

Identification of polymorphisms in Protein Coding Genes which affect eggshell quality traits in layers

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Identification of polymorphisms in Protein Coding Genes which affect eggshell quality traits in layers

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Background

- Chicken egg is a high quality food, at a low cost
- The eggshell constitutes a natural physical barrier against bacterial penetration
- Microbial spoilage of eggs is promoted by presence of eggshell cracks or micro-cracks





Micro-cracks promote bacterial penetration







Context: set hens free!

- Consumer and big brands demand
 - Cage-free eggs production
 - Sustainability -> Long-life laying hen









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- Increased risk of
 - Microbial contamination
 - Weaker eggshells









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Importance of eggshell quality







Factors influencing shell integrity and quality

- Egg manipulation: collecting, grading, packing processes and transportation
- Management / housing systems: nutrition, temperature and lightning conditions
- Eggshell biomineralization process: oviposition time, age of bird
- Genetics : breeds, polymorphisms









Genetic determinism of eggshell quality

- A large number of QTLs influencing eggshell quality traits (stiffness, strength, shape, diameter)
- Several candidate genes

- Causal polymorphism identification
 - Key step to increase the evaluation accuracy (genomic selection).
 - Link between genes, biological functions and traits.







Overall approach

- Polymorphisms in genomic sequences from 1000 Gallus genome project (laying hens, broilers, local breeds) Tixier-Boichard et al., 2020 doi:10.20870/productions-animales.2020.33.3.4564
- Functional candidate genes
- QTL affecting eggshell quality (stiffness, strength, shape, diameter)



Putative causal mutations, localized in candidate genes for eggshell formation and quality.

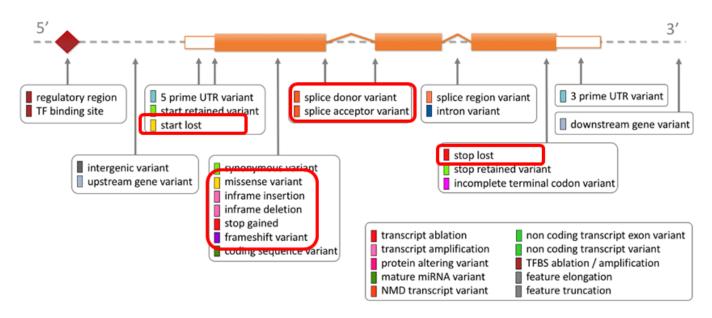






Deleterious polymorphisms identification

May affect protein structure and function









Deleterious polymorphisms identification

- May affect protein structure and function
- Thousand of deleterious variants identified in genomic sequences

	Library	n	Variant	Deleter
Broilers	Chickseq	24	12 898 316	67 986
	Acrigen	16	11 465 902	62 650
	SABRE	6	9 187 271	50 394
Layers	Utopige	90	9 947 217	52 270
	FEEDaGENE	19	7 121 799	40 107
	Epibird	12	7 364 408	38 494
	QTLDJ	4	5 795 085	28 057
	FEEDaGENE_AgENC	4	5 314 924	29 427
Local breeds	Domestic (Diversité)	36	33 410 400	207 596







<u>Deleterious polymorphism in functional candidate</u> <u>genes</u>

- 465 candidate genes:
 - 333 genes known to be involved in calcification process
 - 225 differentially expressed proteins during biomineralization process



4849 deleterious loci in 418 candidate genes







<u>Deleterious polymorphism in functional candidate</u> <u>genes</u>

4 849 deleterious loci in 418 functional candidate genes

<u>Deleterious variant in QTL affecting eggshell quality</u> (stiffness, strength, shape, diameter)

- 5 607 deleterious loci located in 1560 genes
- of which 566 are located in 44 functional candidate genes







Genotyping

- Consolidated list of 255 deleterious polymorphisms
 - 240 SNP + 15 InDels
 - Corresponding to 46 genes of which 34 are candidate genes
- Amplicon sequencing genotyping on 480 laying hens from 8 different lines (White Leghorn and Rhode Island)
- Identification of 693 polymophisms in the targeted regions







Within line and overall to support the hypothesis of a direct effect







Within line and overall to support the hypothesis of a direct effect









Within line and overall to support the hypothesis of a direct effect

No effect
Never significant effect

Indirect effect (association)
Significant effect but

only within line



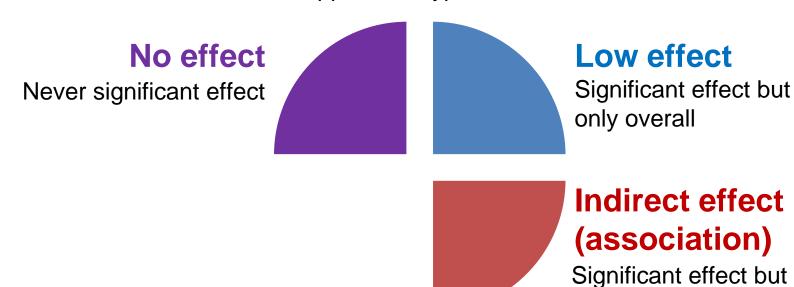




only within line

Association study strategy

Within line and overall to support the hypothesis of a direct effect

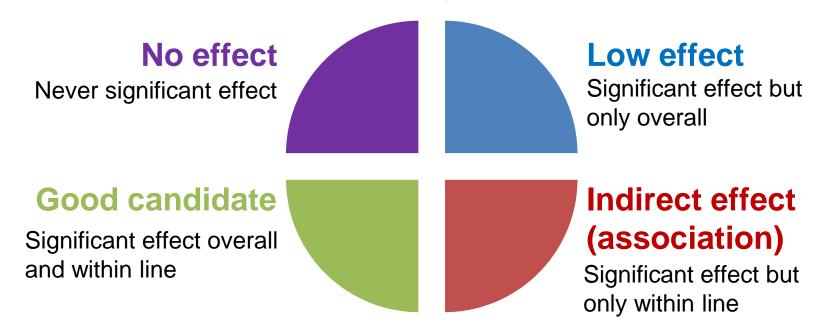








Within line and overall to support the hypothesis of a direct effect





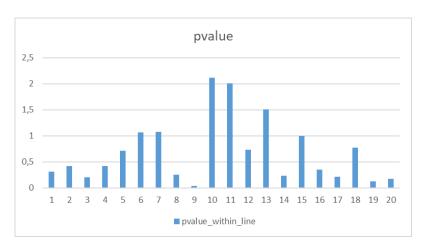




Example results

Association study of twenty polymorphisms (MAF>1%) identified in one gene

Within line analysis









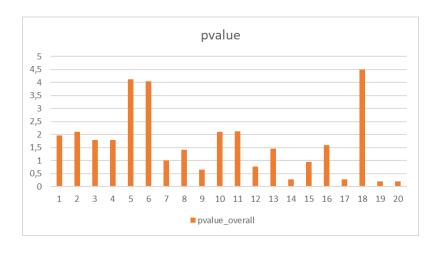
Example results

Association study of twenty polymorphisms (MAF>1%) identified in one gene

Within line analysis

pvalue 2,5 1,5 1 0,5 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 pvalue_within_line

Overall line analysis

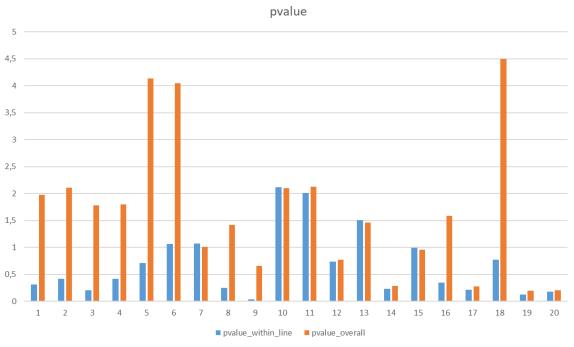








Example results









Results





Low effect

Significant effect but only overall

No Good candidate

Overall and within line effect



Indirect effect (association)







Results



- Identification of 64 deleterious polymorphisms associated with eggshell strength or eggshell stiffness
- 9 deleterious polymorphisms are predicted to have a high impact of amino acid substitution on protein function







Next step

- 6 putative causal mutations will be investigated on several laying hen and broiler lines to confirm their causative status
- Functional and structural characterization of protein isoform products from genes carrying these polymorphisms
 - Transcript expression and protein level
 - 3D structure of protein isoforms







Concluding remarks

- Polymorphisms in coding regions are a small proportion of all polymorphisms
- It's more obvious to draw a link between polymorphism and protein function and trait
- This strategy is generic and can be applied to other species and traits







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