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DR. ITAY BUDIN (Orcid ID : 0000-0001-9706-4294)

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## **Distinct functional roles for hopanoid composition in the chemical tolerance of *Zymomonas mobilis***

Running title: Hopanoids in bacterial ethanol tolerance

Léa Brenac<sup>1†</sup>, Edward E.K. Baidoo<sup>1</sup>, Jay D. Keasling<sup>1,2,3-8</sup>, and Itay Budin<sup>1,2,9\*</sup>

<sup>1</sup>. Joint BioEnergy Institute, 5885 Hollis Street, Emeryville, CA 94608

<sup>2</sup>. Department of Chemical & Biomolecular Engineering, University of California, Berkeley, Berkeley CA 94720

<sup>3</sup>. Department of Chemistry, University of California, Berkeley, Berkeley, CA 94720

<sup>4</sup>. Department of Bioengineering, University of California, Berkeley, Berkeley CA 94720

<sup>5</sup>. QB3 Institute, University of California, Berkeley, Berkeley, CA 94720

<sup>6</sup>. Biological Systems & Engineering, Lawrence Berkeley National Laboratory, Berkeley, CA 94720

<sup>7</sup>. The Novo Nordisk Foundation Center for Sustainability, Technical University of Denmark, Denmark

<sup>8</sup>. Center for Synthetic Biochemistry, Institute for Synthetic Biology, Shenzhen Institutes for Advanced Technologies, Shenzhen, CN

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<sup>9</sup> Department of Chemistry & Biochemistry, University of California, San Diego, La Jolla, CA 92093

<sup>†</sup> Current affiliation: Lonza Ltd, Visp Switzerland

\*Correspondence: [ibudin@ucsd.edu](mailto:ibudin@ucsd.edu)

### Summary:

Hopanoids are a class of membrane lipids found in diverse bacterial lineages, but their physiological roles are not well understood. The ethanol fermenter *Zymomonas mobilis* features the highest measured concentration of hopanoids, leading to the hypothesis that these lipids can protect against solvent toxicity. However, the lack of genetic tools for manipulating hopanoid composition in this bacterium has limited their further functional analysis. Due to the polyploidy (> 50 genome copies per cell) of *Z. mobilis*, we found that disruptions of essential hopanoid biosynthesis (*hpn*) genes act as genetic knockdowns, reliably modulating the abundance of different hopanoid species. Using a set of *hpn* transposon mutants, we demonstrate that both reduced hopanoid content and modified hopanoid polar head group composition mediate growth and survival in ethanol. In contrast, the amount of hopanoids, but not their head group composition, contributes to fitness at low pH. Spectroscopic analysis of bacterial-derived liposomes showed that hopanoids protect against several ethanol-driven phase transitions in membrane structure, including lipid interdigitation and bilayer dissolution. We propose that hopanoids act through a combination of hydrophobic and inter-lipid hydrogen bonding interactions to stabilize bacterial membranes during solvent stress.

### Keywords:

Hopanoids, membrane lipids, ethanol, fermentation, cell membrane structures

## Introduction:

Triterpenoids are a class of cyclized lipids used by cells as bulk membrane building blocks. The canonical triterpenoids are eukaryotic sterols, in which squalene is oxidized before cyclization, leaving a hydroxyl to act as a polar head group. With notable exceptions (Pearson, Budin, & Brocks, 2003; Wei, Yin, & Welander, 2016), bacterial triterpenoids are hopanoids, in which squalene is first cyclized into hopene and then derivatized with polar groups (Ourisson & Rohmer, 1992). Hopanoids are thought to mimic the well-known effects of sterols on membrane ordering and permeability (Kannenbergh, Blume, McElhaney, & Poralla, 1983; Poger & Mark, 2013; Saenz, Sezgin, Schwille, & Simons, 2012). Unlike the bulk sterols in metazoans and fungi, however, they are generally present in complex mixtures of several derivatives, which could diversify their functions. They are also not nearly as widespread, being absent from a majority of cultured bacterial strains (Rohmer, Bouvier-Nave, & Ourisson, 1984) and environmental samples (Pearson, Flood Page, Jorgenson, Fischer, & Higgins, 2007).

In bacteria with non-essential hopanoids, hopanoid biosynthesis (*hpn*) mutants have been used to identify functional roles related to chemical stress. In *Burkholderia cenocepacia*, hopanoid-free cells were found to be sensitive to low pH and detergents (Schmerk, Bernards, & Valvano, 2011), while in *Rhodopseudomonas palustris* they are more sensitive to both low and high pH (Welander et al., 2009) as well as bile salts (Welander et al., 2012). In *Bradyrhizobium diazoefficiens*, mutants lacking extended hopanoids that feature sugar-derived head groups showed membrane defects and were sensitive to antibiotics, acid, and detergent (Kulkarni et al., 2015). The biophysical basis for these phenotypes has not been well studied, nor have physiological roles been characterized in bacteria where hopanoids are essential.

Because of its unusual glycolytic metabolism (Flamholz, Noor, Bar-Even, Liebermeister, & Milo, 2013), the alphaproteobacterium *Z. mobilis* produces ethanol approaching theoretical yields (Sprenger, 1996), leading to its adoption for industrial fermentation applications (Ming He et al., 2014). Native to palm wine fermenters (Swings & De Ley, 1977), *Z. mobilis* features a remarkable tolerance to ethanol, with reported growth in

media containing up to 16% (v/v) ethanol (Lee, Skotnicki, Tribe, & Rogers, 1980). It also features a high abundance of hopanoids in its membranes – up to 50% of all lipids in the cell (Hermans, Neuss, & Sahm, 1991) – suggesting that these lipids could be important for its ability to withstand ethanol.

Like other solvents, ethanol alters the lipid packing (Vierl, Löbbecke, Nagel, & Cevc, 1994) and phase properties (Gurtovenko & Anwar, 2009) of model membranes. In principle, the condensing effect of hopanoids, analogous to eukaryotic sterols (Perzl et al., 1998; Saenz et al., 2012), could buffer against changes to membrane structure induced by solvents. However, in contrast to longer chain alcohols that fluidize membranes, the physicochemical effects of ethanol are complex, and include the induction of membrane phase transitions that increase membrane ordering (Vierl et al., 1994). In other ethanol-tolerant microbial fermentors (budding yeast), ethanol tolerance is partly mediated by unsaturated fatty acids (Thomas, Hossack, & Rose, 1978; You, Rosenfield, & Knipple, 2003), which can have opposing biophysical effects compared to triterpenoids. In *Z. mobilis*, early lipid analyses using thin layer chromatography reported an increase in hopanoids during ethanol exposure (Bringer, Thomas, Poralla, & Sahm, 1985), but later work using modern mass spectrometry tools and transcriptomics showed no link between ethanol and hopanoid biosynthesis (Hermans et al., 1991; Moreau, Powell, Fett, & Whitaker, 1997) or *hpn* expression (Ming-xiong He et al., 2012), respectively. Treatment of cells with the squalene hopene cyclase (SHC) competitive inhibitor 2-aza-2,3-dihydrosqualene has been observed to decrease growth rates in ethanol, suggesting a functional role for total hopanoid content (Horbach, Neuss, & Sahm, 1991). However, it is still not established what specific hopanoid species contribute to ethanol tolerance and how they act on membrane structure to do so.

Testing physiological functions for hopanoid composition requires genetic tools to modulate their abundance and stoichiometry in cells. In *Z. mobilis*, a transposon-based gene disruption has previously been used to generate loss of function mutants to carry out systematic fitness analyses (Skerker et al., 2013). Surprisingly, this effort yielded transposon insertions in essential genes, e.g. those encoding for RNA polymerase and

cell division machinery. Such an effect was proposed to result from polyploid cells containing both mutant alleles, carrying antibiotic resistance markers, and functional ones, carrying essential genes. We hypothesized that this dynamic could reduce the copy number of hopanoid biosynthetic genes, thereby acting as genetic knockdowns and allowing for functional studies of this lipid class in *Z. mobilis*.

## Results:

### *Genetic, chemical, and biophysical characterization of hopanoid biosynthesis mutants*

We first collected a redundant set of 25 Tn5 mutants of the base strain ZM4 covering annotated genes in the hopanoid biosynthesis pathway (Fig. 1A). Mutants with transposons at different positions in the same genes showed identical fitness profiles (Fig. S1), suggesting that insertions acted as null alleles. When grown under antibiotic selection for the transposon, PCR analysis of transposon-inserted *hpn* genes showed the existence of both wild-type and mutated alleles (Fig. 1B), with varying apparent abundances. To confirm that heterozygosity was due to polyploidy, we measured chromosome numbers per cell directly using a qPCR-based approach (Fig. 1C). We found that *Z. mobilis* cells were highly polyploid, containing > 50 copies of two different genomic loci under our growth conditions. In contrast, a monoploid bacterium (*E. coli* in minimal medium) featured 1-2 genome copies per cell by this method. We quantified the transposon insertion rate for *hpn* mutants using high coverage genome sequencing, quantifying the number of reads matching to each allele (Fig 1D). The mutant allele frequency ranged from 31 to 100%, with non-duplicated genes early in the pathway featuring the lowest abundance and genes later in the pathway mimicking full knockouts (Table S1). Notably, the mutant alleles for either of the two SHC genes (*shc* and *hpnF*) were near 100%, indicating that not-essential genes (in this case because of duplication) could approximate knockouts despite the high chromosome number.

Since *hpn* mutants reduce the fraction of functional alleles in a cell, we hypothesized that they would reduce the abundance of the downstream product of each Hpn enzyme. To test this, we used a combination of mass spectrometry approaches to characterize the hopanoid composition of mutants grown under transposon selection. The products of squalene cyclization, hopene (Fig. 2A) and diplopterol (Fig. 2B), were measured by gas chromatography coupled to mass spectrometry (GC-MS) of silylated lipid extracts (Fig. S2A). Both showed decreased abundance in squalene synthase (*hpnC*, *hpnD*) mutants, consistent with their position upstream in the pathway. Lipids from *hpnF* and *shc* mutants, which exhibited almost complete disruption, showed distinct distributions of squalene cyclization products: the *shc* mutant accumulated less hopene, while the *hpnF* mutant accumulated less diplopterol. This difference suggests differing product preferences for these SHCs. Lipids from the *hpnH* mutant exhibited higher hopene levels, consistent with the role of HpnH in converting hopene to adenosylhopane. Later genes in the pathway (*hpnG*, *hpnI*, *hpnK*, *hpnJ*) mildly altered levels of these products.

We next analyzed the distribution of extended hopanoids, which compose the majority of final hopanoid products in *Z. mobilis*, using liquid chromatography coupled to atmospheric pressure chemical ionization time of flight mass spectrometry (LC-APCI-TOF-MS) (Fig. 2C-E, Fig. S2B-C). Mutants targeting enzymes upstream of the extended hopanoids all showed reduced abundance of all these products, but did not alter their stoichiometry. Instead, it was mutants of the three genes downstream of bacteriohopanetetrol (BHT) in the pathway (*hpnI*, *hpnK* and *hpnJ*) that altered extended hopanoid distribution. The *hpnI* mutant exhibited an accumulation of BHT accompanied by a reduction of the BHT derivatives. Analyses of the *hpnK* mutant was hindered by the acetylation of BHT glucosamine during lipid derivatization, which prevents distinction between BHT glucosamine and the acetylated precursor made by HpnI. However, the increased ratio of BHT glucosamine to BHT cyclitol ether (2:1) we observed was consistent with its expected role as a deacetylase and its position upstream from HpnJ, which produces BHT cyclitol ether. In the *hpnJ* mutant, no BHT cyclitol ether could be detected, in agreement with it being near complete gene knock out (98% mutant alleles).

Lipid analysis confirmed the proposed biosynthetic route for hopanoids in *Z. mobilis* and showed that transposon disruptions act as functional knockdowns, resulting in changes in hopanoid abundance and distribution (Fig. 2F). We tested whether these changes modulate the physical properties of lipid bilayers using the anisotropy-based probe diphenyl-hexatriene (DPH), a classic test of ordering in the hydrophobic membrane core (Suurkuusk, Lentz, Barenholz, Biltonen, & Thompson, 1976). Membranes prepared from extracted lipids with reduced hopanoid content showed significantly lower DPH anisotropy (Fig. 3), while those with altered head group composition showed a milder effect. This pattern is consistent with the hopene moiety – common to all hopanoids – being responsible for increasing hydrocarbon packing in the membrane, similar to the effect of sterols. All *Z. mobilis* compositions featured a higher anisotropy compared to membranes assembled from lipids extracted from *E. coli* MG1655, which lack hopanoids.

#### *The effect of changes in hopanoid composition on ethanol tolerance*

We sought to use *hpn* mutants to assess the proposed physiological role for hopanoid composition in *Z. mobilis* ethanol tolerance. In standard rich media (RM), exponential growth rates of different mutants were correlated to their total hopanoid content, likely reflecting physiological roles for these lipids under non-stressed conditions (Fig. S3). We focused further investigation on a set of strains that sampled different aspects of hopanoid composition: reduced total hopanoid content (*hpnC* or *hpnD*), reduced accumulation of sugar-decorated hopanoids (*hpnI*), or absence of BHT cyclitol ether (*hpnJ*), comparing each with the behavior of a kanamycin-resistant control in medium with and without 8% v/v ethanol (Fig. 4A-B). We found that the ethanol caused *hpn* mutants to show a significantly larger growth defect compared to the control (Fig. 4C). This effect was significant both for mutants with reduced hopanoid content and those with altered extended hopanoids. A similar pattern was found for toxicity, measured by colony forming units, after acute (30 min) exposure to high ethanol concentration (20%), with each mutant featuring significantly reduced survival (Fig. 4C). Both hopanoid

abundance and stoichiometry are thus functional for *Z. mobilis* ethanol fitness.

### *Comparison to hopanoid function during acid stress*

In addition to ethanol, we considered other forms of chemical stress tolerance that would be characteristic of the native environment for *Z. mobilis*. Fermentation is characterized by acidic conditions, and *Z. mobilis* grows robustly between pH 3 and 4, matching the acidity of palm wine (Swings & De Ley, 1977). As discussed above, hopanoids have been known to increase low pH tolerance in other bacteria in which they are not essential. Accordingly, we found that *hpn* mutants with reduced total hopanoid content (*hpnC* and *hpnD*) showed reduced growth rates at pH 3.9 (Fig. 5A) and survival at pH 2.5 (Fig. 5B). However, mutants that altered hopanoid composition, but not total abundance (*hpnI* and *hpnJ*), showed no significant change in acid tolerance. The presence of hopanoids is likely essential for *Z. mobilis* to thrive in acidic conditions, but the stoichiometry of head group species is less important as compared to that for ethanol toxicity.

The discrepancy the role of hopanoid stoichiometry in acid vs. ethanol could reflect different modes of lethality imposed by these chemical stresses. We hypothesized that while solvent exposure (e.g. ethanol) would lead to a loss of membrane structure, acid toxicity would occur by a different mechanism – such as passive permeability of protons leading to cytoplasmic acidification – that is not dependent on loss of membrane integrity. To test this difference, we first assayed membrane integrity using SYTOX staining. Cells incubated with ethanol exposure showed an increase membrane permeability at 20 and 30% v/v ethanol, corresponding to the toxicity threshold (Fig. 5C). However, those exposed to lethal acidic conditions (pH 2.0) did not show increased staining (Fig. 5D), indicating that acid does not lead to a loss in membrane integrity as ethanol exposure does. To confirm this result, we tested the leakage of the polar fluorophore 2,7-dichlorofluorescein (DCF) by fluorescence microscopy (Fig. 5E). We incubated cells with a high concentration of DCF in either acidic (pH 2.5) or ethanoic (25% v/v) media before dilution back into neutral, ethanol-free imaging buffer. Only cells

that underwent the ethanol incubation showed cytoplasmic staining, indicating the permeabilization of dye during the incubation.

### *Hopanoids mediate membrane structural changes in response to ethanol exposure*

To further explore the mechanisms by which hopanoids protect membranes against ethanol-mediated permeabilization, we carried out spectroscopic assays using liposomes assembled from *hpn* mutant lipid extracts. Because of its hydrophilicity, ethanol interacts with lipid membranes at the solvent-bilayer interface (Holte & Gawrisch, 1997). We therefore employed the fluorescent probe Laurdan, whose emission is sensitive to solvent access near the head group interface (Parasassi, Krasnowska, Bagatolli, & Gratton, 1998), to track changes to membrane structure in response to ethanol. As bilayers become disordered, they allow in more polar solvents, and Laurdan emission becomes red-shifted. This emission shift is quantified with a General Polarization (GP) ratio. Because Laurdan remains partitioned in lipid membranes independent of ethanol concentration (Zeng & Chong, 1995), changes in GP reflect changes in membrane ordering.

We found that Laurdan GP had a triphasic dependence on ethanol concentration, which track previously identified membrane structural changes (Fig. 6A-C). Initially, ethanol acts to disorder membranes, increasing head group spacing (bilayer expansion) and solvent accessibility, thereby reducing GP (regime I). At a critical concentration (~10%), the trend is reversed as phospholipid acyl chains become interdigitated across the bilayer, a gel-like phase transition (Mou, Yang, Shao, & Huang, 1994; Simon & McIntosh, 1984) that increases GP (regime II). At a second critical concentration (>25%), Laurdan emission strongly red shifts, reflecting the dissolution of the bilayer structure at high ethanol concentrations that correspond to lethality in cells (regime III). The three regimes of the ethanol concentration vs. Laurdan GP relationship can thus be used to interrogate the specific structural effects on lipid membranes. Notably, incubation of liposomes at pH 2.0 did not lead to large effects on Laurdan emission (Fig. S4C), consistent with acid toxicity not being the result of envelope dissolution.

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As predicted by our physiological data, hopanoid content and composition mediated the changes to membrane structure induced by ethanol (Fig. 6D). We compared the changes to Laurdan GP in liposomes made from extracts with mutants with reductions in total (*hpnC*) and extended (*hpnI*) hopanoids. Under basal conditions (0% ethanol), reductions in total (*hpnC*) and extended (*hpnI*) hopanoids led to decreased membrane ordering, with the latter having the larger effect (Fig. S4). This is in contrast with membrane ordering of the hydrophobic core measured with DPH (Fig. 3), likely reflecting the importance of the hopanoid polar head group in driving ordering at the solvent-bilayer interface, which Laurdan is sensitive to. This trend continued during bilayer expansion at 8% ethanol, which led to uniform decrease in Laurdan GP among all compositions. However, at higher ethanol concentrations (20%), ordering was significantly higher in hopanoid-depleted (*hpnC*) membranes, indicating a more pronounced interdigitated phase compared to membranes with wild type levels of hopanoids. At 25% ethanol, both *hpnC* and *hpnI* liposomes showed a dramatic drop in Laurdan GP, indicating a loss of membrane structure while control liposomes remained intact. Therefore, both hopanoid abundance and head group composition act to prevent membrane dissolution at high ethanol concentrations.

### Discussion:

Although widespread among bacteria, hopanoids remain a poorly understood class of membrane lipids. To better understand their function, we sought a genetic system for modulating the composition hopanoids in *Z. mobilis*, a bacterium in which these lipids are highly abundant. Because of its high polyploidy, we found that transposon mutants of essential *hpn* genes – when grown under selection – act as specific knockdowns of several steps in hopanoid biosynthesis. The resistance of many *hpn* genes, especially the non-duplicated genes early in the pathway, to complete disruption when grown under selection mimics that of essential genes (*ftsZ*, *rpoB*, *leuS*) that were previously tested (Skerker et al., 2013). In contrast, duplicated *hpn* genes (that encoded SHCs) or ones late in the pathway (*hpnJ*, *hpnK*) could be almost completely knocked out. These

features are consistent with at least the core set of hopanoids (e.g. up to BHT) being essential for *Z. mobilis* growth under the standard conditions tested here.

Using a subset of *hpn* mutants, we characterized the effects of changes in hopanoid abundance and composition on the *Z. mobilis* physiology and the biophysical properties cell-derived membranes. Notably, we established that both the abundance of hopanoids and their polar head groups play key roles in dictating ethanol tolerance. A role for hopanoids in the ability of *Z. mobilis* to grow and survive in high ethanol concentrations has been hypothesized, but had been previously difficult to test. Because of the importance of this bacterium to industrial ethanol production, we expect that further engineering of hopanoid biosynthesis could be an avenue to tune its fermentation capabilities or to increase solvent tolerance in other, less-robust hosts.

We contrasted the role of hopanoids in ethanol tolerance with that of another chemical stress, acid. The ability for hopanoids to impart acid tolerance has been previously demonstrated in other bacteria. By controlling both total abundance and the stoichiometry of different hopanoid species, we showed that only the former dictated survival at low pH. This finding suggests distinct mechanisms by which these two chemical stresses influence membranes, and therefore how this class of lipids can protect against them. Specifically, low pH does not disrupt the integrity of *Z. mobilis* membranes *in vivo* (Fig. 5D-E) or lead to large effects on membrane ordering *in vitro* (Fig S4C). In contrast, ethanol acts as a solvent stress on lipids membranes and does have such effects.

Using a spectroscopic probe for membrane structure (Laurdan), we characterized the interplay of increasing ethanol concentrations and hopanoid composition on membrane structure. These experiments showed that *Z. mobilis*-derived membranes undergo ethanol-mediated structural changes previously identified in model bilayers. Hopanoids alter the magnitude of these effects and the ethanol concentrations at which they take place. Although the parameters for phase transitions in extracted membranes might not exactly correspond to those in intact cells, it is worth considering their physiological

relevance. The toxicity threshold for ethanol in cells – around 20% v/v – corresponds to an interdigitated state we observed in liposomes. Although membranes are ordered in this state, they are also highly leaky (Zeng, Smith, & Chong, 1993), consistent with increased SYTOX staining of cells in 20% ethanol. Accordingly, the mutant with reduced hopanoid amount (*hpnC*) showed the strongest interdigitated effect, as measured by increase in Laurdan GP, and also the lowest survival under acute ethanol toxicity. Evaluating how hopanoids modulate ethanol-membrane interactions *in vitro* thus provides a mechanism by which they could act to increase physiological tolerance *in vivo*.

Hopanoids are commonly thought to mimic the effects of eukaryotic sterols, whose planar structures condense lipid bilayers, reducing the area per phospholipid, and acyl chain mobility (Yeagle, 1985). These effects on membrane ordering (Fig. 3) lower the permeability of polar molecules across the bilayer, including protons (Deamer & Nichols, 1989). A reduction in proton leakage into the cytoplasm provided by the presence of abundant hopanoids or sterols provides a straightforward mechanism for acid tolerance imparted by these lipids. During ethanol stress, hopanoids instead act to mediate the phase properties of membranes: bilayer expansion at low concentrations, interdigitation at medium concentrations, and dissolution at higher concentrations. All these transitions are likely resisted by the increased packing of lipids that is caused by triterpenoids. Notably, cholesterol has previously been shown to resist the interdigitated phase transition in lipid vesicles (Tierney, Block, & Longo, 2005). In this way the interplay of hopanoids and ethanol mimics that of sterols or other triterpenoids.

One way hopanoids differ from other triterpenoids is in their polar head groups, which feature extended polyhydroxylated moieties. Extended hopanoids make up ~90% of all species in *Z. mobilis* and we found that their composition also mediates ethanol tolerance. We propose a very different functional analogue for these structures: di-acyl glycerol lipids modified by one or more sugar groups (glycolipids), which are highly abundant in plant thylakoid and in cell-wall less bacteria. Glycolipids promote membrane ordering through hydrogen bonding interactions between adjacent lipid head

groups (Curatolo, 1987). The phase behavior of glycolipid-containing membranes can be mediated by changes in head group structure, such as the anomeric configuration of the glycosidic linkage in a disaccharide (Iwamoto, Sunamoto, Inoue, Endo, & Nojima, 1982). Sugar-modified lipids, including glycolipids, hopanoids, and ceramides, could act as a general mechanism to buffer membrane structure against chemical agents (solvents, detergents) or other physical stresses (temperature, shear forces) that alter hydrophobic interactions. Hopanoids, however, are unique in that they feature both hydrocarbon and polar structural elements that promote bilayer stability. It is likely that the combination of these features allows different hopanoids species to maintain membrane stability in response to the wide-range of environmental challenges experienced by bacterial cells.

#### Figure legends:

**Fig. 1:** Genetic characterization of *hpn* transposon mutants in *Z. mobilis*. **(A)** Hopanoid biosynthesis in *Z. mobilis* occurs via a multistep pathway catalyzed by products of highly conserved *hpn* genes. Colored species indicate mature products and their reported (Hermans et al., 1991) abundance in wild type cells (as a % of total hopanoid weight content). **(B)** Characteristic colony PCRs showing the *hpn::Tn5* strains contain both native *hpn* alleles and mutant *hpn::Tn5* ones in varying amounts. In mutants early in the pathway (e.g. *hpnC*), the native allele is dominant over the mutant, but this is reversed for those late in the pathway (e.g. *hpnJ*). **(C)** Measurement of ploidy in *Z. mobilis* using qPCR of DNA extracted from counted cells, whose amplification was normalized with that of purified template standards. For *Z. mobilis* (left), this analysis yielded high genome copy numbers (60-100) for two different loci (Z1 and Z2). In contrast, *E. coli* grown in minimal media, where it is monoploid, showed a low copy number (1-2, E1 and E2) by the same method (right). Values represent mean  $\pm$  SEM, n=3. **(D)** Quantification of mutant allele abundance by deep sequencing of genomic DNA. Reads for each mutant were mapped to the genome sequence containing the transposon, and read coverage in the transposon was used to quantify the fraction of genome copies

carrying the mutant allele. Shown are three examples that correspond to colony PCRs in panel (B); for each, a gene map with the transposon insertion is shown above the coverage plot. Quantification for the rest of the mutants is found in Table S1.

(2 columns)

**Fig. 2:** Composition of mature hopanoid species in *hpn* mutants or control cells (-). Cells were grown in RM media for 20-22 hours (early stationary phase) under kanamycin selection for the transposon and lipids were extracted as described in the Methods. Each species is color coded by their structures in Fig. 1A, and values are normalized to control cells. The abundance of hopene (A) and diplopterol (B) were measured by GC-MS of silylated lipid extracts, while BHT (C), BHT glucosamine (D) and BHT cyclitol ether (E) were measured by LC-APCI-TOF-MS of acetylated lipid extracts. Due to derivatization, BHT glucosamine is indistinguishable from its acetylated precursor; its accumulation in the *hpnK* mutant likely reflects that of the HpnI product (acetylated BHT glucosamine). (F) Total hopanoids are normalized by the absolute abundance of each species in wild type background as previously measured (Hermans et al., 1991). Error bars indicate mean +/- SD, n = 3 independent cultures.

(2 column)

**Fig. 3:** The dependence of bilayer order, as measured by DPH anisotropy, on hopanoid composition in liposomes. Liposomes were prepared using lipids extracted from early-stationary phase cultures for each *hpn* mutant, cells with intact hopanoids (-), or hopanoid-free *E. coli* (MG1655). Steady-state anisotropy of DPH incubated with the liposomes was measured as a unit-less ratio  $R = (I_A - I_B) / (I_A + 2 I_B)$ , where  $I_A$  and  $I_B$  are the emission (430 nm) intensities parallel and perpendicular, respectively, to the polarization of the excitation (360 nm). Cartoons on the left diagram the compositional differences for each sample, as well as the relative motion of the probe within the bilayer's hydrophobic core. In the diagrams, the blue and red species are phospholipids

and hopanoids, respectively. Error bars indicate mean  $\pm$  SEM (n=3). Unpaired t-tests compare indicated lipid composition against the control (-): \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ .

(1 column)

**Fig. 4:** The effect of hopanoid knockdowns on *Z. mobilis* ethanol tolerance. A subset of *hpn* mutants sampling hopanoid composition were chosen for analysis. **(A)** Under standard conditions on rich medium (RM), *hpn* mutants show mild ( $\leq 25\%$  loss in rate) growth defects compared to control cells (-), which feature a kanamycin cassette in non-essential lysine exporter. **(B)** However, *hpn* mutants show noticeably larger growth defects in 8% (v/v) ethanol. The ranges for each curve show indicate  $\pm$  SEM for three independent cultures. **(C)** The relative growth rates in 8% vs. 0% ethanol ( $\mu$ , 8% /  $\mu$ , 0%) are significantly reduced for all *hpn* mutants compared to the control. **(D)** The *hpn* mutants also show significant increases in acute toxicity to ethanol, as measured by their survival rate after 30 min in 20% v/v ethanol. Error bars indicate mean  $\pm$  SEM, n = 3 independent cultures. Unpaired t-tests were used to assess significance against control cells (-): \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ .

(1 column)

**Fig. 5:** In contrast to ethanol, acid tolerance is dependent on hopanoid abundance, but not head group composition. **(A)** Mutants (*hpnC* and *hpnD*) with reduced hopanoid abundance show impairment in growth at pH 3.9 vs. pH 6.2, while those that affected hopanoid composition (*hpnI* and *hpnJ*) do not. **(B)** A similar pattern was observed for acute toxicity at high acidity (30 min at pH 2.5), as measured by colony forming units. Error bars indicate mean  $\pm$  SEM, n = 3 independent cultures. Unpaired t-tests were used to assess significance against control cells (-): \*,  $p < 0.05$ ; \*\*,  $p < 0.01$ ; \*\*\*,  $p < 0.001$ . **(C)** SYTOX staining of wild-type *Z. mobilis* cells with increasing ethanol concentrations shows that cell death between 20 and 30% (v/v) ethanol corresponds to a loss of membrane integrity. When permeabilization occurs, the polar dye can bind to cellular nucleic acids, leading to increased fluorescence. **(D)** In contrast, staining of cells

in extreme acidity (pH 2.0) did not exhibit a loss in membrane integrity. Cells under these conditions showed no survival in physiological tests, suggesting that a loss of membrane structure is the cause of ethanol but not acid toxicity. (E) Micrographs showing the ethanol-dependent leakage of the polar fluorophore DCF is specific to ethanol stress. Samples were incubated for ten minutes in the given conditions before being diluted 1:5 in DCF-free Tris pH 7.0 for imaging. Cells incubated at low pH did not exhibit internalization of DCF. Scale bars, 5  $\mu$ .

(1 column)

**Fig. 6:** The hopanoid composition of *Z. mobilis*-derived liposomes mediates changes to bilayer structure induced by ethanol. (A) Cartoon showing the sequential phase transitions in membranes caused by increasing ethanol concentrations, including bilayer expansion (I), lipid interdigitation (II), and membrane dissolution (III). The blue and red species representing phospholipids and hopanoids, respectively. (B) Emission spectra of Laurdan in liposomes reconstituted from extracted *Z. mobilis* lipids with different amounts of ethanol. At low concentrations (0-10% v/v), ethanol red-shifts Laurdan emission, indicating more solvent access to the bilayer. At intermediate concentrations (10-25%), this effect is reversed due to an ordered membrane phase with interdigitated lipids. At high concentrations (> 30%), emission is strongly red-shifted, indicating solubilization of the membrane. (C) Quantification of membrane ordering, measured as Laurdan GP, and its triphasic dependence on ethanol concentration in membranes containing *Z. mobilis* lipids. Each of the three regimes (I, II, III) corresponds to a structural transition diagrammed in panel a. (D) The effect of mutant lipid compositions with hopanoid content (*hpnC*) or changes in its head group composition (*hpnI*) on changes to Laurdan GP with increasing ethanol concentrations. Mutant liposomes show a stronger increase in GP in moderate ethanol concentrations (12-20%), indicating a more pronounced interdigitated phase, as well as a reduced threshold for bilayer dissolution at high ethanol concentration. Error bars indicate mean  $\pm$  SD, n = 3 independent liposome preparations. Unpaired t-tests were used to assess significance against liposomes with intact hopanoids: \*, p < 0.05; \*\*, p < 0.01; \*\*\*, p < 0.001.

(1 column)

### Experimental procedures:

*Cell growth and physiology:* *Z. mobilis* strains were grown in rich medium (RM) (10 g/L yeast extract (Becton Dickinson), 2 g/L potassium phosphate dibasic, and 20 g/L glucose, pH 6.2) in culture tubes shaking at 200 rpm at 30°C, unless otherwise noted. For mutants, the medium was supplemented with kanamycin (100 µg/mL). For each culture, 5 mL of medium was inoculated from a glycerol stock and strain was allowed to grow for 2 to 3 days under selection. Cultures were then back-diluted into 10 mL fresh medium; the inoculation ratio was varied across ZM4 mutants (from 0.1% to 2.5% v/v) to account for growth rate variability and enable harvesting after 20-22 hours in early stationary phase. Cells were then harvested for lipid, DNA extraction, or toxicity tests. For lipid analysis, characteristic cultures of each mutant were also dried to completeness and massed, in order to correlate optical density to cell dry mass.

For *E. coli* experiments, K12 cells (MG1655) were grown in MOPS minimal medium pH 7.2 (Teknova) with 0.6% (w/v) succinic acid as the carbon source. Cells were grown to early stationary phase (OD ~ 1.0) at 30°C in 10 mL cultures before being harvested for ploidy quantification and to stationary phase (OD ~ 2.0) in 50 mL Luria Broth medium for lipid extractions.

For fitness analysis, *Z. mobilis* growth curves were recorded in 1 mL cultures in 24-well plates (Falcon) inoculated with 10 µL of overnight culture. The plates were sealed with a semi-permeable film (Thermo Fischer) and incubated at 30°C in a Synergy 4 plate reader (BioTek) with shaking and absorbance readings (600 nm) every five minutes, for 24 to 72 hours. For acute toxicity measurements, cells were spun down in early stationary phase and resuspended in RM (control) and RM supplemented with ethanol (20% v/v) or HCl (until pH 2.5). After incubation (30 min), cells were serially diluted and

plated on RM agar plates in technical triplicates. Cell survival was measured by the ratio of colony forming units (CFUs) compared to the control condition.

For assaying of permeabilization by flow cytometry, cells were incubated with 30 nM of SYTOX Green Dead Cell Stain (Invitrogen) for 15 minutes. The fluorescence intensity of 100,000 cells was then measured on an Accuri flow cytometer (BD) using a GFP fluorescence filter set. Data was analyzed and plotted using FlowJo. For analysis of permeabilization by fluorescence microscopy, cells were incubated under the given conditions with DCF (Sigma-Aldrich) and then diluted 1:5 in 50 mM Tris to a final pH of 7.0 before imaging. Fluorescence (GFP filter) and transmitted illumination (phase contrast) images were acquired using LAS X software (Leica Microsystems) from a Leica DM6B epifluorescence microscope equipped with a mercury lamp (Leica Microsystems) and a Hamamatsu C11440 camera.

*Genetic analysis:* The function of each *hpn* gene was deduced from their roles described by loss of function studies in other bacteria (Bradley, Pearson, Saenz, & Marx, 2010; Schmerk et al., 2015; Welander et al., 2012). For PCR and copy number measurements, 2 mL of cultures grown to early stationary phase and genomic DNA extracted with a Wizard Genomic DNA Purification Kit (Promega). Outside-in colony PCR of a subset of *hpn* genes was performed with PrimeSTAR DNA polymerase (TaKaRa) using the following primers:

*hpnC*: CCACATGATTTCCCGTTCAGCTTATG and CCGGTTCTTTCAGAAAAGCGGC

*hpnI*: GCCAAGGGCTTCGAGTTACTATAAACT and TGACTTTTTTAAGAGCCGCTACGGT

*hpnJ*: CGGAAGTGCGGTCAGTTATCCC and ACTGAGAAGCCCTTAGAGCC

For quantifying transposon insertion rates, genomic DNA libraries were prepared using NEBnext DNA Library Prep Master Mix Set for Illumina (New England Biolabs) following the instructions for 400 bp insert libraries. Sequencing was performed using the 600-cycle Miseq Reagent Kit v3 (Illumina) on the MiSeq system (Illumina). For analysis, the online platform Galaxy (usegalaxy.org) was used, with alignments performed with the

Map with BWA-MEM tool to ZM4 genomes to which a typical transposon sequence (KanR Tn5 with an inserted TagModule) had been juxtaposed. The resulting alignment file was opened with UGENE and the fragments aligned to the border of the transposon were examined to find the transposon insertion locus. The genome files were updated with actual transposon insertions and the alignment was repeated. The coverage depth was calculated with *plotCoverage* tool. To estimate the transposon insertion rate, the mean coverage depth over the whole genome was computed and compared to the mean coverage depth of a 500 bp conserved region inside the transposon's KanR cassette.

Quantification of ploidy was performed using qPCR as previously described (Pecoraro, Zerulla, Lange, & Soppa, 2011). Briefly, cells were harvested at early stationary phase and serially diluted. A hemocytometer was used to count the density of cells in the dilutions, and solutions containing discrete number of cells were then prepared. From these, genomic DNA was quantitatively extracted using phenol:chloroform extraction after cell lysis, as previously described (Thompson et al., 2018). Separately, standards containing the two targeted loci were amplified from *Z. mobilis* (Z1, Z2) and *E. coli* genomic DNA (E1, E2) using the following primers:

Z1 standard: TTGTGTTAAAGGGAGCGAGAC and AGACATATGTCCACGGACTTCTAA

Z2 standard: AATTTCAAAGGGGCCTTAGCT and TTAAAGACCCTCCTACTGCTTGT

E1 standard: ATTGCCCATAAACGAGAATACC and GGAAGCTTGGATCAACCG

E2 standard: TAACGCGTCGTCTGAAACC and TAGACGCCAGCATGTTTCGTAA

The single-product amplification of the resulting standards, 1 KB in length, was confirmed by agarose electrophoresis, which was then purified by a PCR cleanup kit (Qiagen). The concentration of the standard was quantified by absorbance at 260 nm and then serially diluted to prepare a standard curve. PCR reactions for both gDNA samples and the standards was prepared with SYBR Green Master Mix (Invitrogen), using primer pairs that amplified a ~250-bp insert in the standards above:

Z1 analysis: TAAACAGCCTTTAAAATTTTGTGTTCTTG and

GTTTATTTTCGGTATTTTGGACGCAG

Z2 analysis: ATTTGATATTGTTCTGCAGTATCG and

TACTCAAGACCTTCAATATTGTTTAAACAT

E1 analysis: AAACGGATACCCGCCTG and CCTTTGACGTCATCATCATTG

E2 analysis: ATCCGTGATGAAGTG GGG and AATGCAGTAACCACAGCC

Amplification was measured on a StepOnePlus Real-Time PCR System (Applied Biosystems). Quantification of gDNA abundance relative to the standard curve was performed using the  $\Delta C_T$  method.

*Lipid analyses:* The lipid extraction protocol used in this study was adapted from Bligh and Dyer (Bligh & Dyer, 1959). Cell pellets from 10 mL of culture were resuspended in a 400 microliters of water and sonicated for 10 minutes at 50°C. Chloroform and methanol (1:1, 5 mL) were added and the monophasic extraction mixture was bath sonicated for 1 hour at 50°C and then left to shake for 3 hours at 37°C. Water (2.5 mL) was then added and complete separation of the organic (chloroform) and water/methanol phases was achieved through centrifugation. The organic phase was collected and evaporated to dryness under N<sub>2</sub> flux.

For analysis of hopene and diplopterol by GC-MS, dry lipids were silylated in 150  $\mu$ L of N,O-Bis (trimethylsilyl) trifluoroacetamide (BSTFA kit, Supelco) and 150  $\mu$ L of pyridine for 2 hours at 50°C. The solvent was then evaporated under N<sub>2</sub> flux. The product was then extracted in hexane (100  $\mu$ L) and filtered (Nylon 0.2  $\mu$ m 500  $\mu$ L centrifugal filters, VWR) before analysis. Gas chromatography was performed on an HP 6890 Series GC-System (Hewlett Packard) equipped with a DB-5MS capillary column (30 m length x 0.25 mm internal diameter, 25  $\mu$ m film; J&W). 1  $\mu$ L of sample was injected at a temperature of 250°C and the GC was run in splitless mode with a Helium (carrier gas) flow rate of 1 mL/min at a pressure of 9.36 psi. The temperature program of the oven was as follows: held at 80°C for 1 min after injection, heated to 280°C at 20°C/min, held at 280°C for 15 min, heated to 300°C at 20°C/min and held for 7 min. The column was

coupled to a HP 5973 Mass Selective Detector (Hewlett Packard). The source and quad temperature were set to 300°C and 200°C, respectively. The solvent delay was set to 9 min. For quantification of C<sub>30</sub> hopanoids, the SIM mode (191 *m/z* for hopene and 131 *m/z* for diplopterol) was used with a dwell time of 100 ms and 3 cycles/s. Data collection and processing were performed with HP Enhanced ChemStation software (Agilent Technologies).

For analysis of extended hopanoids, lipid extraction was performed as described above, with a known amount (100 µg) of an internal standard (5α-pregnane-3β,20β-diol) added to the extraction mixture. The following derivatization procedure was adapted from Talbot et al. (Talbot, Summons, Jahnke, & Farrimond, 2003) The dried chloroform extract was acetylated in 3 mL of acetic anhydride/pyridine (1:1 v/v) at 50°C for 1 hour and left stand overnight at room temperature. The solvent was then evaporated under N<sub>2</sub> flux and the acetylated lipids were dissolved in 250 µL of methanol/isopropanol (6:4 v/v). The samples were centrifuged for 10 minutes at maximum speed and transferred to glass vials. Liquid chromatography was performed with a Kinetex XB-C18 column (100 mm length x 2.1 mm internal diameter, 2.6 µm particle size; Phenomenex) at 50°C, with a 1200 Series HPLC system (Agilent Technologies). The injection volume was 3 µL and separation was achieved with a flow-rate of 0.45 mL/min and the following mobile phase gradient profile: 20% to 42% B in 2.2 min, held at 42% B for 3.6 min, 42% to 100% B in 0.1 min, held at 100% B for 2.1 min, 100% to 20% B in 0.1 min, held at 20% B for 4.3 min (where solvent A is composed of 30% isopropanol/40% methanol/30% water, and solvent B of 90% isopropanol/10% water; HPLC grade, Honeywell Burdick & Jackson). The HPLC system was coupled to an Agilent Technologies 6210 time-of-flight mass spectrometer (LC-TOF MS), with 1/5 post-column split, via a LAN card. Nitrogen was used as nebulizing (6 L/min) and drying (300°C, 30 lb/in<sup>2</sup>) gases. The vaporizer temperature was 250°C. The corona was set to 7 µA. Atmospheric pressure chemical ionization (APCI) was conducted in the positive ion mode with a capillary voltage of 3000 V. Full-scan mode (100–1500 *m/z*) at 1 spectrum/s was used for MS experiments. TOF-MS was calibrated with Agilent APCI TOF tuning mix. Data acquisition and integration were performed by the MassHunter Workstation (Agilent Technologies) and

MassHunter Qualitative Analysis (Agilent Technologies), respectively. The targeted ions are presented in Table S2; quantified analytes were normalized to the internal standard in order to correct for variations in ionization strength.

*Biophysical analyses:* Liposomes were prepared from lipids extracted from early stationary phase cells (100 mL) using a scaled-up version of the procedure described above. Upon complete drying of the organic phase under vacuum, the extracted lipids were massed and solubilized in chloroform at 1 mg/mL. For each liposome preparation, 300  $\mu$ L of the lipid solution was transferred to a borosilicate test tube and dried with Argon. The resulting film was further dried for 1 hour under vacuum. Liposomes were formed by resuspending the film in buffer (20 mM HEPES, pH 7.0), followed by overnight incubation with gentle agitation. Liposome formation was confirmed by microscopy of the samples labeled with Rhodamine 6G, a membrane dye. Before analysis, liposomes were extruded to 100 nm with a miniextruder (Avanti Polar Lipids).

For DPH experiments, liposomes were incubated with 0.5% (v/v) of a 5 mM DPH (Sigma) stock solution in ethanol. Samples were then incubated for at least one hour under gentle agitation. Steady-state anisotropy was measured using a Fluorolog spectrofluorometer (Horiba) with automated polarizers; excitation was set to 360 nm, and emission at 430 nm. For Laurdan experiments, liposomes were incubated with 1.0% (v/v) of a 1 mg/ml stock solution of Laurdan (Invitrogen) in DMSO. Laurdan emission was measured from 380 to 600 nm upon excitation at 365 nm. Laurdan GP was calculated as the ratio of integrated emission intensities at two different ranges of wavelengths:  $GP = (I_{420-440nm} - I_{490-510nm}) / (I_{420-440nm} + I_{490-510nm})$ . For testing the effects of ethanol or low pH, preformed and labelled liposomes were diluted 1:10 into HEPES buffer with ethanol or that was acidified and allowed to incubate an additional 15 minutes before measurement.

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**Author contributions:** L.B., J.K.D., and I.B. conceived the study and designed the experiments. L.B. and E.E.K.B. performed lipid analysis. L.B. and I.B. performed all other experiments. All authors discussed the results and wrote the paper.

**Data availability:** All strains are available from the Joint BioEnergy Institute public registry (<https://public-registry.jbei.org/folders/473>). Next-generation sequencing data is available through Galaxy (<https://usegalaxy.org/u/ibudin/h/hopanoids>). All other data are available from the corresponding author (I.B.) upon request.

**Abbreviated Summary:** A set of knockdown, transposon mutants was used to analyze the physiological functions of hopanoid composition in the ethanologenic bacterium *Zymomonas mobilis*. Both the abundance of hopanoids and their stoichiometry mediated growth and survival in ethanol-rich medium. Liposome-based experiments showed that hopanoids mediate the concentrations at which ethanol-induced transitions in membrane structure occur, providing a mechanism for their protective effects.

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