Trends in molecular genetic studies of livestock in Indonesia

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Introduction

Van Vleck (1990) mentioned **that** the history of molecular biology began when the Watson - Crick Model for genetic material around 50 years ago. They had **worked** out, rather amazingly, the structure **and coding pattern** for **DNA.** Enthusiasts, no **doubt,** through that all **genetic** mysteries would **soon be** solved. **However** quantitative animal breeder **was** naturally skeptical. Who would have predicted that the gene for making bovine growth **hormone** (bGH) could **be cut** out of the chromosome of a **cow and** inserted into bacteria which then manufactures rather cheaply so much bGH that perhaps 20% **fewer dairy cows will be needed?** Who **would** have thought **that** the DNA structure **of** an **entire** chromosome might be sequenced? Who would **have** thought a gene from a man can be added to the genome of a mouse, or a **pig** or a sheep to create what are called transgenic. That **much** of chromosome seems to contain non-essential information? That some genes **are** repeated in the same **and** different chromosome? That a **couple** of missing **base pairs** are implicated **in** cystic fibrosis? **That** chromosome can be biologically **sliced** at predictable break point **and** them sorted **by** size – the restriction fragment **length** polymarphism?

Quantitative geneticist, however quickly recover **after** acknowledging the impossible and **ask** the **skeptic's** question: what, of all that has been learned from molecular biology, **can be** applied to livestock improvement? **At** present, **and** after 50 **years** of exiting and **amazing** discovery, **the answer seems to be not** much. If anything, from molecular can be applied to animal improvement.

For the last 12 years, **the** trends of molecular biology research in Indonesia **showed** a good progress. It should be noted that although **the** research budget provided by university **and funding agencies** is still not appropriate, the research trends **is** still **following the latest** science and **research** development. In order to describe the trends in molecular **biology** research for livestock, I **have examined and studied** the research that **have been conducted only for** the major **universities** and research centers.

The trends of molecular biology research

Bali cattle are **one** on Indonesian native cattle's that famous for their **ability** to adapt to tropical conditions. For the last 30 **years,** indiscriminate crossbreeding **using** artificial insemination (AI) might be **has** contaminated the purity **of** Bali **cattle. In** order to utilize as well to conserve Bali cattle **it is** necessary to develop **an** accurate **and** simples method **to** detect the purity of Bali cattle.

In order to identify the purity **of Bali cattle some molecular** biology **techniques have been** applied including kariotype analysis (Noor et. al., 2000, Hardiman, 2000 **and** Sutrisna, 2002); hair structure **analyses using scanning electron** microscope (Noor et al., 2000); Haemoglobin **analysis using Isoelectric focusing** methods (Karmita, 2000; Noor el al., 2001) and DNA microsatelite (Noor et al.,2000; Handiwirawan et al, (2003). **The** results show that **by** combining different methods of molecular biology **we can** get more accurate result, **because each** technique has **some** strengths and **weaknesses.** In addition, these techniques **can** be **used** to differentiate

Bali **cattle and** other domestic **species.** Some microsatelite loci (HEL 1, INRA035, CSSM66 and INRA037) **of** Bali cattle **have** specific band patterns that differ from those of Simmental, Brangus and Limmousin. The hair structure analyses using scanning electron microscope indicates that Bali cattle hair **has** specific pattern **that** different from those **of** Simmental, **Brangus** and Limmousin. In **the** same manner the lsoelectric focusing Methods can differentiate the differences of hemoglobin band patterns between Bali cattle and other species. Kariotype analyses results **show** a variation on ideogram profile among Bali cattle collected from different regions in Bali Island.

Another microsatellite experiment **has** been conducted **by** Noor, et al., 2001b) by analyzing **the** genetic variation of Bali, Madura, PO and **Brangus** cattle's. ETH225 microsatelite of Madura **cattle has five** alleles. The results give **us** early indication that **the** techniques can be **used** to differentiate among the breeds. **A** more intensive research to test **the** specificity of HEL9 **and** INRA035 microsatellite **markers** in Bali cattle **was** conducted by Handiwirawan et al (2003). The result **show** that **A and** B alleles at INRA035 microsatellite locus are **monomorphic** and can **be used** for a **specific** markers for Bali cattle. Allele **A** at **locus** HEL9 that **has high** frequency (92.90%) in Bali cattle and 100% in Banteng **can** also he used a supporting marker.

The **same microsatelite technique** has been applied to identify the genetic variation of among Padang Coastal area cattle's (Noor and Anwar, 2002). Sarbaini (2004) conducted a study of **microsatellite** DNA variation of West Sumatra Pesisir cattle using six microsatellite markers i.e., ETH225, HEL9, BM2113, ILST006, INRA037 and ETH3. The **PCR** analysis showed that **the** average **number** of allele of the six **microsatellite** were 9.6 and 11, **and** the heterozygosity average were 0.85731 ± 0.00014 and 0.8738 ± 0.00012 for Pesisir Selatan and Padang Pariaman subpopulation respectively.

Attempts to associate the **microsatellite** allele variation with quantitative trait for beef **and** dairy cattle have been conducted by **Maskur** (2005) and Sumantri et al., (2001, 2002). Maskur (2005) used 16 microsatellite **markers** to analyze genetic identification of Bali cattle, Brangus and their crossed. The result shows **that the** average number of detected allele **was** 2.31, 2.56 and 2.75 for Bali cattle, Brangus and the **crossed,** respectively. They claimed **that** the INRA037, HEL9, CSSM66, INRA035 and ETH225 **have** significant effect on average daily gain. **The** INRA037 have significant affect on Birth weight. Sumantri et al. (2001 **and** 2002) stated **that** kappa casein BB significantly affected milk quality, especially protein content. The **above** results are still questionable, **because their** sample size is small and the basic quantitative genetics theory **does** not support their conclusion.

Abdullah (2005) **is using** DNA mitochondria in order to analyze **the** genetic characterization of beef cattle at Nanggroe Aceh Darussalam. Unfortunately the **result** cannot be presented **because** the experiment is still going.

Conclusion

Considering the research budget **and** the capability of university and research centers to do molecular biology research to improve livestock production in Indonesia, the conventional quantitative genetic techniques still play a major **role. However, this** techniques should be **combined with** molecular biology techniques such us **microsatellite** and mitochondria in order to get **rapid** progress. The molecular biology research is needed to get supporting information, especially to describe the genetic variation of domestic animal.

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