Detection of Feral Hog Impacts on Water Quality



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Negatively impact native wildlife

- Wood and Barrett 1979; Singer et al. 1984; Elsey et al. 2012

Reservoirs for disease

- Wood et al. 1992; Mason and Fleming 1999

Harmful to native vegetation - Bratton 1975; Mitchell and Mayer 1997



Complex legal status

Popular with some hunters - Wood and Barrett 1979

Water Quality



Mallin et al. 1997; Stone et al. 1998

Belden and Pelton 1975, 1976 Kaller and Kelso 2003 Kaller et al. 2007



West Bay and Ft. Polk WMAs 2002-2005 Excessive Fecal Coliforms (*E. coli*) - 8 of 20 samples

Identified pathogens: Aeromonas, Enterococcus, Staphlococcus auerus, and Shigella.

Statistical and DNA fingerprinting association with feral hogs

Significant impacts to aquatic organisms and habitat







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Kisatchie National Forest Summer 2014 Excessive Fecal coliforms (E.coli) **17 of 31 sites** Leptospira and Klebsiella **19 of 31 sites** Salmonella 8 of 31 sites Yersinia 6 of 31 sites











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Voges-Proskauer (VP) utilized as confirmatory test only. Voges-Proskauer (VP) wird nur als Zusatztest verwendet. Voges-Proskauer (VP) utilisé seulement comme test complémentaire. Voges-Proskauer (VP) utilizzato solamente come test di conferma. Voges-Proskauer (VP) se utiliza sólo como prueba de test suplementaria.





Summer 2015 Excessive Fecal coliforms (E.coli) 9 of 40 sites Leptospira 34 of 40 sites Klebsiella 40 of 40 sites Yersinia 29 of 40 sites Salmonella (including Swine Cholera) 9 of 40 sites

2014 and 2015 Combined Excessive Fecal coliforms (E.coli) 26 of 71 sites Leptospira 53 of 79 sites Klebsiella 59 of 71 sites Yersinia 35 of 71 sites Salmonella (including Swine Cholera) **17 of 71 sites**

No Detections Multiple Hog Sources 2015 KNF Hogs 2015 LDWF Hogs Pre-2005 KNF Hogs

Natchitoches



Preliminary Implications

Human and wildlife pathogens present and associated with feral hogs.

DNA fingerprinting (22 of 40 sites) detected individual and/or matrilineal connection (i.e., same sounder – 12 of 39 sampled hogs).

Feral hogs may be spreading by natural demographic processes or anthropogenic actions.



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