GENOME ANALYSIS AND EXPERIMENTAL EVIDENCE OF HORIZONTAL TRANSMISSION OF NERVOUS NECROSIS VIRUS (NNV) INFECTING HATCHERY STOCKS OF MARINE FISH



BORNEO MARINE RESEARCH INSTITUTE UNIVERSITI MALAYSIA SABAH 2011

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THESIS SUBMITTED IN FULFILLMENT FOR THE DEGREE OF MASTER OF SCIENCE

BORNEO MARINE RESEARCH INSTITUTE UNIVERSITI MALAYSIA SABAH 2011

DECLARATION

I hereby declare that the material in this thesis is my own except for quotations, excerpts, equations, summaries and references, which have been duly acknowledged.

21 October 2011

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ABSTRACT

GENOME ANALYSIS AND EXPERIMENTAL EVIDENCE OF HORIZONTAL TRANSMISSION OF NERVOUS NECROSIS VIRUS (NNV) INFECTING HATCHERY STOCKS OF MARINE FISH

High stocking density in larviculture is important for successful production of marine fish species in hatchery. However, mass mortality due to nervous necrosis virus (NNV) often occurred in newly hatched fish larvae. This reduces the marine fish seed production in hatcheries throughout the country. Hence, this study was conducted to analyze the genomes of NNV and examine the possibility of horizontal transmission of the virus in fish larvae through viral-contaminated fish. In the first experiment, NNV was detected using RT-PCR and histopathological methods from twenty sampling sets of fish larvae collected from different hatcheries and aquaculture farms. The collected fish specimens represented the four most cultured marine fish species in the South East Asian region. The RT-PCR analysis revealed that 60.98% of the fish specimens were infected by NNV. The designed PCR primers in this study were suitably used for the purpose of detection of NNV in marine fish species. The histopathological study showed that cell vacuolation has been observed in brain and retina tissues of infected fish. In the second experiment, the complete coding sequence of both genomes (RdRp and Cp genes) in NNV was successfully PCR amplified and sequenced. The complete coding sequence of RdRp gene consisted of 3024 nucleotides and 982 amino acids. Meanwhile the complete coding sequence for Cp gene consisted of 1363 nucleotides and 338 amino acids. The analysis of nucleotide sequences revealed that both RdRp and Cp genes in NNV isolates in Malaysia had 94.5 - 99.7% and 95.9 – 99.8% similarity to RGNNV genotype, respectively. This shows that only RGNNV genotype of the virus exists in Malaysia. In the third experiment, amplified fragments of RdRp and Cp genes of NNV were restricted using six different restriction enzymes. The result showed that RdRp and Cp genes produced five and seven different RFLP-PCR profiles, respectively. The phylogenetic tree further showed that the RGNNV genotype in Malaysia could be clustered into five main clusters based on RdRp gene and seven main clusters based on Cp gene. In the last experiment, clinically healthy Asian seabass, Lates calcarifer and tiger grouper, Epinephelus fuscoguttatus larvae were exposed to pure culture of GPNNV and tissue homogenates of infected fish. The transmission of NNV was evaluated using RT-PCR, histopathological, RFLP-PCR and DNA sequencing methods. The results showed that horizontal transmission of NNV has successfully occurred in the exposed fish groups except for groups D2 and E2, respectively. The exposed fish specimens showed cell vacuolations in brain and retina tissues similar to those observed in naturally infected fish. The cDNA of Cp gene in NNV isolated from the exposed fish showed 100% similarity in RFLP-PCR profiles and nucleotide sequence to the viral sources. Overall, this study has provided scientific evidence that aquaculture industry in Malaysia is threatened by NNV infection. This requires holistic management approaches to be adopted in both hatcheries and aquaculture farms to prevent spreading of the pathogen thus ensuring the sustainability of sea food security in the country.

ABSTRAK

Penstokan pada kepadatan yang tinggi semasa peringkat larvikultur adalah sangat penting untuk produksi vang beriava bagi spesis ikan marin di hatceri. Walau bagaimanapun, kematian yang tinggi disebabkan oleh nervous necrosis virus (NNV) sering terjadi pada anak ikan yang baru menetas. Ini telah mengurangkan pengeluaran benih ikan marin di semua hatceri di seluruh negara. Maka, kajian ini dijalankan untuk menganalisis kedua-dua genom NNV dan kemungkinan berlakunya jangkitan secara melintang virus tersebut pada anak ikan melalui ikan yang telah dijangkiti. Dalam eksperimen pertama, NNV telah dikesan dengan menggunakan kaedah RT-PCR dan kaedah histopatologi dari dua puluh set sampel anak ikan yang diperolehi secara berasingan dari pusat-pusat hatceri dan ladangladang akuakultur. Ikan-ikan yang dikumpul mewakili empat daripada spesis ikan marin yang paling banyak dikultur di Asia Tenggara. Analisis RT-PCR mendapati bahawa 60.98% daripada spesimen-spesimen ikan tersebut telah dijangkiti oleh NNV. PCR primer yang direka dalam eksperimen ini adalah sesuai untuk tujuan pengesanan NNV pada ikan marin. Kajian histopatologi menunjukkan bahawa vakulasi sel diperhatikan di dalam tisu-tisu otak dan retina ikan yang telah dijangkiti. Dalam eksperimen kedua, jujukan pengekodan lengkap bagi kedua-dua genom (gen RdRp dan gen Cp) dalam NNV telah berjaya diamplifikasikan dan dijujukkan. Jujukan pengekodan lengkap bagi gen RdRp terdiri daripada 3024 nukleotida dan 982 asid amino. Sementara itu, jujukan pengekodan lengkap bagi gen Cp mengandungi 1363 nukleotida dan 338 asid amino. Analisis jujukan nukleotida mendedahkan bahawa kedua-dua gen RdRp dan gen Cp daripada NNV yang dipencilkan di Malaysia masing-masing adalah 94.5-99.7% dan 95.9-99.8% menyerupai genotip RGNNV. Ini menunjukkan bahawa hanya genotip RGNNV bagi virus tersebut wujud di Malaysia. Dalam eksperimen ketiga, gen RdRp dan gen Cp yang diamplifikasi dari NNV telah dibatasi menggunakan enam jenis enzim pembatasan yang berbeza. Keputusan menunjukkan bahawa gen RdRp menghasilkan lima dan gen Cp menghasilkan tujuh profil RFLP-PCR yang berbeza. Pokok filogenetik seterusnya menunjukkan bahawa genotip RGNNV di Malaysia boleh dirumpunkan ke dalam lima rumpun utama berdasarkan gen RdRd dan tujuh rumpun utama berdasarkan gen Cp. Dalam eksperimen terakhir, anak ikan siakap, Lates calcarifer dan anak ikan kerapu harimau, Epinephelus fuscoguttatus yang secara klinikalnya sihat didedahkan kepada kultur tulen GPNNV dan homogenat tisu-tisu ikan yang dijangkiti. Transmisi NNV dianalisa dengan menggunakan kaedah-kaedah RT-PCR, histopatologi, RFLP-PCR dan jujukan DNA. Keputusan menunjukkan bahawa transmisi NNV secara melintang telah berlaku dengan jayanya kecuali kumpulan D2 dan E2. Spesimen-spesimen ikan yang terdedah menunjukkan vakulasi sel di dalam tisu-tisu otak dan retina sama seperti yang diperhatikan pada ikan yang dijangkiti secara semulajadi, cDNA bagi gen Cp dalam NNV yang dipencilkan semula dari ikan yang terdedah menunjukkan bahawa 100% persamaan dalam profil RFLP-PCR dan jujukan DNA dengan sumber virus. Pada keseluruhannya, kajian ini menyediakan bukti saintifik bahawa industri akuakultur di Malaysia sedang dibebani dengan jangkitan NNV. Ini memerlukan adaptasi pengurusan holistik di hatceri-hatceri dan ladang-ladang akuakultur bagi menghalang penyebaran patogen tersebut dan memastikan kemampanan sumber makanan laut negara.

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	Malaysia 2, Lana 20, CR 0000 Candalyan Malaysia 2, Lana	
	inalaysia J, Lahe JU, JD UJUJ Jahluakali Malaysia J, Lalie	
	SI. SD USUS Saliudkali Malaysia S; Lane 32: SB USUS	06
	Sanuakan Malaysia 8.	86