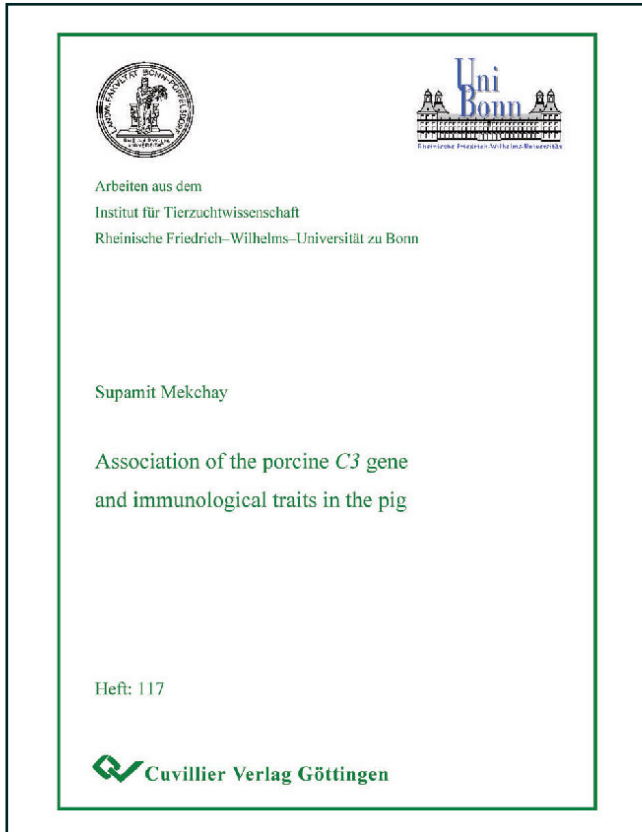




Supamit Mekchay (Autor)
**Association of the porcine C3 gene and
immunological traits in the pig**



<https://cuvillier.de/de/shop/publications/3336>

Copyright:
Cuvillier Verlag, Inhaberin Annette Jentsch-Cuvillier, Nonnenstieg 8, 37075 Göttingen,
Germany
Telefon: +49 (0)551 54724-0, E-Mail: info@cuvillier.de, Website: <https://cuvillier.de>

1 Introduction

Infectious diseases in livestock are still a major constraint on production efficiency. Economic losses from disease of farm animals have been estimated to account for 10-20 % of the total production costs (Müller and Brem 1991). Normally, antibiotics, vaccination, sanitation and eradication are used to control and prevent the animal pathogens. Recently, the growing consumer's concerns about the antibiotics and chemical residue in animal products, including an emergence of the food-borne disease, increased more demand on safety and quality of animal products (Huh 2000).

Breeding for disease resistance is an alternative to solve these problems in a long term perspective and can contribute to reduce the costs of disease control. In the past, the conventional methods of animal breeding were used to improve genetics for disease resistance. However, the progress was slow due to environmental factors and traits controlled by many complex genes. More recently, molecular genetic methods have shown a high power to identify genes or DNA loci which affect disease resistance or susceptibility traits in porcine and other farm animals, to provide a means for selecting animals with the best combination of genes for disease resistance. This methodology reveals a great importance for enhancing animal health, animal productivity, animal welfare and quality of animal products, in addition to relating a sustainable animal production system (Olesen et al. 2000).

Disease resistance in animals involve immune response which is manifested by the host ability to eliminate pathogens. The immune response consists of many systems to protect animal's body from pathogens, of which the complement system is the one and a powerful effector of the immune system. It is a part of innate immunity that plays a role of host defence mechanism against general microorganisms. C3 complement is a major component and plays a major role as a central molecule of the complement cascade. The activated C3 molecules attach to the pathogenic cells that induce opsonization of phagocytic cells and triggers the activation of the lytic pathway of complement leading to lyse the pathogenic cells. Moreover, some cleavage products of the C3 complement are involved in inflammation response and antibody production in a specific immunity response. The C3 complement is an important molecule in host defence mechanism against general and specific microorganisms. Hence, the *C3* complement gene is a

potential candidate gene for complement activity. By that implication, a high complement activity can be expected to contribute to the power of a general defence mechanism against microorganisms.

The objectives of this study are:

- (1) to analyse the nucleotide sequence of porcine *C3* gene including the 5' and 3' flanking regions.
- (2) to identify the polymorphism in porcine *C3* gene.
- (3) to develop simple methods to identify the polymorphic sites of the porcine *C3* gene.
- (4) to analyse an association between the genotype of the *C3* gene and immunologic parameters that include alternative and classical pathway complement activity, serum *C3* concentration, antibody titre against microorganisms (*Mycoplasma*, Aujeszky and PRRS) and lymphocyte proliferation.

2 Literature review

2.1 Molecular genetic approach for disease resistance and improved health in porcine

In farm animals, breeding for disease resistance by traditional phenotype selection is difficult to practise. Because most disease resistance or susceptibility traits are controlled by polygenic loci and also influenced by environmental factors (Rothschild 1991), there are also difficulties associated in measuring the phenotypic disease resistance traits. There is also increasing concern that selection for resistance to one disease might increase susceptibility to other disease (Mallard et al. 1998). Moreover, disease resistance traits have been ignored in most selection programs (Rothschild 1991). These are some of the reasons for a slow progress of conventional breeding approach to improve disease resistance in farm animals in the past. A better alternative would be to select for immune response parameters. Immune responsiveness has been suggested as an indirect indicator of disease resistance (Buchmann et al. 1985, Gavora and Spencer 1983, Mallard et al. 1998) and selection for it is a feasible indirect approach to enhance disease resistance and productivity in porcine (Mallard et al. 1998, Wilkie and Mallard 2000).

Molecular genetics is a powerful tool for identification of important genes or DNA regions for disease resistance or immune responsiveness. This methodology identifies the potential genetic markers which could be used for marker assisted selection (MAS). The MAS can enable selection for disease resistance without exposure to disease challenge and allows high accurate selection which is unaffected by environmental factors (Soller and Andersson 1998). Reviews of molecular genetic approach to disease resistance or immune capacity in livestock have been described by several authors (Archibald 1991, Blattman and Ben 1995, Crawford et al. 2000, Edfors-Lilja 1999, Hawken et al. 1998, Müller and Brem 1991, Soller and Andersson 1998). The strategies of molecular genetic approach for selecting disease resistance genes (Figure 1) begins by choosing a general or specific disease resistance candidate gene from known function (e.g. biological function and physiological function) or unknown functions through informations from the gene maps (linkage map, physical map, comparative map, QTL-linkage map or expressed sequence tags (ESTs)) to analyse nucleotide sequence and identify polymorphisms in this gene.

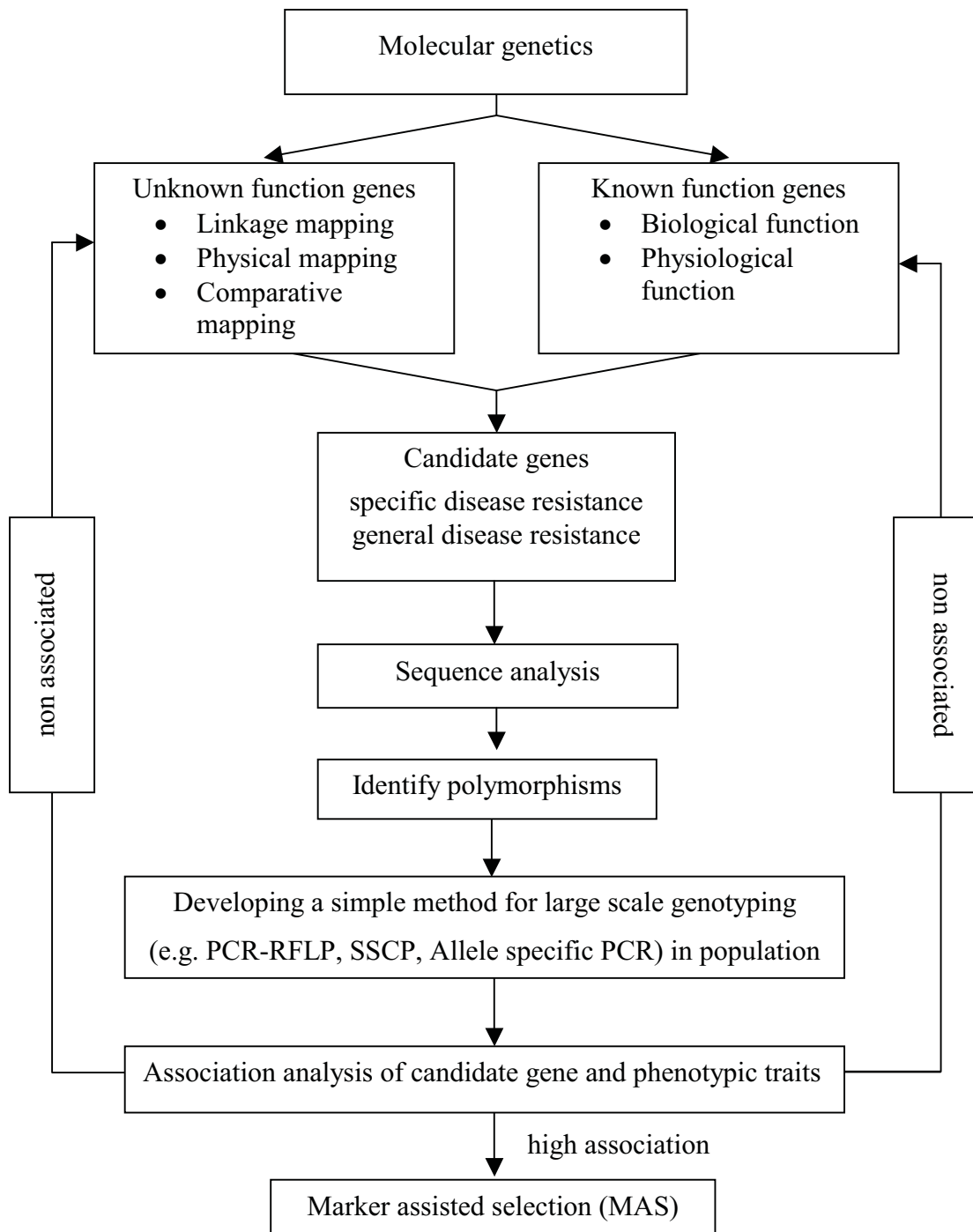


Figure 1: Molecular genetic approach to identify candidate genes or potential DNA region fragments as marker assisted selection for disease resistance and enhancing health in porcine (review from Soller and Andersson 1999)