ATP translocator were essential for the survival and growth of yeast presenting long range deletion (ρ^-) or complete loss of their mitochondrial genome (ρ°) (Dupont et al., 1985; Kovácová et al., 1968; Subík et al., 1972). This specific sensitivity prompted scientist to hypothesize that the F_1 subcomplex driven ATP hydrolysis together with the electrogenic activity of the ADP/ATP translocator could be key to maintain the proton electrochemical potential across the mitochondrial inner membrane and therefore essential for the growth and survival of ($\rho^-/\circ$) yeast (Giraud and Velours, 1997; Chen and Clark-Walker, 1999; Clark-Walker, 2007). Our analyses demonstrated that the loss of IF1/STF1 associated with drastic loss of F_1 subcomplex does not prevent the yeast to undergo $\rho^-/\circ$ conditions nor impact their growth under

fermentative carbon source (Figure 6). Consequently, our results corroborate original analyses from Tzagaloff and Schatz demonstrating that the loss of subunits forming the F_1 sector did not preclude the conversion into $\rho^{-/o}$ cells (Tzagoloff et al., 1975).

For endogenous peptide inhibitors, the free F_1 subcomplex is a priority target because of its potential toxicity for the cell energy metabolism. In contrast to the fully assembled F_1F_0-ATP synthase, the toxicity of the free F_1 subcomplex stems from its lack of thermodynamic feedback inhibition by the proton electrochemical potential. The novel IF1/STF1-mediated mechanism of action identified in the present work, elegantly circumvents any potential uncontrolled ATP hydrolysis from the yeast free F_1 subcomplex. Our present work demonstrates that in the presence of IF1/STF1 the free F_1 subcomplex is tightly regulated and inhibited, whereas in the absence of IF1 the free F_1 subcomplex is not maintained (Figure 1 and 2). Altogether, our data suggest that the IF1 binding to the free F_1 subcomplex is not only preventing potential toxic ATP hydrolysis, but also stabilizing this assembly intermediate (Figure 3A). This peculiar interplay between IF1 and the yeast free F_1 subcomplex is in agreement with the parallel increase in IF1 and ATP synthase subassemblies we previously characterized in cardiac-specific knockouts developing a progressive cardiomyopathy associated with mitochondrial genome expression deficiency (Mourier et al., 2014).

Interestingly, the loss of the IF1/STF1 inhibition on the fully assembled F_1F_0-ATP synthase was associated with a mild stress increasing cell respiration capacity, but without affecting the growth rate (Figure 4). However, the CCCP-induced OXPHOS uncoupling stress unmasks the crucial role played by IF1 under a very specific metabolic condition associated with the glycerol carbon source. The systematic comparison of cell respiration of cell growing under fermentable (glucose 0.5%, galactose 2%) and non-fermentable (glycerol 2%, lactate 2%) demonstrated that the mitochondrial respiration alone was insufficient to comprehend the unique metabolic specificity of cell metabolizing glycerol (Figure 4). In contrast to the glucose and lactate conditions presenting striking differences in their respirations, it was impossible to discriminate on the basis of their endogenous respiration of yeast grown on galactose (non-fermentable) and glycerol (fermentable) (Figure 4). This observation prompted us to develop a new screen using genetically modified yeast presenting defective mitochondrial or glycolytic-driven ATP production to decipher the respective implication of the two pathways in energy balance and yeast growth (Figure 5C). This strategy demonstrated that in contrast to lactate medium where yeast growth was exclusively dependent on the mitochondrial pathway, the growth on

glycerol also relied on the Pyk1 glycolysis activity. This observation demonstrated that the glycerol, in contrast to lactate, is not a strict ‘non-fermentable’ carbon source strictly relying on mitochondrial energy metabolism. This observation corroborates recent hypothesis based on transcriptomic and metabolomic analyses and challenging the classification of glycerol as a ‘non-fermentable’ carbon source (Aßkamp et al., 2019; Xiberras et al., 2019). Assessing the relative dependence of cell energy metabolism on glycolysis and oxidative phosphorylation was more pertinent for understanding the role of IF1/STF1 in OXPHOS uncoupling stress in glycerol, than simply characterizing metabolism through respiro-fermentative properties. Accordingly, the specific IF1/STF1 dependency of cells under glycerol, redefined here as a glyco-oxidative metabolic condition, suggests that preventing mitochondrial ATP hydrolysis is crucial for cell growth only when energy metabolism evenly relies on both glycolysis and OXPHOS processes (Figure 5 C-E). In contrast, the unrepressed ATPase activity did not affect the cell growth on highly glycolytic conditions (glucose and galactose) and conversely could not be compensated under highly oxidative metabolic conditions (lactate). We believe that this new approach deciphering the respective role of glycolysis and OXPHOS in cell energy balance applied to the mammalian context could help understanding the intriguing role of IF1 in numerous tumors undergoing hypoxic stress and overexpressing this inhibitory peptide (Sánchez-Aragó et al., 2013; Sgarbi et al., 2018).

_ Figure 1 _

IF1/STF1 are required to maintain the F_1F_0-ATP synthase free F_1 subcomplex levels.

(A) Western blot performed on total cell protein extracts purified from WT, *inh1*Δ, *stf1*Δ and *inh1*Δ *stf1*Δ mutants, grown on glycerol 2% medium. (representative of n = 5 independent experiments)

(B) Growth of WT (black) and *inh1*Δ *stf1*Δ (red) mutant on lactate 2% medium, following the optical density of the culture at 550 nm. (n = 5 independent experiments).

(C) CN-PAGE (3-12%) electrophoresis performed with purified mitochondria from WT and *inh1*Δ *stf1*Δ cells grown on lactate 2% medium, solubilized with GDN at a GDN to protein ratio of 0.5 g/g protein. The F_1F_0-ATP synthase assemblies were revealed by F_1F_0-ATP synthase hydrolytic activity in gel (CV IGA). (representative of n = 3 independent experiments)

(D) CN and BN-PAGE (3-12%) electrophoreses performed with total cell extract from WT and *inh1*Δ *stf1*Δ grown on glycerol 2% medium solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. The F_1F_0-ATP synthase assemblies were revealed by F_1F_0-ATP synthase hydrolytic activity in gel (CV IGA). (representative of n = 3 independent experiments)

(E) CN and BN-PAGE (3-12%) electrophoreses performed with total cell extract, membrane and soluble fraction obtained after ultracentrifugation from WT cell grown on glycerol 2% medium solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. The F_1F_0-ATP synthase assemblies were revealed by F_1F_0-ATP synthase hydrolytic activity in gel (CV IGA). (representative of n = 3 independent experiments)

_ Figure 2 _

IF1 binds and inhibits ATP synthase oligomers, monomers and free F_1 subcomplexe.

(A) Western blot following 2D-BN/SDS-PAGE performed with total cell extracts from WT and the *inh1*Δ *stf1*Δ grown on glycerol 2% medium. During the extraction and solubilization, the pH was conserved at 6.4 to preserve the IF1/STF1 binding. (representative of n = 3 independent experiments)

(B) Densitometric quantification of western blot following 2D-BN/SDS-PAGE performed with total cell extracts from WT cell grown on glycerol 2% medium. For each F_1F_0-ATP synthase assemblies, the western blot signal obtained with IF1 signal was normalized to the β or γ subunit.

(C) Measurement of the ATP hydrolysis flux performed on total cell extracts from WT (black bars) and *inh1*Δ *stf1*Δ (red bars) grown on glycerol 2% medium by monitoring the

ATP induced phosphate production over several minutes. Experiments were performed at pH 9 (inactive inhibitors) and pH 6.4 (active inhibitors). (n = 3 independent experiments, t test unpaired, Error bars ± SEM **p<0.005)

(D) Measurement of the ATP hydrolysis flux performed on total cell extracts from WT (black bars) and *inh1*Δ *stf1*Δ (red bars) grown on glycerol 2% medium by monitoring the ATP induced phosphate production over several minutes. Experiments were performed at pH 9 (inactive inhibitors) in absence or presence of oligomycin. (n = 3 independent experiments, t test unpaired, Error bars ± SEM *p<0.05)

(E) Measurement of the ATP hydrolysis flux performed on the soluble fraction purified from total cell extracts from WT (black bars) and *inh1*Δ *stf1*Δ (red bars) grown on glycerol 2% medium by monitoring the ATP induced phosphate production over several minutes. Experiments were performed at pH 9 (inactive inhibitors) and pH 6.4 (active inhibitors), in absence or presence of oligomycin. (n = 3 independent experiments, t test unpaired, Error bars ± SEM

_ Figure 3 _

IF1 and STF1 are specifically involved in free F_1 subcomplex stabilization.

(A) BN-PAGE (3-12%) electrophoresis performed with total cell extracts, from WT and *inh1*Δ *stf1*Δ grown on glycerol 2% medium subjected to cycloheximide (250 µg/ml) during 0, 30 and 90 minutes. Samples were solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. The F_1F_0-ATP synthase assemblies were revealed by F_1F_0-ATP synthase hydrolytic activity in gel (CV IGA). (representative of n = 3 independent experiments)

(B) Western blot (left) and densitometric analysis (right) of the relative abundance of IF1 (black) and STF1 (gray) from total cell extract, from WT grown on glycerol 2% medium subjected to cycloheximide (250 µg/ml) during 0, 30 and 90 minutes. Densitometric signals were normalized to the t_0-condition without cycloheximide. The ponceau staining as well as the Coomassie blue staining presented in the upper part demonstrate (i) that samples are evenly loaded and (ii) that the tagged IF1 and STF1 produced *in vitro and used* for relative quantification levels are equally loaded in the standard. (n = 3 independent experiments, 2-way ANOVA, Error bars ± SEM)

(C) CN and BN-PAGE (3-12%) electrophoresis performed with total cell extracts, from WT, *inh1*Δ *stf1*Δ, *atp18*Δ and *atp18*Δ *inh1*Δ cell grown on glycerol 2% medium solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. The F_1F_0-ATP synthase assemblies were revealed by F_1F_0-ATP synthase hydrolytic activity in gel (CV IGA). (representative of n = 4 independent experiments)

(D) Growth of WT (black circles), *atp18*Δ (orange circles) and *atp18*Δ *inh1*Δ (brown circles) on glycerol 2% medium, following the optical density of the culture at 550 nm. (n = 3 independent experiments)

_ Figure 4 _

IF1/STF1 mitigate the impact of mitochondrial depolarizing stress on glycerol medium.

(A) Drop test performed on WT and *inh1*Δ *stf1*Δ grown on different fermentable (glucose 0.5%, galactose 2%) and non-fermentable (glycerol 2%, lactate 2%) culture media supplemented or not with CCCP (representative of n = 3 independent experiments)

(B) Growth of WT (black circles and black cross when supplemented with CCCP), and *inh1*Δ *stf1*Δ (red circle and red cross when supplemented with CCCP) cells on different fermentable (glucose 0.5%, galactose 2%) and non-fermentable (glycerol 2%, lactate 2%) culture media supplemented (cross) or not with CCCP (circle) , following the optical density of the culture at 550 nm. (n = 3 independent experiments)

(C) High resolution respirometry performed on WT (black bars and hatched black bars in presence of CCCP) and *inh1*Δ *stf1*Δ cells (red bars and hatched red bars in presence of CCCP), collected during exponential phase on different fermentable (glucose 0.5%, galactose 2%) and non-fermentable (glycerol 2%, lactate 2%) culture media supplemented (hatched bars) or not (empty bars) with CCCP (9h incubation). The oxygen consumption fluxes were normalized to optical density assessed extemporaneously. The cell respiration was measured under endogenous state and in the presence of ethanol, under endogenous, non-phosphorylating (triethyltin titration) and uncoupled (CCCP titration) states. (n ≥ 3 independent experiments, two-way ANOVA, Error bars ± SEM *p<0.05, **p<0.005, ***p<0.0005)

_ Figure 5 _

F_1F_0-ATP synthase peptide inhibitors activity is crucial to preserve energy metabolism under glyco-oxydative metabolism.

(A) Western blot and (B) densitometric analysis of the relative abundance of IF1 and STF1 in regards of the F_1F_0-ATP synthase β subunit level. Denaturing electrophoreses were performed using total cell extract of WT grown on different fermentable (glucose 0.5%, galactose 2%) and non-fermentable (glycerol 2%, lactate 2%) culture media. Densitometric signals were normalized to the glycerol condition. The ponceau staining as well as the Coomassie blue staining presented in the upper part demonstrate (i) that samples are evenly loaded and (ii) that the tagged IF1 and STF1 produced *in vitro* and used for relative

quantification levels are equally loaded in the standard. (n = 8 independent experiments, two-way ANOVA, Error bars ± SEM *p<0.05, **p<0.005).

(C) Drop test performed on WT, *pyk1Δ* thermosensitive (*ts*) mutant (37°) and *atp18Δ* mutant grown on different fermentable (glucose 0.5%, galactose 2%) and non-fermentable (glycerol 2%, lactate 2%) culture media. (representative of n = 3 independent experiments)

(D) Scheme of the main metabolic pathways involved in the ATP/ADP maintenance characterizing the so-called glyco-oxidative metabolism observed under glycerol 2% conditions.

(E) HPIC quantification of adenylic energy charge in WT (black) and *inh1*Δ *stf1*Δ (red) cells grown in the absence (circle) or presence (cross) of CCCP (1h incubation) on glycerol 2% medium. (n = 3 independent experiments, one-way ANOVA, Error bars ± SEM ***p<0.0005)

(F) BN-PAGE (3-12%) electrophoreses performed with total cell extracts from WT and *inh1*Δ *stf1*Δ grown on glycerol 2% medium solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. NADH dehydrogenases, complex IV (CIV) and F_1F_0-ATP synthase (CV) in gel activities (IGA) were performed. (representative of n = 3 independent experiments)

(G) Enzymatic activity of the respiratory chain complex III (CIII) performed on total cell extracts from WT and *inh1*Δ *stf1*Δ cultivated on glycerol 2% medium, in the presence or absence of CCCP (6h incubation). All the fluxes were normalized to WT condition without CCCP. (n ≥ 9 independent experiments, Error bars ± SEM (**p<0.005))

(H) Quantitative PCR quantification of the mitochondrial DNA to nuclear DNA ratio performed on total DNA extracted from WT and *inh1*Δ *stf1*Δ grown on glycerol 2%, in the presence (hatched bars) or absence (solid bars) of CCCP (6h incubation). (n = 3 independent experiments, 2-way ANOVA, Error bars ± SEM)

(I) Western blot (left) and densitometric (right) analysis of the relative abundance of COX2, a subunit of complex IV. Denaturing electrophoresis were performed using total cell extracts of WT and *inh1*Δ *stf1*Δ grown on glycerol 2% medium in the presence or absence of CCCP (6h incubation). Immunodecoration signals were normalized to ponceau signal. (n = 3 independent experiments, one-way ANOVA, Error bars ± SEM)

_ Figure 6 _

The IF1/STF1 inhibitors as well as F_1F_0-ATP synthase free F_1 subcomplex are both dispensable for the viability of ρ-/° yeasts

(A) Percentage of WT and *inh1*Δ *stf1*Δ cells that spontaneously partially (long range deletion) or totally lost their mitochondrial genome **$\rho^-/°$**. (n = 8 independent experiments, t test unpaired, Error bars ± SEM ***p<0.0005)

(B) Western blot (left) and densitometric analysis (right) of the relative abundance of IF1 and STF1 in regards of the F_1F_0-ATP synthase β subunit level. Denaturing electrophoresis were performed on total cell extract from WT (black) and WT $\rho^-/°$ (grey) grown on glucose 0.5% medium. (n = 3 independent experiments, t-test unpaired, Error bars ± SEM *p<0.05)

(C) Growth of WT (black circle) or WT $\rho^-/°$ (black triangle), *inh1*Δ *stf1*Δ (red circle) and *inh1*Δ *stf1*Δ $\rho^-/°$ (red triangle) cell on glucose 0.5% medium, following the optical density of the culture at 550 nm. (n = 3 independent experiments)

(D) Measurement of the ATP hydrolysis flux performed on total cell extracts from WT (black bars) and *inh1*Δ *stf1*Δ (red bars) and their $\rho^-/°$ variants, grown on glucose 0.5% medium by monitoring the ATP induced phosphate production over several minutes. Experiments were performed at pH 9 (inactive inhibitors). (n = 3 independent experiments, t test unpaired, Error bars ± SEM **p<0.005)

(E) BN-PAGE (3-12%) electrophoreses performed with total cell extracts from WT and *inh1*Δ *stf1*Δ and their respective $\rho^-/°$- variants, grown on glucose 0.5% medium. Cell extracts were solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. NADH dehydrogenases and F_1F_0-ATP synthase (CV) in gel activities (IGA) were performed. (representative of n = 3 independent experiments)

(F) BN-PAGE (3-12%) electrophoreses performed with highly concentrated total cell extracts from WT, WT $\rho^-/°$ and *inh1*Δ *stf1*Δ $\rho^-/°$ grown on glucose 0.5% medium. Cell extracts were solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. The F_1F_0-ATP synthase assemblies were revealed by ATP synthase hydrolytic activity in gel (CV IGA). (representative of n = 3 independent experiments)

SUPPLEMENTAL

_ Figure S1 _

(A) BN-PAGE (3-12%) electrophoresis performed with total cell extracts, from WT, *inh1*Δ *stf1*Δ *and atp18*Δ grown under glycerol 2% medium. Cell extracts were solubilized with increasing digitonin to protein ratio ranging from 0.5 to 6 g/g protein. The ATP synthase assemblies were revealed by F_1F_0-ATP synthase (CV) hydrolytic activity in gel (IGA). (representative of n = 3 independent experiments)

_ Figure S3 _

(A) Measurement of the ATP hydrolysis flux performed on the purified mitochondria extract from total cell extracts from WT (black bars) and *inh1*Δ (red bars) grown on lactate 2% medium by monitoring the ATP induced phosphate production flux over several minutes. Experiments were performed at pH 9 (inactive inhibitors) and pH 6.4 (active inhibitors). (n ≥ 7 independent experiments, t test unpaired, Error bars ± SEM ***p<0.0005)

_ Figure S5 _

(A) Western blot (left) and densitometric analysis (right) of the relative abundance of IF1 and STF1, using PGK1 as loading control. Denaturing electrophoreses were performed with total cell extracts grown on glycerol 2% medium supplemented or not with CCCP. The Coomassie blue staining on the upper panel demonstrates the equal loading of the IF1 and STF1 tagged produced in vitro and used for the relative quantification of inhibitors (* signal remaining from anti-STF1 antibody). (n = 3 independent experiments, t test unpaired, Error bars ± SEM)

(B) BN-PAGE (3-12%) electrophoreses performed with total cell extract from WT grown on different fermentable (glucose 0.5%, galactose 2%) and non-fermentable (glycerol 2%, lactate 2%) culture media. Cell extracts were solubilized with digitonin at a digitonin to protein ratio of 1.5 g/g protein. 150 µg of protein were loaded for glucose and galactose condition and 100 µg of protein were loaded for glycerol and lactate conditions. The F_1F_0-ATP synthase assemblies were revealed by F_1F_0-ATP synthase (CV) hydrolytic activity in gel (IGA). (representative of n = 2 independent experiments)

Mat & meth

Yeast strains

The *Saccharomyces cerevisiae* strain used in this study is the strain D273-10B/A/H/U (MAT α, met6, ura3, his3) for referred to as the wild type (WT)(Paul et al., 1989) and strain BY4741 Euroscarf (*MAT α; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0*). The mutants D273 were obtained by homologous recombination of the following deletion cassette in the wild type strain: D273 *inh1Δ* (*MAT α, met6, ura3, his3, inh1::HIS3-kanMX6),* D273 *stf1Δ* (*MAT α, met6, ura3, his3, stf1::NatR*), D273 *inh1Δ stf1Δ* (*MAT α, met6, ura3, his3, stf1::NatR, inh1::HIS3-KanMX6*), D273 *atp18Δ* (*MAT α, met6, ura3, his3, atp18::HIS3*), D273 *atp18Δ inh1Δ* (*MAT α, met6, ura3, his3, inh1::HIS3-kanMX6, atp18::NatR*). The plasmids used for the cassette HIS3-kanMX6 and nourseothricin resistance (*NatR*) were respectively pFA6a-His3MX6 and pUG-natNT2. The generated mutants were validated with PCR and Western blot. D273 $\rho^{-/\circ}$ strain was obtained after growing cells on rich medium with glucose 2% for two days before spreading on rich medium with 0.5% of glucose. The $\rho^{-/\circ}$ colonies were identified and counted after a replicate on glycerol medium where only the ρ^{+} colonies were able to grow. The wild type (*MAT a; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0)* and mutants strains BY4741 were provided by Euroscarf: BY4741 *atp18*Δ (*MAT a; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; YML081c-a::kanMX4*), BY4741 *pyk1*Δ (*MAT a; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0; cdc19-1::kanMX4* (lethal at 37°C)).

Yeast growth and media

Cells were grown aerobically at 28°C with shaking at 180 rpm. Growth was followed by measuring the optical density at 550 nm using a Jasco V-760 spectrophotometer. The composition of rich medium was: 1% (w/v) yeast extract, 0.12% (w/v) $(NH_4)_2SO_4$, 0.1% (w/v) KH_2PO_4, 2% or 0.5% (w/v) carbon source, pH 5.5 and for solid medium bacto agar 2% (w/v) was added. For the drop test done with *pyk1Δ* and *atp18Δ* strain, cells were grown in the following minimum medium: 0.175% (w/v) yeast nitrogen base w/o amino acids and ammonium sulfate, 0.5% (w/v) $(NH_4)_2SO_4$, 0.1% (w/v) KH_2PO_4, 0.2% (w/v), 2% or 0.5% (w/v) carbon source, bacto agar minimum medium 2% (w/v), pH 5.5, casein hydrolysate 0.2% (w/v), leucine 100 mg/L, histidine 20 mg/L methionine, 20 mg/L uracil. A filtered solution of casein and amino acids was added to the sterilized medium. Different carbon sources were used: D,L-lactic acid, glycerol, D(+)-galactose or D(+)-glucose. The carbon source selected for the experimentation is indicated in the legends. The uncoupler agent CCCP was added in the liquid culture medium, thermostated at 28°C, a few minutes

before inoculating the cells at 0.1 OD_{550nm} for growth curves and at 1 OD_{550nm} for HPIC experiment. For solid culture medium CCCP was added in the tepid medium just before solidification of agar and used within one day. A CCCP concentration titration was performed for each experiment and condition (between 1.25 and 7.5 µM). The inhibitor of cytosolic translation, cycloheximide (250 µg/ml) was added in the culture medium, at 2 OD_{550nm} culture. Cells were harvested on exponential growth.

Mitochondria preparation

Yeast cells grown in the presence of 2% lactate were collected in the exponential growth phase and mitochondria were prepared by enzymatic digestion of the cell wall with Zymolyase®-20T (nacalai tesque®, référence 07663-04) according to (Guérin et al., 1979).

High-resolution oxygen consumption measurement on yeast cells and isolated mitochondria.

Oxygen consumption of cells harvested during the exponential phase of their growth on different culture media was measured at 28°C using an Oxygraph-2k (OROBOROS INSTRUMENTS, Innsbruck, Austria). Oxygen consumption rates of cells were measured under endogenous state and in presence of ethanol substrate (85 mM) under endogenous conditions, under the non-phosphorylating state with addition of TET (25 µM) and under the uncoupled state by successive addition of CCCP titration (around 2.5 µM). When necessary, cells were diluted with the culture medium.

Protein extraction

100 units of OD_{550nm} were harvested, pelleted and washed with cold water before being broken by vigorous shaking for 4 min in 250 µl of extraction buffer containing Bis-Tris-HCl (10 mM pH 6.4), EDTA (1 mM) and a mixture of protease inhibitors (Complete EDTA-free™, Roche) with an equal volume of glass beads (0.4 mm diameter). Protein concentrations were then determined using the DC assay according to manufacturer's instructions (Bio-Rad). To detect the free F_1 subcomplex in the $\rho^{-/o}$, we obtained concentrated solubilized cell protein extract using concentrated with a centrifugal Concentrator (Corning® Spin-X® UF 500 µL, molecular weight cut-offs 100 kDa). The supernatant was collected after a centrifugation at 12,000xg for 10 min at 4°C. To obtain the membrane and soluble fractions, the total cell extract was centrifuged at 30,000xg during 30 min at 4°C. The supernatant (containing the soluble fraction) and pellet (containing the membrane fraction), were collected and subjected to protein quantification.

The pellet was resuspended in a volume of extraction buffer equivalent to that of the harvested supernatant.

Enzymatic activities determination

The activity of cytochrome c reductase (complex III) was determined measuring the cytochrome c reduced form, absorbing the light at 550 nm in presence in the following buffer: KH_2PO_4 (50 mM, pH 7.4), KCN (0.5 mM), succinate (10 mM), G3P (10 mM) and bovine heart cytochrome c (200 µg/ml). The specificity of the assay was validated by the addition of antimycin A (0.5 µM), the cytochrome c reductase (complex III) being defined as the Antimycin A sensitive flux. The measurement of enzymatic activity was done on 250 µg protein and performed in a quartz spectrophotometer cell at 28°C with stirring at 1,000 rpm with a Jasco V-760 spectrophotometer.

The hydrolytic activity of ATP synthase (complex V) on cell extract was determined at 28°C with shaking at 750 rpm with a thermomixer in the following buffer: triethanolamine (75 mM), $MgCl_2$ (5 mM) pH 9.0 or pH 6.4 with alamethicin (2 µg/ml). The measures were done with 0.8 mg cell extract proteins. The reaction started with the addition of ATP (5 mM). Every 2 min (or 6 min for ρ^-/°) an aliquot was collected and added to the following solution: sulfuric acid 0.38 M, ammonium heptamolybdate tetrahydrate (5 µM), iron(II) sulfate heptahydrate (29 µM). The Pi product was quantified following changes in the absorbance assessed at 750 nm. The same experimentation was performed after 2-min pre-incubation with oligomycin (19 µg/ml) to assess the oligomycin insensitive ATP hydrolysis flux. The hydrolytic activity of ATP synthase (complex V) on purified mitochondria was determined at 28°C with shaking at 750 rpm in an oroboros chamber in the following buffer: triethanolamine (75 mM), $MgCl_2$ (5 mM) pH 9.0 or 6.4 with alamethicin (1 µg/ml). The measures were done with 0.035 mg of mitochondrial proteins. The reaction started with the addition of ATP (5mM). Every 30 s an aliquot was collected and added to the following solution: sulfuric acid 0.38 M, ammonium heptamolybdate tetrahydrate (5 µM), iron(II) sulfate heptahydrate (29 µM). The Pi product was quantified following changes in the absorbance assessed at 750 nm. The same experimentation was performed after 2 min pre-incubation with triethyltin (4 ng/ml) to assess the oligomycin insensitive ATP hydrolysis flux.

BN-PAGE analyses and two-dimensional electrophoresis on total yeast cells protein extracts

For CN and BN-PAGE, 100 or 200 µg of total cell protein extract were solubilized with Glyco-diosgenin (GDN) (0.5g/g) or high-purity digitonin (1.5 g/g) in extraction buffer (see

above) with 0.0125 kU/µl of nuclease. Membranes were solubilized by vortexing for 30 min at 4°C and incubated at room temperature for 10 min. Supernatants were collected after centrifugation of the solubilized protein extract at 30,000g for 30 min. The loading buffer containing 6-aminohexanoic acid (0.15 M) was used for CN-PAGE and this loading buffer was supplemented with glycerol (20%), Coomassie brilliant blue G-250 (0.0125 % (w/v)) for BN-PAGE. Proteins samples were loaded on Bis-Tris Invitrogen™ Novex™ NativePAGE™ 3-12% acrylamide gradient. Gel migration was performed at 10 mA, 3h at 4°C. At the three-quarters of migration, the BN-PAGE buffer was removed and replaced by a CN-PAGE buffer to decrease the blue coloration of gel.

Protein complexes were detected by in-gel activity as previously described (Molinié et al., 2022). Native gels were incubated with buffer activity containing KH_2PO_4 (50 mM, pH 7.4) and iodonitrotetrazolium (0.5 mg/ml). The buffer was complemented with NADH (400 µM, pH 7.0) to reveal NADH dehydrogenases. For cytochrome c reductase in gel activity, native gels were incubated in the following buffer: KH_2PO_4 (50 mM, pH 7.4), sucrose (75 mg/ml), 3,3'-Diaminobenzidine (0.5 mg/ml) and cytochrome c (1 mg/ml). For ATP synthase in-gel activity, native gel was incubated in the following buffer: glycine (50 mM), lead acetate (1.32 mM), Triton X-100 (0.1 % (w/v)), and supplemented with $MgSO_4$ (5 mM) and ATP (4 mM, pH 7.0) to start the reaction. After revelation of ATPase activity, native gel was incubated with HCl (0.1% (v/v)) to remove lead precipitate before Coomassie staining (Coomassie 0.125% (w/v), ethanol 50% (v/v), acetic acid 10% (v/v)). After 45 min, gels were distained with a destaining solution (ethanol 25% (v/v) and acetic acid 8% (v/v)). After in gel activity, Native gels were imaged using ImageQuant (Amersham) and the Optical Density was determined using FIJI analyzer.

For two-dimensional electrophoresis (2D-BN/SDS-PAGE), the first dimension BN-PAGE bands were excised and incubated for 15 min in denaturing and reducing buffer containing SDS 1% and β-mercaptoethanol 1% pH 6.4, and then incubated in a second buffer containing SDS 1% pH 6.4 for 15 min. Each lane was placed at the top of Bis-Tris Invitrogen™ Novex™ NuPAGE™ 4–12% acrylamide gradient and a gel solution (4% of acrylamide) was poured to seal the lane. A PageRuler™ Plus (10 to 250 kDa) were loaded as MW ladder. The Novex™ MES running buffer according to the manufacturer recommendations. The migration was performed at 100V during 1h30.

Quantitative Western-blot analyses

For quantitative Western-blot analyses, 50 or 100 µg of protein extract were solubilized in standard RIPA buffer (NaCl 150 mM, tris-base 25 mM, NP40 1% (w/v), SDS 1% (w/v),

deoxycholate 0.25% (w/v) and EGTA 1 mM, pH 8.0) for 30 min at 4°C. The loading buffer (0.3 M Tris pH 6.8, glycerol 50% w/v, thioglycerol 30% v/v, SDS 10% w/v, bromophenol blue 0.05% w/v) was added to the samples before incubating them at 75°C for 5 min. To obtain a good separation of small proteins we performed a denaturing Schägger gel using 15% of acrylamide gels as previously described (Schägger and von Jagow, 1987). A size marker PageRuler™ Plus (10 to 250 kDa) was loaded on gel. The denaturing ectrophoresis gel was subjected to 100V for 2h. Proteins were then transferred onto nitrocellulose Amersham Protran Premium membrane (Amersham) (0.2 µm) with transfer buffer (25 mM Tris, 192 mM glycine, 0.1% SDS (w/v)) at 100V during 1h at 4°C. Membranes were stained with ponceau red solution (2 mg/ml with acetic acid 31% (v/v)) before incubation with blocking buffer containing 5% (w/v) skimmed milk diluted in PBS-tween buffer (10 mM NaH_2PO_4 pH 7.2, 0,14 M NaCl, 0,1% Tween-20 (w/v)). For immunodetection, membranes were incubated with primary antibody diluted in PBS tween 0.1% and detected by a peroxidase-conjugated secondary antibody Clarity ECL reagent (Bio-Rad). The chemiluminescence signals were recorded using an ImageQuant (Amersham) and then quantified using ImageJ software.

IF1 and STF1 proteins were produced and purified to determine the relative abundance of both inhibitors in cells.

IF1 was expressed and purified as mentioned in (Corvest et al., 2007), except that the His-tag was not removed. The STF1 gene was amplified by PCR using the 5' - CGCGCGCCATGGCTGTTCTCATCATCATCATCACGACGGTCCTCGTGTGTGTGTGCCGG - 3' forward primer to introduce a N-terminal His-tag and the 5' CGCGCGCCATGGCTGTTCTCATCATCATCATCACGACGGTCCTCTCGTGTGTGTGTGTGCCGG - 3' reverse primer. The PCR product, digested by Nco1 and BamH1, was inserted into the pIVEX2.3 vector, digested with the same restriction enzymes. The protein was produced in cell-free expression system (Larrieu et al., 2017). After 18h of production at 28°C, the reaction mix was centrifuged (10 min, 12,000xg, 4°C) and the supernatant containing STF1 was diluted 10-fold and loaded onto a Nickel NTA column. The column was washed with 25 CV of washing buffer 1 (150 mM NaCl,10 mM imidazole, 20 mM Tris-HCl pH8, containing protease inhibitors Pierce) and 20 CV of washing buffer 2 (150 mM NaCl,20 mM imidazole, 20 mM Tris-HCl pH8) and eluted with 4 CV of elution buffer (150 mM NaCl, 250 mM Imidazole**,** 20 mM Tris-HCl pH8 containing protease inhibitors Pierce).

Antibodies

Primary antibody: PGK1 mouse monoclonal antibody 22C5D8 (CiteAb 459250), MTCO2 (COX2) mouse monoclonal antibody (Thermo Fisher 12C4F12). Rabbit polyclonal antibodies raised against purified subunits β, ɣ, and Su 4 were obtained in the laboratory. Rabbit polyclonal antibodies raised against the INDPRNPRFAKGGK peptide of subunit i were purchased from Neosystem. Anti-IF1 antibodies were kindly provided by K. Tagawa (Osaka, Japan). The STF1 protein produced in vitro was used by Covalab society to raise polyclonal rabbit antibodies.

The secondary antibodies used were: ECL Plex goat-mouse IgG, Cy5 (GE Healthcare PA45009); ECL Plex goat-rabbit IgG, Cy5 (GE Healthcare PA45011).

Metabolites quantifications

Cells were cultured during 12 h before adding CCCP treatment (1 µM) at 1 OD_{550nm}. After 1 h of treatment, size and number of cells were defined with a multisizer instrument. 20 ml of culture were filtered (Sartolon polyamid 0.45 µm) and the filter was rapidly rinsed twice with ice-cold water to stop reactions. Metabolites were extracted using an ethanol/HEPES 20 mM pH 7.2 (2/8 v/v) solution as described (Ceschin et al., 2014). Metabolites were separated, detected and quantified on a High Performance Ionic Chromatography (HPIC) station as described (Pinson et al., 2023). The intracellular concentration of nucleotides was determined using standard curves obtained with pure compounds. Adenylic energy charge was defined as AEC = [ATP] + ½ [ADP] / [ATP] + [ADP] + [AMP] (Atkinson and Walton, 1967).

Mitochondrial DNA quantification

For the extraction of DNA, cells were washed and broken by shaking during 1 min with an equal volume of glass beads (0.4 mm) in following buffer: Tris (10 mM, pH8.0), EDTA (1 mM), NaCl (100 mM), Triton X-100 (2% v/v), SDS (1% v/v) and chloroform/phenol (1:1) (50% v/v). Equal volumes of Tris (10 mM, pH8) and EDTA (1 mM) buffer was added and vortexed during 5 min. The supernatant was added with an equal volume of chloroform during 1 min and centrifuged at 12,000xg. The supernatant was mixed with a double volume of glacial ethanol and centrifuged at 12,000xg. The pellet was dried at room temperature before being resuspended in water nuclease free.

Quantitative PCR for mtDNA content performed with qPCRBIO SyGreen Blue Mix Lo-ROX (Eurobio®). Based on the manufacturer’s instructions, 0.1 ng of DNA used to quantify mtDNA and nuclear DNA with two different set of primer. The first mtDNA primer set (fw: TTGAAGCTGTACAACCTACC, rv: CCTGCGATTAAGGCATGATG) targeted a region of

COX3 gene, the second primer set (fw: AACAATTGGTTTATTAGGAGCAGGTATTGG, rv: TATACACCGAATAATAATAAGAATGAAACC) targeted a region of *ATP9* gene. The nDNA primer set (fw: CACCCTGTTCTTTTGACTGA, rv: CATAGAAGGCTGGAACGTTG) targeted a region of *ACT1* gene, and the other primer set (fw: TGCTTTGTCAAATGGATCATATGG, rv: CCTGGAACCAAGTGAACAGTAC) targeted a region of *GAL1* gene.

Statistical analyses

Data are presented as mean SEM. Sample numbers (different culture) and experimental repeats are indicated in legends. Data were analyzed with the GraphPad Prism software using unpaired Student's t-test, one-way ANOVA or two-way ANOVA. A 0.05 p-value was considered statistically significant.

AUTHOR CONTRIBUTIONS

Orane Lerouley performed and analyzed experiments. Dr. Benoit Pinson determined the quantification of metabolites. Isabelle Larrieu managed the production of the antibody STF1. Dr. Marie-France Giraud did the production and purification of IF1 and STF1 for quantitative Western blot. Dr Arnaud Mourier and Dr Marie-France Giraud co-supervised the project, interpreted results and provided funding. AM administered, provided funding for the project and wrote the manuscript and all authors reviewed and edited the manuscript.

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Figure 1

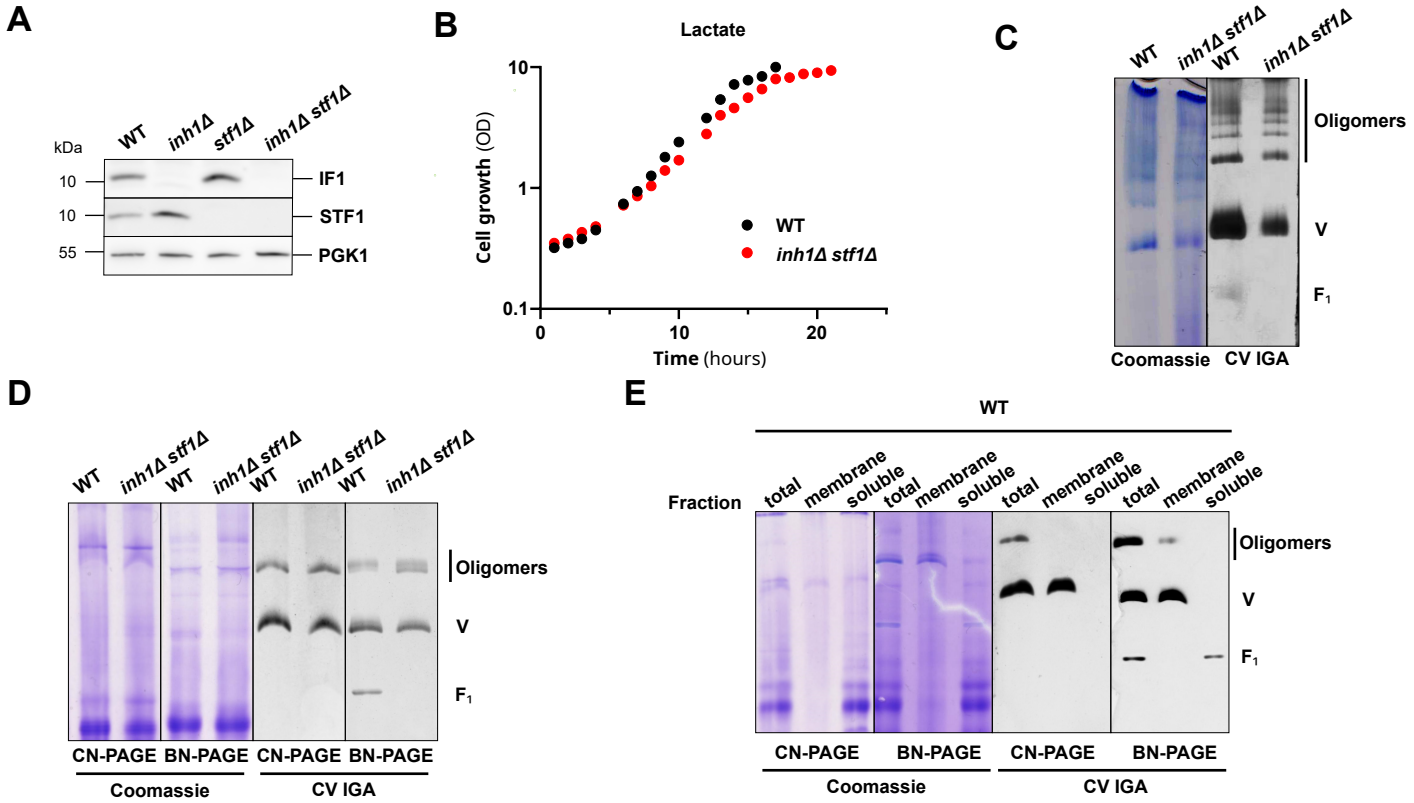

A
kDa
WT
inh1Δ
stf1Δ
inh1Δ stf1Δ
10
10
55
IF1
STF1
PGK1
B
Lactate
Cell growth (OD)
10
1
0.1
0
10
20
Time (hours)
WT
inh1Δ stf1Δ
C
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
Oligomers
V
F1
Coomassie
CV IGA
D
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
Oligomers
V
F1
CN-PAGE
BN-PAGE
CN-PAGE
BN-PAGE
Coomassie
CV IGA
E
WT
Fraction
total
membrane
soluble
total
membrane
soluble
total
membrane
soluble
total
membrane
soluble
Oligomers
V
F1
CN-PAGE
BN-PAGE
CN-PAGE
BN-PAGE
Coomassie
CV IGA

Figure 2

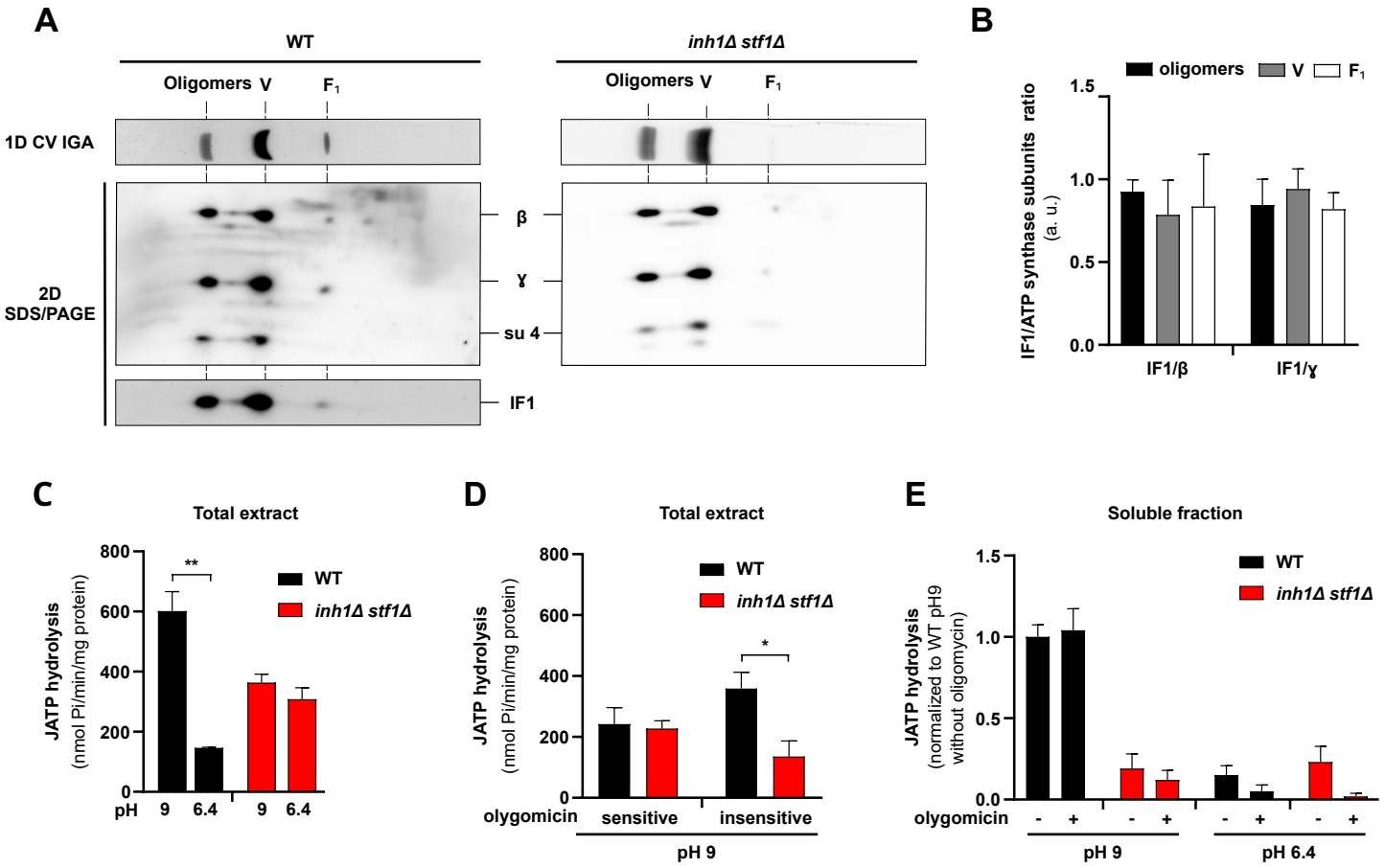

A
WT
inh1Δ stf1Δ
Oligomers V
F1
1D CV IGA
2D SDS/PAGE
β
γ
su 4
IF1
B
oligomers
V
F1
IF1/ATP synthase subunits ratio (a. u.)
1.5
1.0
0.5
0.0
IF1/β
IF1/γ
C
Total extract
JATP hydrolysis (nmol Pi/min/mg protein)
800
600
400
200
0
**
WT
inh1Δ stf1Δ
pH 9 6.4 9 6.4
D
Total extract
JATP hydrolysis (nmol Pi/min/mg protein)
800
600
400
200
0
*
WT
inh1Δ stf1Δ
olygomicin
sensitive
insensitive
pH 9
E
Soluble fraction
JATP hydrolysis (normalized to WT pH9 without oligomycin)
1.5
1.0
0.5
0.0
WT
inh1Δ stf1Δ
olygomicin
- + - + - + - +
pH 9
pH 6.4

Figure 3

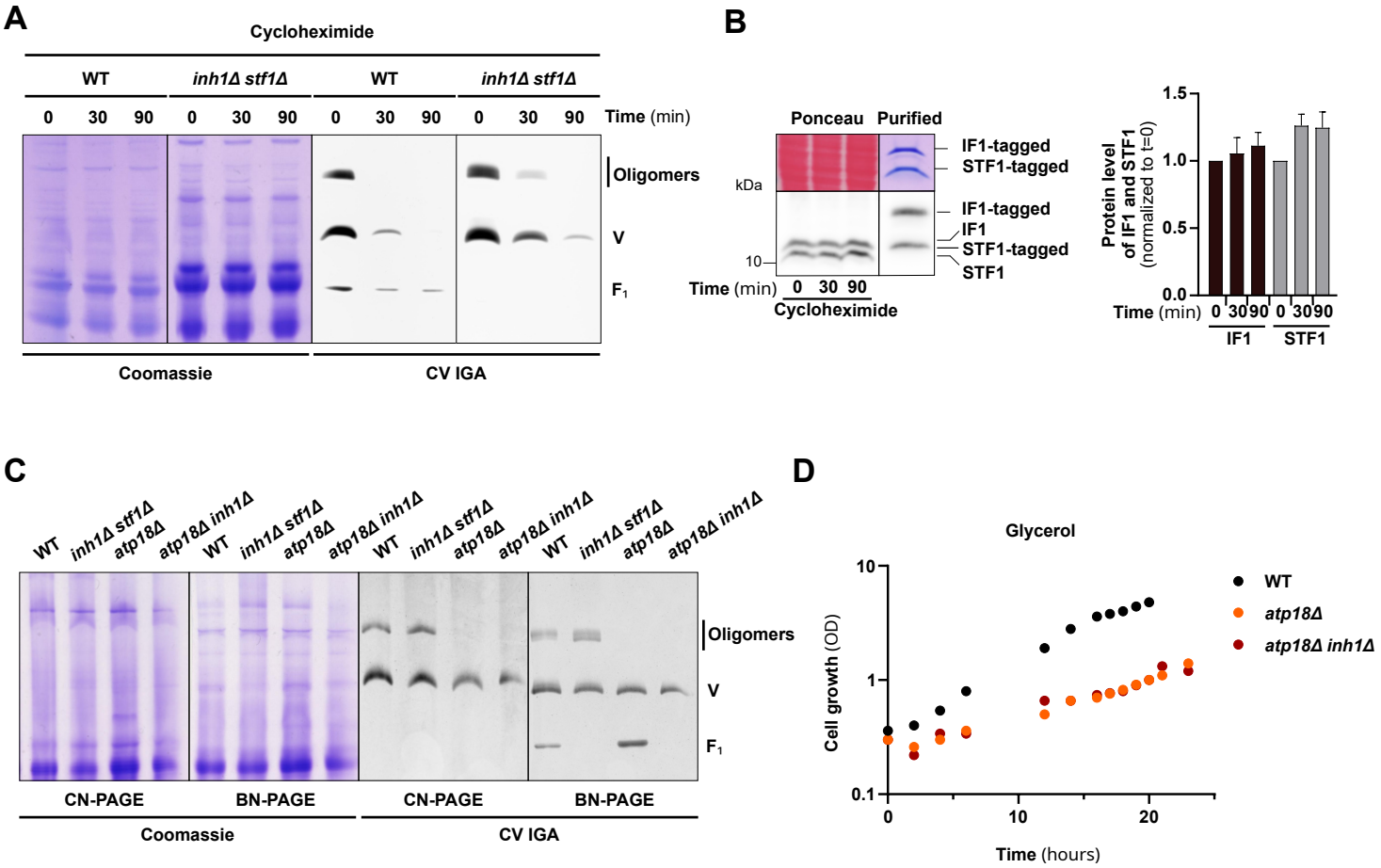

A
Cycloheximide
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
0 30 90 0 30 90 0 30 90 0 30 90
Time (min)
Oligomers
V
F1
Coomassie
CV IGA
B
Ponceau
Purified
kDa
10
IF1-tagged
STF1-tagged
IF1-tagged
IF1
STF1-tagged
STF1
Time (min) 0 30 90
Cycloheximide
Protein level of IF1 and STF1 (normalized to t=0)
1.5
1.0
0.5
0.0
Time (min) 0 30 90 0 30 90
IF1
STF1
C
WT
inh1Δ stf1Δ
atp18Δ
atp18Δ inh1Δ
Oligomers
V
F1
CN-PAGE
BN-PAGE
CN-PAGE
BN-PAGE
Coomassie
CV IGA
D
Glycerol
Cell growth (OD)
10
1
0.1
0
10
20
Time (hours)
WT
atp18Δ
atp18Δ inh1Δ

Figure 4

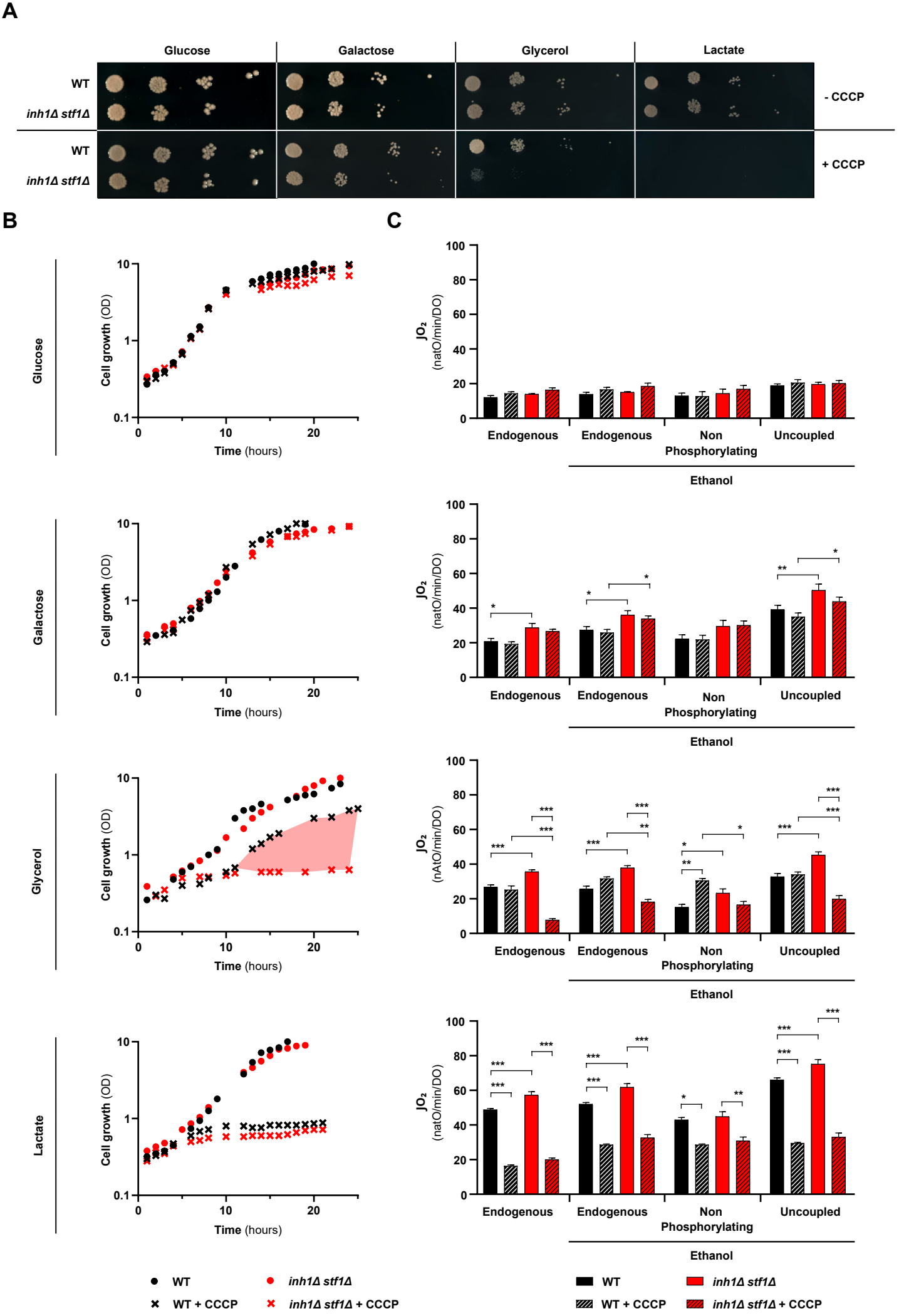

A
Glucose
Galactose
Glycerol
Lactate
WT
inh1Δ stf1Δ
- CCCP
+ CCCP
B
C
Glucose
Galactose
Glycerol
Lactate
Cell growth (OD)
Time (hours)
JO2 (natO/min/DO)
JO2 (nAtO/min/DO)
Endogenous
Endogenous
Non Phosphorylating
Uncoupled
Ethanol
WT
inh1Δ stf1Δ
WT + CCCP
inh1Δ stf1Δ + CCCP

Figure 5

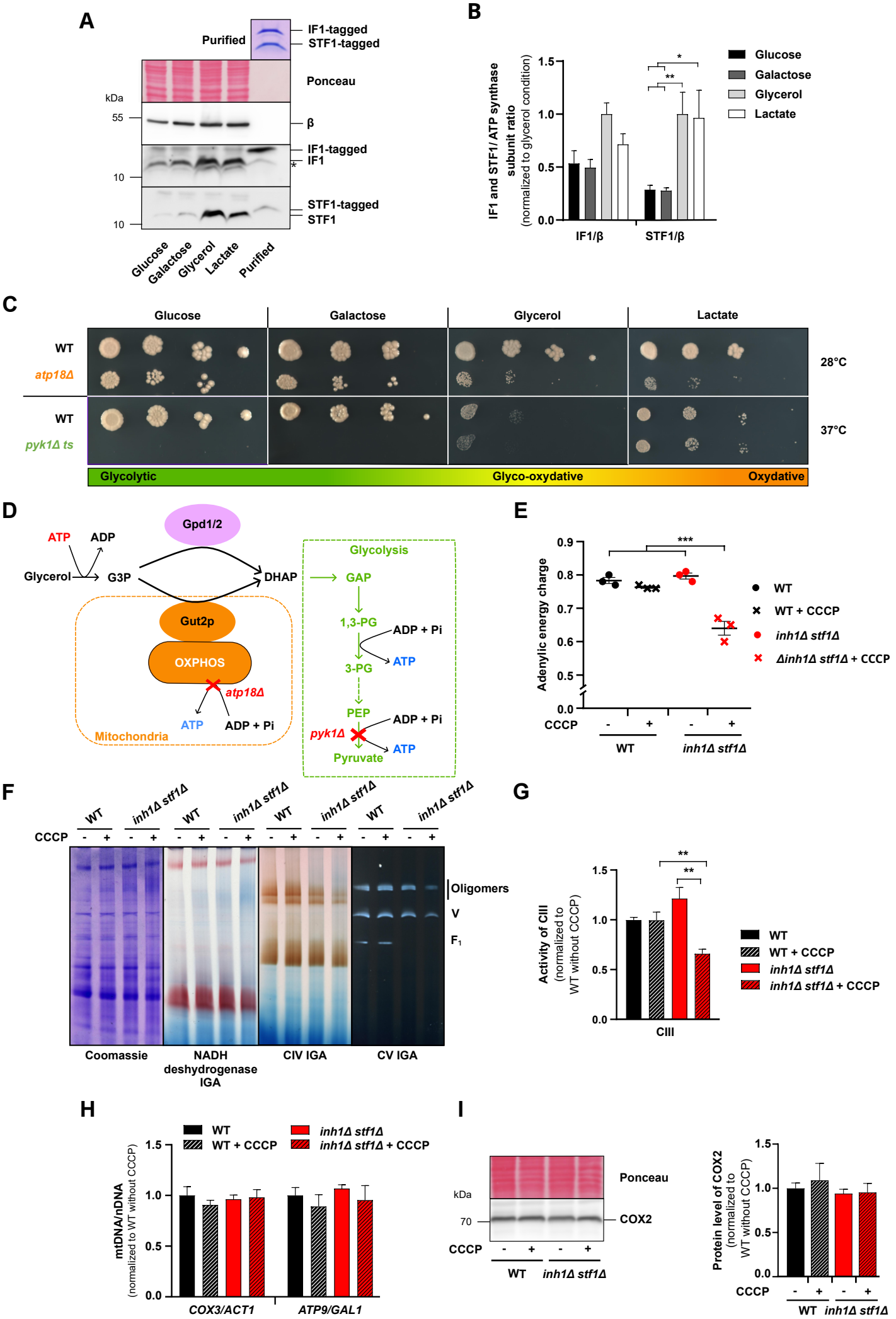
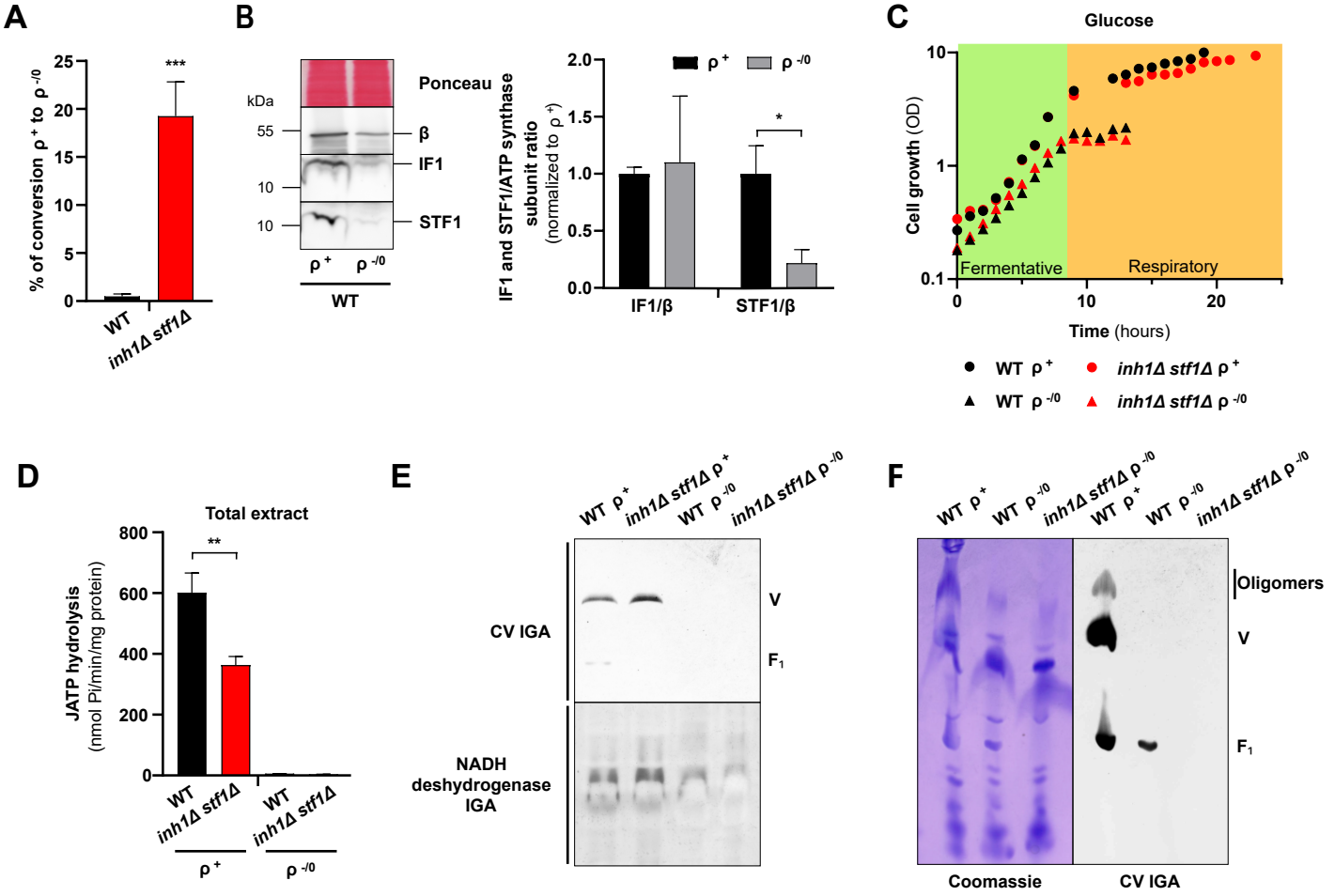
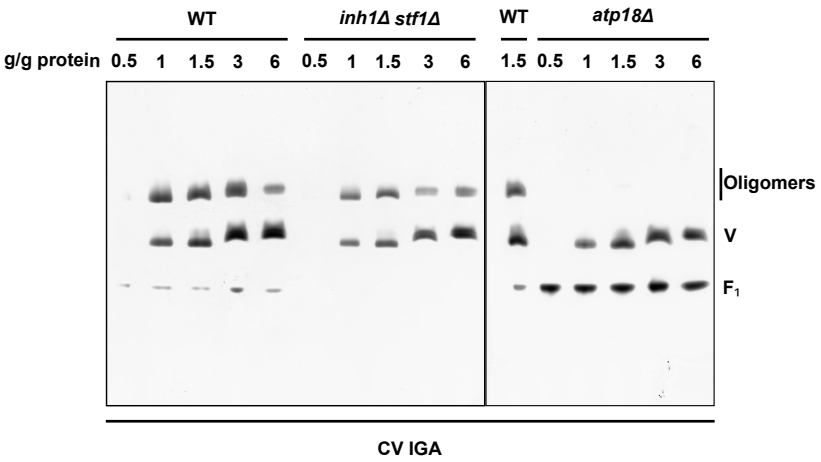

A
Purified
IF1-tagged
STF1-tagged
Ponceau
kDa
55
β
IF1-tagged
IF1
10
STF1-tagged
STF1
10
Glucose
Galactose
Glycerol
Lactate
Purified
B
IF1 and STF1/ ATP synthase subunit ratio (normalized to glycerol condition)
1.5
1.0
0.5
0.0
*
**
Glucose
Galactose
Glycerol
Lactate
IF1/β
STF1/β
C
Glucose
Galactose
Glycerol
Lactate
WT
atp18Δ
28°C
WT
pyk1Δ ts
37°C
Glycolytic
Glyco-oxydative
Oxydative
D
Gpd1/2
ATP
ADP
Glycerol
G3P
DHAP
Gut2p
OXPHOS
atp18Δ
ATP
ADP + Pi
Mitochondria
Glycolysis
GAP
1,3-PG
ADP + Pi
ATP
3-PG
PEP
ADP + Pi
pyk1Δ
ATP
Pyruvate
E
Adenylic energy charge
0.9
0.8
0.7
0.6
0.5
0.0
***
WT
WT + CCCP
inh1Δ stf1Δ
Δinh1Δ stf1Δ + CCCP
CCCP
-
+
-
+
WT
inh1Δ stf1Δ
F
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
CCCP
- + - + - + - + - + - + - + - +
Oligomers
V
F1
Coomassie
NADH deshydrogenase IGA
CIV IGA
CV IGA
G
Activity of CIII (normalized to WT without CCCP)
1.5
1.0
0.5
0.0
**
**
WT
WT + CCCP
inh1Δ stf1Δ
inh1Δ stf1Δ + CCCP
CIII
H
WT
WT + CCCP
inh1Δ stf1Δ
inh1Δ stf1Δ + CCCP
mtDNA/nDNA (normalized to WT without CCCP)
1.5
1.0
0.5
0.0
COX3/ACT1
ATP9/GAL1
I
Ponceau
kDa
70
COX2
CCCP
-
+
-
+
WT
inh1Δ stf1Δ
Protein level of COX2 (normalized to WT without CCCP)
1.5
1.0
0.5
0.0
CCCP
-
+
-
+
WT
inh1Δ stf1Δ

Figure 6


A
% of conversion ρ+ to ρ-/0
25
20
15
10
5
0
***
WT
inh1Δ stf1Δ
B
kDa
55
10
10
Ponceau
β
IF1
STF1
ρ+
ρ-/0
WT
IF1 and STF1/ATP synthase subunit ratio (normalized to ρ+)
2.0
1.5
1.0
0.5
0.0
ρ+
ρ-/0
*
IF1/β
STF1/β
C
Glucose
Cell growth (OD)
10
1
0.1
Fermentative
Respiratory
0
10
20
Time (hours)
WT ρ+
inh1Δ stf1Δ ρ+
WT ρ-/0
inh1Δ stf1Δ ρ-/0
D
Total extract
JATP hydrolysis (nmol Pi/min/mg protein)
800
600
400
200
0
**
WT
inh1Δ stf1Δ
WT
inh1Δ stf1Δ
ρ+
ρ-/0
E
WT ρ+
inh1Δ stf1Δ ρ+
WT ρ-/0
inh1Δ stf1Δ ρ-/0
CV IGA
V
F1
NADH deshydrogenase IGA
F
WT ρ+
WT ρ-/0
inh1Δ stf1Δ ρ-/0
WT ρ+
WT ρ-/0
inh1Δ stf1Δ ρ-/0
Oligomers
V
F1
Coomassie
CV IGA

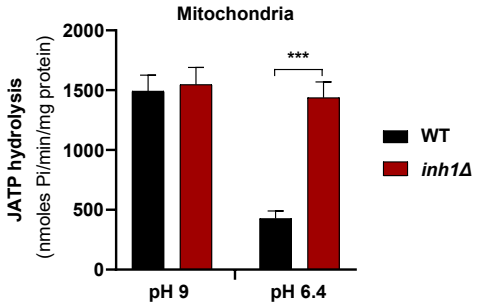
Supplemental Figure 1

S1A



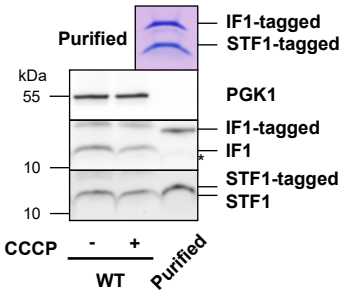
Supplemental Figure 3

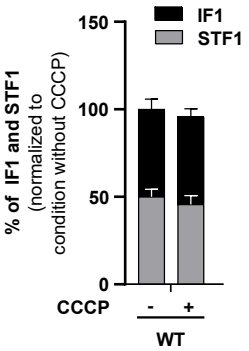
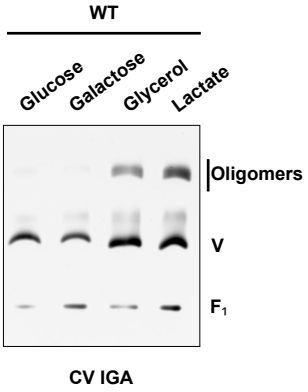
S3A



Supplemental Figure 5

S5A





S5B