Enzymatic Characterization of *Leishmania major* Phosphatidylethanolamine Methyltransferases *Lmj*PEM1 and *Lmj*PEM2

Stergios Bibis[a,b], Kelly Dahlstrom[c], Tongtong Zhu[b], Rachel Zufferey[b,c]

[a] Biology Department, University of Bridgeport, 126 Park Ave, CT 06604
[b] Department of Biological Sciences, St. Johns University, 8000 Utopia Pkwy, Jamaica, NY 11439, USA
[c] Department of Biochemistry, Kansas State University, Manhattan, KS 66506, USA

Abstract

Phosphatidylcholine (PC) is the most abundant phospholipid in the membranes of the human parasite *Leishmania*. It is synthesized via two metabolic routes, the de novo pathway that starts with the uptake of choline, and the threefold methylation of phosphatidylethanolamine.

Choline was shown to be dispensable for *Leishmania*; thus, the methylation pathway likely represents the primary route for PC production. Here, we have identified and characterized two phosphatidylethanolamine methyltransferases, *Lmj*PEM1and *Lmj*PEM2. Both enzymes are expressed in promastigotes as well as in the vertebrate form amastigotes, suggesting that these methyltransferases are important for the development of the parasite throughout its life cycle.

Heterologous expression in yeast has demonstrated that *Lmj*PEM1 and *Lmj*PEM2 complement the choline auxotrophy phenotype of a yeast double null mutant lacking phosphatidylethanolamine methyltransferase activity. *Lmj*PEM1 catalyzes the first, and to a lesser extent, the second methylation reaction. In contrast, *Lmj*PEM2 has the capacity to add the second and third methyl group onto phosphatidylethanolamine to yield (lyso)PC; it can also add the first methyl group, albeit with very low efficiency.

Fig. 1. General PC biosynthetic pathways. 1. PEMT; 2. choline kinase; 3. phospho-choline cytidylyltransferase; 4. choline phosphotransferase; 5. PC synthase. DAG,diacylglycerol; DM, dimethyl; MM, monomethyl; P, phosphate.

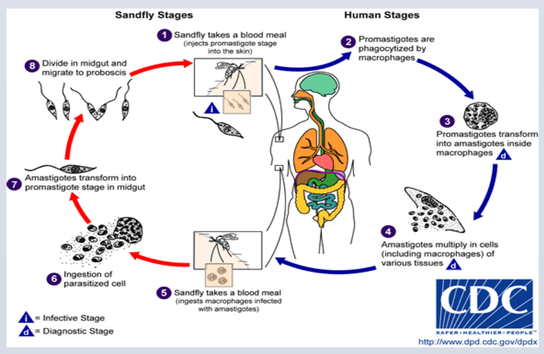

Fig. 2. Life cycle of *Leishmania*

Objectives

1. Establish that *Leishmania major* utilizes the methylation pathway involved in PC biosynthesis.
2. Identify putative *Leishmania major* genes involved in the PE methylation pathway.
3. Verify that these putative PE methyltransferase genes are expressed in *L. major* and determine their ability to complement auxotrophy in *Saccharomyces cerevisiae* lacking PE methyltransferase activity.
4. Determine substrate specificities of these enzymes

Results

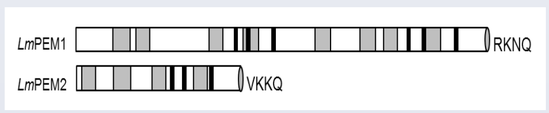

Fig. 3. Schematic representation of the PE methyltransferases LmjPEM1 and LmjPEM2 of *L. major*.
The grey rectangles represent the putative transmembrane spans, the black rectangles depict the conserved amino acids diagnostic of PE methyltransferases, and the grey ovals symbolize the putative endoplasmic reticulum retention motif.

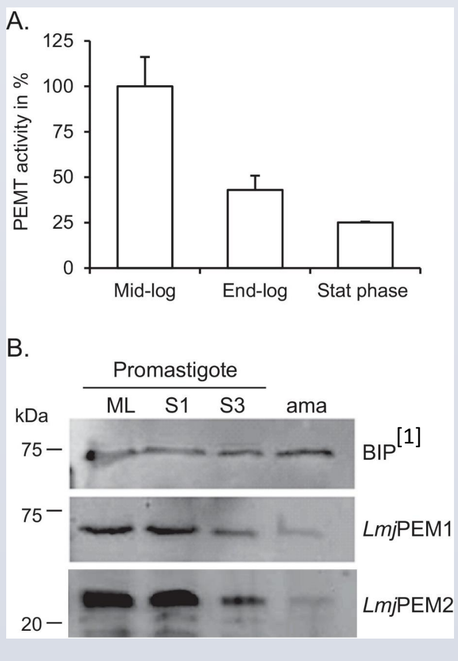

Fig. 3. *Lmj*PEM1 and *Lmj*PEM2 are expressed throughout the life cycle of *Leishmania*.

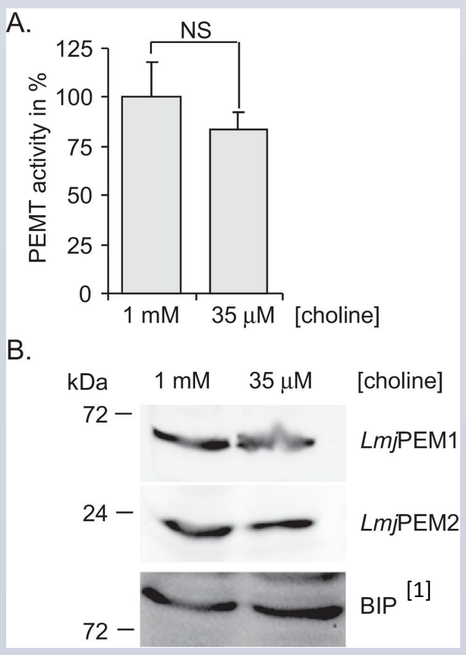

Fig. 4. Expression of *Lmj*PEM1 and *Lmj*PEM2 is choline independent.

Results

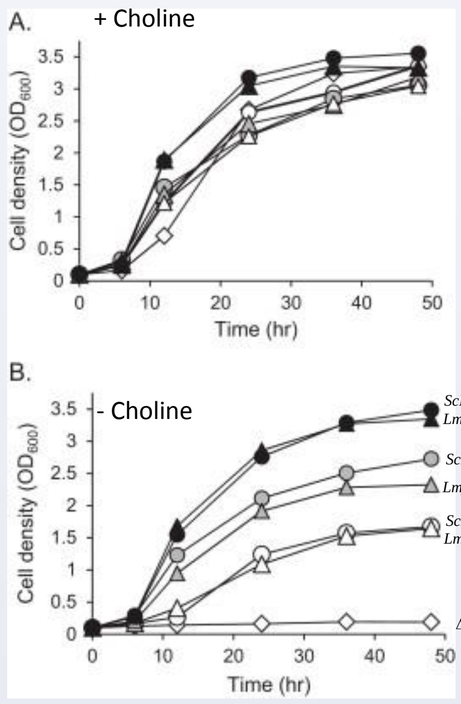

Fig. 7. *Lmj*PEM1 and *Lmj*PEM2 complement the choline auxotrophy phenotype of *S. cerevisiae* double null mutant *scpem1Δscpem2Δ* that lacks PEMT activity

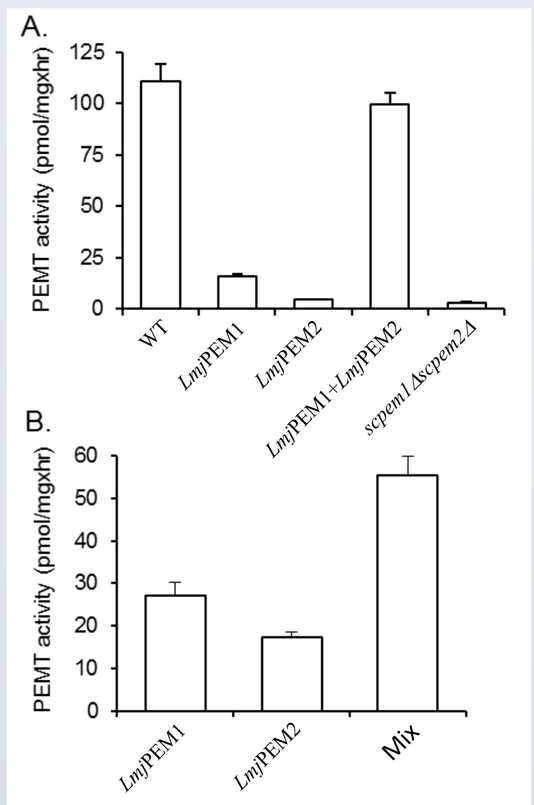

Fig. 8. LmjPEM1 and LmjPEM2 act as PEMT enzymes.

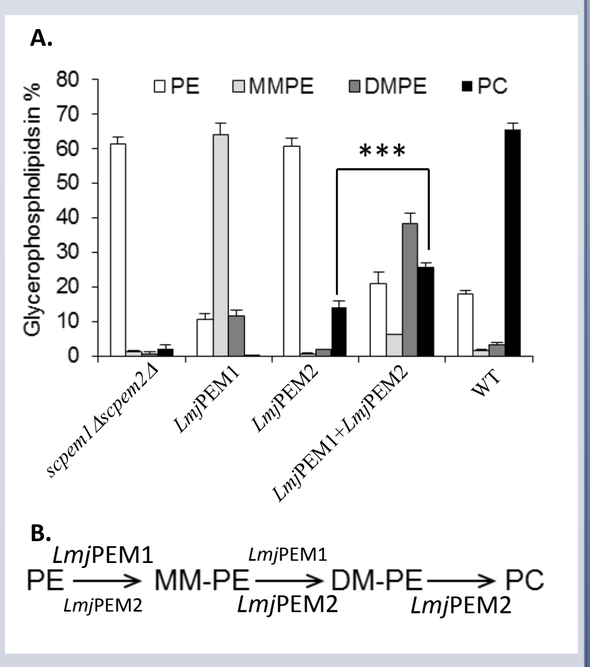

Fig. 9. *Lmj*PEM1 and *Lmj*PEM2 substrate specificities.

Conclusion

- ✓ *Leishmania major* posses two PE-methyltransferase genes, *LmjPEM1* and *LmjPEM2*
- ✓ *Leishmania major* express both *LmjPEM1* and *LmjPEM2* in both promastigotes and amastigotes in a cell cycle dependent manner
  - ✓ Which correlates to PE-methyltransferase activity
- ✓ Expression of *LmjPEM1* and *LmjPEM2* is independent of choline
  - ✓ As is PE-methyltransferase activity
- ✓ *LmjPEM1* and *LmjPEM2* complement the choline auxotrophy of *scpem1Δscpem2Δ* yeast deficient of PE-methyltransferase activity
- ✓ *Lmj*PEM1 catalyzes the first and second methylations of PE producing MM-PE and DM-PE
  - ✓ Albeit with lower affinity for the second methylation
- ✓ *Lmj*PEM2 catalyzes all three methylations of PE producing MM-PE, DM-PE, and PC
  - ✓ Albeit with a lower affinity for the first methylation

References

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Acknowledgements

This project was supported by the American Heart Association award 0630001N, the NIH grant P20 RR016475 from the INBRE Program of the National Center for Research Resources and the NIH grant ARRA 1 R03 AI078145 to RZ. The lipid profile data were acquired at Kansas Lipidomics Research Center (KLRC). Instrument acquisition and method development at KLRC were supported by NSF grants MCB 0455318, MCB 0920663,DBI 0521587, DBI 1228622, Kansas INBRE (P20 GM103418 from the National Institute of General Medical Sciences), NSF EPSCoR grant EPS-0236913, Kansas Technology Enterprise Corporation, and Kansas State University.