Curriculum vitae

VAYSSE Amaury
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CURRENT EMPLOYEMENT

Reasercher Statistical Genetics G5. Institut Pasteur

EDUCATION

PhD « Identification of genetic signatures of selection in dog » (2011)
Université de Rennes 1, Rennes (France)

Master - M2 Complementary skill in informatics (2005)
Institut de Formation Supérieure en Informatique et Communication, Rennes (France)

Master - M2 Biology and health (2004)
Université de Rennes 1, Rennes (France)

COMPLEMENTAIRY TRAINING

- Structuring Machine Learning projects (deeplearning.ai on Coursera) Dec. 2017
- Improving deep neural networks (deeplearning.ai on Coursera) Nov. 2017
- Neural Networks and Deep Learning (deeplearning.ai on Coursera) Nov. 2017
- Workshop on Machine Learning for Personalized Medicine, Barcelone (Espagne), 2016
- The 5th International Workshop on Genomic Epidemiology, Paris (France), 2013
- Atelier INSERM n°222: « Méthodes statistiques et nouvelles stratégies de recherche de gènes impliqués dans les maladies communes à l'ère du séquençage haut débit », Bordeaux (France), 2013
- The 3rd International Workshop on Genomic Epidemiology, Paris (France), 2009
- Workshop on data management and association analysis (BC|SNPmax), Uppsala (Suède), 2008

PROFESSIONNAL EXPERIENCES

Researcher in genetic epidemiology (2018)
Statistical Genetics G5, Institut Pasteur

Post-doctoral fellow in genetic epidemiology of melanoma and asthma (2012-2017)
UMR-946, Inserm-Université Paris Diderot, Paris, (director: Florence Demenais)

PhD in Bioinformatics (Defended in 2011)
« Identification des signatures génétiques de la sélection chez le chien », under the supervision of Christophe Hitte. IGDR UMR-6061, CNRS-Université de Rennes 1, Rennes (France),

Developer (2006-2008)
Creation of a relational database with a web interface for the handling of biological samples

AWARDS

- Thesis Prize, Rennes 1 Foundation "Progressing, Innovate, Initiate," University of Rennes 1, Rennes (France), 2012
- Winner of a grant from the French Society of Genetics, Montpellier (France), 2010

REASEARCH PROJECTS IN STATISTICALGENETICS

Study of genetic mechanism using summary statistic from GWAS

Development of a strategy extending the medelian randomisation approach to decipher causal pattern between phenotypes with Application on Body Mass Index (BMI - proxy of fat content of the body) and Wiast-to-Hip Ratio.

Study of human melanoma

Development of a multi-marker strategy combining pathways analysis on summary statistics from pan-genomic association studies (GWAS) and tests of the interactions effects between DNA markers to identify sets of genes that jointly influence the trait:

- Application to the risk of melanoma (6,803 subjects in two studies)
- Application to the Breslow index, a prognosis factor (2,506 subjects in two studies)

Inter-species study of melanoma

Development of an inter-species comparative genomic strategy (human-pig-dog) to identify new genes for susceptibility to melanoma in humans (project funded by INCa).

- GWAS adapted to related populations (mixed model), meta-analyzes..
- Comparative mapping to define orthologous regions and compare the results between species.

Contribution to other multifactorial disease study projects

- Identification of rare mutations of a new gene (POT1) associated with the risk of familial melanoma (Nature Genetics, 2017, in collaboration with an American team at NCI).
- Pathway analysis to contribute to the discovery of the association between the gene RAB27A and the exhaled nitric oxide fraction in families of asthmatics.
- Integration of interaction analyzes among genes selected by text mining in a study that identified an interaction between two genes involved in allergy using data from 3,244 subjects.
- Functional annotation of the results of the Trans-National Asthma Genetic Consortium (meta-analysis of 66 GWAS of asthma totalling 142,486 subjects) using public results from SNPs-gene expression (eQTL) assays and chromosome conformation (HiC).

Development and dissemination of pipelines and procedures

- Pipeline to search for genomic regions in which markers show differences in allele frequencies between populations
- Procedures for implementing pathway and gene interaction methods
- Procedures for implementing pan-genomic analysis methods adapted to canine populations
- Procedures to establish orthologous regions between the human and dog genomes and produce the integrated graphical representation of the results of pan-genomic association studies for both species.

SKILLS AND EXPERTISE

In-depth knowledge of methods and tools of statistical genetics

- Imputations of genetic data (Shapeit2, IMPUTE2)
- Single and multi-marker analyzes on individual data (PLINK, GEMMA, script to test gene-gene interactions, meta-analyzes, survival analyzes)
- Multi-marker analysis on summary statistics (GCTA, VEGAS)
- Pathways-based analysis (GSEA, DAVID)
- Functional annotation (use of eQTL chromosome conformation data bases)

Computer skills

- General programming (mainly in Shell, Python and PERL languages, notions of Java, C ++)
- Statistical programming (R et STATA)
- Database Development (MySQL)

LANGUAGE:

- English (read, write and speak fluently)
- French (native speaker)

SCIENTIFIC PRODUCTION

Publications in peer-reviewed international journals

1. Bourneuf E, Estellé J, Blin A, *et al.* Mapping of susceptibility loci for cutaneous melanoma occurrence and progression using a porcine model. *In Prep*
2. Demenais F, Margaritte-Jeannin P, Barnes KC, Cookson W *et al.* Multi-ancestry genome-wide association study identifies new asthma susceptibility loci that co-localize with immune cell enhancer histone marks. 2017, *Nat Genet. 2018;50(1):42-53*
3. Sugier P-E, Brossard M, Sarnowski C, **Vaysse A**, *et al.* A novel role for cilia function in atopy: ADGRV1 and DNAH5 interactions. 2017, JACI, *doi:10.106/j.jaci.2017.06.050*
4. Liu Y*, Brossard M* (co-1er auteurs), Sarnowski C, **Vaysse A**, *et al.* Network-assisted analysis of GWAS data identifies a functionally-relevant gene module for childhood-onset asthma. *Sci Rep. 2017;7(1):938.*
5. Fang S*, **Vaysse A*** (co-1er auteurs), Brossard M, *et al*. Novel melanoma expression genes identified through genome-wide association study of Breslow tumor thickness. *J Invest Dermatol. 2016 doi: 10.1016/j.jid.2016.07.032.*
6. **Vaysse A***, Fang S*, Brossard M* *et al.* A comprehensive genome-wide analysis of melanoma Breslow thickness identifies interaction between *CDC42* and *SCIN* genetic variants. *Int J Cancer. 2016. 139(9):2012-20.*
7. Brossard M*, Fang S* (co-1er auteurs), **Vaysse A** *et al.* Integrated pathway and epistasis analysis reveals interactive effect of genetic variants at *TERF1* and *AFAP1L2* loci on melanoma risk. *Int J Cancer, 2015, 137(8):1901-9.*
8. Plassais J, Guaguère E, Lagoutte L *et al.* A spontaneous KRT16 mutation in a dog breed: a model for human focal non-epidermolytic palmoplantar keratoderma (FNEPPK). *J Invest Dermatol. 2015; 135(4):1187-90.*
9. Bouzigon E, Nadif R, Thompson E *et al.* A common variant in RAB27A is associated with fractional exhaled nitric oxide levels in adults. *Clin Exp Allergy, 2015, 45(4):797-806.*
10. Shi J, Yang XR, Ballew B, *et al.* Germline POT1 mutations predispose to familial cutaneous malignant melanoma. *Nat Genet. 2014; 46(5):482-6.*
11. Derrien T, **Vaysse A**, André C, Hitte C. Annotation of the domestic dog genome sequence: finding the missing genes. *Mamm Genome. 2012, 23(1):124-131.*
12. **Vaysse A***, Ratnakumar A*, Derrien T, *et al.* Identification of loci governing common and rare phenotypic traits in dog breeds using selection mapping. *PLoS Genet. 2011; 7(10):e1002316.*
13. Rimbault M, Robin S, **Vaysse A**, Galibert F. RNA profiles of rat olfactory epithelia: individual and age related variations. *BMC Genomics. 2009;10:572.*
14. Abadie J, Hédan B, Cadieu E, *et al*. Epidemiology, pathology, and genetics of histiocytic sarcoma in the Bernese mountain dog breed. *J Hered. 2009;100 Suppl 1:S19-27.*
15. Derrien T, Thézé J, **Vaysse A**, *et al*. Revisiting the missing protein-coding gene catalog of the domestic dog. *BMC Genomics, 2009 Feb, 10:62*.
16. Robin S, Tacher S, Rimbault M, **Vaysse A**, *et al*. Genetic diversity of canine olfactory receptors. *BMC Genomics, 2009 10(1):21*.
17. Hubert JF, Duchesne L, Delamarche C, **Vaysse A**, *et al.* Pore selectivity analysis of an aquaglyceroporin by stopped-flow spectrophotometry on bacterial cell suspensions. *Biol Cell, 2005 97(9):675-86.*

Publications and Communications in national and internationals congresses

1. Brossard M, Liu Y, **Vaysse A**, *et al*. The SigMod network analysis method identifies gene modules for cutaneous melanoma and nevus count that share relevant candidates. *International Genetic Epidemiology Society* (IGES), Sept. 2017, Cambridge (UK).

2. Brossard M, **Vaysse A**, Mohamdi H, *et al*. Genetic analysis of the telomere interactome pinpoints new candidate genes for melanoma risk *International Genetic Epidemiology Society*, 2016, Toronto (Canada).

3. **Vaysse A**, Fang S, Brossard M, *et al*. A comprehensive genome-wide analysis of melanoma Breslow thickness identifies interaction between *CDC42* and *SCIN* genes. 49th annual meeting of the *European Society of Human Genetics* (ESHG), May. 2016, Barcelone (Spain). *Abs. published online.*

4. Liu Y, Brossard M, Sarnowski C, *et al*. Network-based analysis of genome-wide association data identifies a gene sub-network underlying childhood onset asthma. *American Society of Human Genetics*, Oct. 2015, Baltimore (USA) – *Abs. published online*

5. Sugier PE, Brossard M, **Vaysse A**, *et al*. Combining text mining and epistasis analyses identifies new atopy genes. *American Society of Human Genetics* (ASHG), Oct. 2015, Baltimore (USA) - *Abs. published online*

6. Liu Y, Brossard M, Margaritte-Jeannin P, *et al*. Network-Assisted Investigation of Signals from Genome-Wide Association Studies in Childhood-onset Asthma. *Capita Selecta on Complex Disease Analysis* (CSCDA), Nov. 2014, Liège (Belgium). *Abs. published online*

7. Sugier P-E, **Vaysse A**, Sarnowski C, *et al*. Integration of gene-based and text mining analyses to discover genes underlying atopy. *Capita Selecta in Complex Disease Analysis* (CSCDA), Nov. 2014, Liège (Belgium). *Abs. published online.*

8. **Vaysse A**, Fang S, Brossard M, *et al*. Combined pathway and gene-gene interaction analysis pinpoints biologically relevant genes for a major melanoma prognosis factor. 64th annual meeting of the *American Society of Human Genetics* (ASHG), Oct. 2014, San Diego (USA). *Abs. published online*

9. Brossard M, Fang S, **Vaysse A**, *et al*. Integrated pathway and gene-gene interaction analysis reveals novel candidate genes for melanoma. 64th annual meeting of the *American Society of Human Genetics* (ASHG), Oct. 2014, San Diego (USA). *Abs. published online.*

10. **Vaysse A**, Fang S, Brossard M, *et al.* Integration of pathway and gene-gene interaction analyses reveal biologically relevant genes for Breslow thickness, a major predictor of melanoma prognosis. *International Genetic Epidemiology Society* (IGES), Août 2014, Vienna (Austria). *Abs. published online.*

11. Brossard M, Fang S, **Vaysse A** *et al.* Pathway and gene-gene interaction analysis reveals new candidate genes for melanoma, *International Genetic Epidemiology Society* (IGES), Août 2014, Vienna (Austria). *Abs. published online.*

12. Brossard M, **Vaysse A**, Corda E, *et al.* Comparison of permutations strategies to assess gene-set significance in gene-set-enrichment analysis, *International Genetic Epidemiology Society* (IGES), Sept. 2013, Chicago (USA). *Abs. published online*

13. Sugier PE, **Vaysse A**, Loucoubar C *et al.* Identification of common and specific genetic determinants to skin prick test reactivity using genome-wide association study and gene-based test approaches. 62nd annual meeting of the *American Society of Human Genetics* (ASHG), Nov. 2012, San Francisco (USA). *Abs. published online.*

14. Loucoubar C, Brossard M, Sugier PE, **Vaysse A**, *et al.* Performances of single-SNP and pathway-based analyses of genome-wide data to detect genetic factors shared by eosinophil and basophil counts in asthma ascertained families. 62nd *Annual Meeting of the American Society of Human Genetics* (ASHG), 6-10 Nov. 2012, San Francisco (USA**).** *Abs. published online*

15. Brossard M, **Vaysse A**, Corda E, *et al.* Pathway-based analysis of genome-wide SNP data reveals new candidate genes for susceptibility to melanoma. 62nd Annual Meeting of the *American Society of Human Genetics* (ASHG), Nov. 2012, San Francisco (USA). *Abs. published online.*

16. Jean-Baptiste-Adolphe H., Emily M, **Vaysse A**, André C, Hitte C. Haplotype-based method for detecting regions under selection in the domestic dog. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Juil. 2012, Rennes (France).

17. Derrien T, **Vaysse A**, Hennuy B, *et al.* Computational detection and expression profiling of conserved long non-coding RNAs in the domestic dog. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Juil. 2012, Rennes (France).

18. Hitte C, Ratnakumar A, **Vaysse A**, *et al*. Identification of loci governing phenotypic traits in dog breeds highlights disease genes of relevance to human health. *European Human Genetics Conference*, May 2011, Amsterdam (the Netherlands). *Abs. published online*

19. Webster MT, **Vaysse A**, Ratnakumar A, *et al.* Identification of common and rare selective sweeps in 36 dog breeds. *The 5th Advances in Feline and Canine Genomics,* Sept. 2010, Baltimore (USA).

20. Hitte C, Ratnakumar A, **Vaysse A**, *et al.* Functional impact of artificial selection in the domestic dog. *The 5th Advances in Feline and Canine Genomics*, Sept. 2010, Baltimore (USA).

21. Grall A, **Vaysse A**, Escriou C, *et al.* Recherche des bases génétiques d'une épilepsie canine : un modèle pour les épilepsies humaines. 5èmes *Assises de Génétique Humaine et Médicale*, Jan. 2010, Strasbourg (France). *Abs. published online.*

22. **Vaysse A**, Ratnakumar A, Derrien T, *et al.* Differentiation of allelic frequencies analysis identifies short genomic regions with signatures of artificial selection between canine breeds. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Sept. 2010, Montpellier (France).
23. **Vaysse A**, Galibert F, André C, Hitte C. Comparative patterns of positive selection between human and five mammalian genomes. 5èmes *Assises de Génétique Humaine et Médicale*, Jan. 2010, Strasbourg (France)*. Abs. published online*
24. **Vaysse A**, Derrien T, André C, Galibert F, Hitte C. Lineage-specific pseudogenes identification through selective constraints analysis in the canine genome. Journées Ouvertes en Biologie, Informatique et Mathématiques(JOBIM), Juin 2009, Nantes (France).
25. André C, Chaudieu G, Herbin L, **Vaysse A**, *et al.* CaniDNA : a French initiative for the collection and distribution of dog DNA samples and distribution of dog DNA samples. *4th International Conference: Advances in canine and feline genomics and inherited diseases*, May 2008, St Malo (France).

TEACHING AND TRAINING

Teaching:
Since 2015 in the of Public Health "Epidemiological Genetics and Biomarkers within the teaching units « *Logiciels d'analyse génétique »* et *« Liaison, Association, Génétique Quantitative et Formelle ».*

Supervision and training:
I contributed to the supervision and training of a master student, 4 engineers and 3 doctoral and post-doctoral students from the laboratory or coming to the laboratory for international exchanges organized within the European network Marie -Curie "Machine Learning for Personalized Medicine".

SCIENTIFIC ANIMATION

Advisory and expertise activity**:**
- Advisory activity for the development and computerized management of the Canine Biological Resource Center for the "Dog Genetics" group (IGDR-UMR6290, Rennes, France)
- Reviewer for PLoS One and BMC vet
- Grant reviewer for the « Netherlands Organisation for Scientific Research » (NWO)

Nationals and internationals Collaborations:
- **Cooperative group MELARISK for the study of melanoma un human:** UMR-946 (INSERM/université Paris Diderot), CHU Cochin, Institut Gustave Roussy and national network of et le réseau national de dermatologists et d'onco-geneticists.
- **Comparative genomic of melanoma in three species (human/pig/dog) :** UMR-946, UMR-6290 (CNRS/Université de Rennes 1), UMR-1314 (INRA/CEA).
- **Study of the selection in the dog genome:** Institut of biology from the "école normale supérieure", Paris.
- **Exome sequencing for familial melanoma:** National Cancer Institute, Rockville; McGill University, Montréal.
- **Genetics of melanoma and Breslow thickness based on pathway analysis** : MD Anderson Cancer Center, Texas; Dartmouth College, New Hampshire, USA
- **Genetic Epidemiology of Melanoma:** International Melanoma Genetics Consortium (GenoMEL) : over 20 groups from Europe, North America and Australia (http://www.genomel.org)
- **Genetic Diversity in Dog:** Department of Medical Biochemistry and Microbiology (IMBIM), Faculty of Medicine, Uppsala University as a member of the European consortium LUPA (over 20 groups from 12 European countries)

Oral presentation in research seminar and workshops:

1. Identification of genetic signatures of selection in dog. Mar. 2011, Rennes.
2. A Knowledge-Integration System for the Multi-Locus Analysis of Genome-Wide Association Studies. Feb. 2012, Paris.
3. Gene ontology: tool for the unification of biology. Mar. 2013, Paris.
4. Integration of GWAS results across species: analysis strategy. Jul. 2013, Rennes.
5. Genome-wide pathway-based analysis. Nov. 2014, Paris.
6. "Etudes pan-génomiques du mélanome dans l'espèce canine". Jul. 2015, Rennes.

Collective life of the team

- Presentations in internal seminars and working groups
- Participation to the Monitoring of scientific literature
- Presentations at journal club organised as part of the "Cercle francilien de Recherche en génétique EPidémiologique et Evolutive" (CREPE)