

Βιογραφικό σημείωμα

Παναγιώτης Ιωαννίδης, PhD
Μεταδιδακτορικός ερευνητής

Διεύθυνση

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Εκπαίδευση

- 2003 BSc. Διαχείριση Περιβάλλοντος και Φυσικών Πόρων.
Πανεπιστήμιο Ιωαννίνων.
- 2008 Ph.D. Διαχείριση Περιβάλλοντος και Φυσικών Πόρων.
Πανεπιστήμιο Ιωαννίνων.
Τίτλος εργασίας: “Μελέτη του συμβιωτικού βακτηρίου *Wolbachia*: μία γονιδιωματική προσέγγιση”.
Επιβλέπων: Κώστας Μπούρτζης, PhD

Εκπαίδευση πριν την απόκτηση διδακτορικού

- 2004 Ερευνητής, Center for Bioinformatics, Department of Genetics, University of Pennsylvania, Philadelphia, USA
Επιβλέπουσα: Άρτεμις Χατζηγεωργίου, PhD
- 2006 Ερευνητής, Marine Biological Laboratory, Woods Hole, MA, USA (1 month).
Επιβλέπων: Seth R Bordenstein, PhD
- 2006 Ερευνητής, The Institute for Genomic Research, Rockville, MD, USA (1 month).
Επιβλέπων: Julie C Dunning-Hotopp, PhD

Μεταδιδακτορική εμπειρία

- 2010-2011 Μεταδιδακτορικός ερευνητής, National Institute for Agricultural Research (INRA), Nancy, France.
Επιβλέπων: Francis Martin, PhD
- 2011-2013 Μεταδιδακτορικός ερευνητής, Institute for Genome Sciences, University of Maryland at Baltimore, School of Medicine, Baltimore, MD, USA.
Επιβλέπουσα: Julie C Dunning Hotopp, PhD
- 2013-2016 Μεταδιδακτορικός ερευνητής, Department of Genetic Medicine and Development, University of Geneva, Geneva, Switzerland.
Επιβλέπων: Evgeny Zdobnov, PhD
- 2018-Παρόν Μεταδιδακτορικός ερευνητής, Ινστιτούτο Μοριακής Βιολογίας και Βιοτεχνολογίας, Ίδρυμα για την Τεχνολογία και Έρευνα, Ηράκλειο, Κρήτη, Ελλάδα.
Επιβλέπων: Γιάννης Βόντας, PhD

Δραστηριότητες που δεν σχετίζονται με την έρευνα

2009 Υποχρεωτική στρατιωτική θητεία στον Ελληνικό Στρατό (8
μήνες). Βάλτος Ορεστιάδας, Ελλάδα

Ερευνητικές δεξιότητες

Βιοπληροφορική: Εκτεταμένη εμπειρία στην ανάλυση γονιδιωμάτων και μεταγραφωμάτων (συναρμολόγηση (assembly) γονιδιωμάτων και μεταγραφωμάτων, πρόβλεψη γονιδίων, υπολογιστικός λειτουργικός χαρακτηρισμός, συγκριτικές αναλύσεις). Εκτεταμένη εμπειρία σε φυλογενετικές και φυλογενωμικές αναλύσεις. Εκτεταμένη εμπειρία στην εργασία σε υπολογιστικές συστοιχίες (high-performance computing clusters) LSF και Slurm. Εκτεταμένη εμπειρία στην χρήση της γλώσσας Perl. Εκτεταμένη εμπειρία στο λειτουργικό σύστημα Linux. Καλή γνώση της στατιστικής γλώσσας R.

Μοριακές τεχνικές: Απομόνωση γενωμικού DNA από έντομα. Χρήση της τεχνικής PCR για την ενίσχυση τμημάτων του DNA. Κλωνοποίηση DNA. Απομόνωση πρωτεΐνων και ηλεκτροφόρηση σε τζελ ακρυλαμίδης. Συντήρηση αποικιών Drosophila.

Συγγραφή επιστημονικών εργασιών: Συγγραφή εργασίας από το αρχικό στάδιο έως την υποβολή στο περιοδικό. Συγγραφή μικρών τμημάτων για να περιληφθούν σε μια μεγαλύτερη εργασία.

Δημοσιεύσεις σε περιοδικά με κριτές

- Skarlas L, Ioannidis P, Likothanassis S (2007). Coding potential prediction in *Wolbachia* using Artificial Neural Networks. *In Silico Biology* **7**, 0010.
- Ioannidis P, Dunning Hotopp JC, Sapountzis P, Siozios S, Tsiamis G, Bordenstein SR, Baldo L, Werren JH, Bourtzis K (2007). New criteria for selecting the origin of DNA replication in *Wolbachia* and closely related bacteria. *BMC Genomics* **8**: 182.
- Ioannidis P, Bourtzis K (2007). Insect symbionts and applications: The paradigm of incompatibility-inducing *Wolbachia*. *Entomological Research* **37**:125-138.
- Siozios S, Sapountzis P, Ioannidis P, Bourtzis K (2008). *Wolbachia* symbiosis and insect immune response. *Insect Science*, **15**: 89-100.
- Ishmael N, Dunning Hotopp JC, Ioannidis P, Biber S, Sakamoto J, Siozios S, Nene V, Werren J, Bourtzis K, Bordenstein SR, Tettelin H (2009). Extensive genomic diversity of closely related *Wolbachia* strains. *Microbiology*, **155**: 2211-2222.
- Siozios S, Ioannidis P, Klasson L, Andersson SGE, Braig HR, Bourtzis K (2013). The diversity and evolution of *Wolbachia* ankyrin repeat domain genes. *PLoS One*, **8**:e55390.
- Uroz S, Ioannidis P, Lengelle J, Cebron A, Morin E, Buee M, Martin F (2013). Functional assays and metagenomic analyses reveals differences between the microbial communities inhabiting the soil horizons of a Norway spruce plantation. *PLoS One*, **8**:e55929.
- Ioannidis P, Johnston KL, Riley DR, Kumar N, White JR, Olarte KT, Ott S, Tallon LJ, Foster JM, Taylor MJ, Dunning Hotopp JC (2013). Extensively duplicated and transcriptionally active recent lateral gene transfer from a bacterial *Wolbachia* endosymbiont to its host filarial nematode *Brugia malayi*. *BMC Genomics*, **14**:639.
- Papasotiropoulos V, Tsiamis G, Papaioannou C, Ioannidis P, Klossa-Kilia E, Papapanagiotou AP, Bourtzis K, Kilias G (2013). A molecular phylogenetic study of aphids (Hemiptera: Aphididae) based on mitochondrial DNA sequence analysis. *Journal of Biological Research - Thessaloniki*. **20**:0.
- Ioannidis P, Lu Y, Kumar N, Creasy T, Daugherty S, Chibucus MC, Orvis J, Shetty A, Ott S, Flowers M, Sengamalay N, Tallon LJ, Pick L, Dunning Hotopp JC (2014). Rapid transcriptome sequencing of an invasive pest, the brown marmorated stink bug *Halyomorpha halys*. *BMC Genomics*, **15**:738.
- Popadin KY, Gutierrez-Arcelus M, Lappalainen T, Buil A, Steinberg J, Nikolaev SI, Lukowski SW, Bazykin GA, Seplyarskiy VB, Ioannidis P, Zdobnov EM, Dermitzakis ET, Antonarakis SE (2014). Gene age predicts the strength of purifying selection acting on gene expression variation in humans. *Am J Hum Genet*, **95**:660-674.
- Kriventseva EV, Tegenfeldt F, Petty TJ, Waterhouse RM, Simao FA, Pozdnyakov IA, Ioannidis P, Zdobnov EM (2014). OrthoDB v8: update of the hierarchical catalog of orthologs and the underlying free software. *Nucleic Acids Res*, **43**:D250-256.

Zhao C, Escalante LN, Chen H, Benatti TR, Qu J, Chellapilla S, Waterhouse RM, Wheeler D, Andersson MN, Bao R, Batterton M, Behura SK, Blankenburg KP, Caragea D, Carolan JC, Coyle M, El-Bouhssini M, Francisco L, Friedrich M, Gill N, Grace T, Grimmelikhuijen CJ, Han Y, Hauser F, Herndon N, Holder M, **Ioannidis P**, Jackson L, Javaid M, Jhangiani SN, Johnson AJ, Kalra D, Korchina V, Kovar CL, Lara F, Lee SL, Liu X, Löfstedt C, Mata R, Mathew T, Muzny DM, Nagar S, Nazareth LV, Okwuonu G, Ongeri F, Perales L, Peterson BF, Pu LL, Robertson HM, Schemerhorn BJ, Scherer SE, Shreve JT, Simmons D, Subramanyam S, Thornton RL, Xue K, Weissenberger GM, Williams CE, Worley KC, Zhu D, Zhu Y, Harris MO, Shukle RH, Werren JH, Zdobnov EM, Chen MS, Brown SJ, Stuart JJ, Richards S (2015). A massive expansion of effector genes underlies gall-formation in the wheat pest *Mayetiola destructor*. *Curr Biol.* **25**:613-620.

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SIB Swiss Institute of Bioinformatics Members. The SIB Swiss Institute of Bioinformatics' resources: focus on curated databases (2016). *Nucleic Acids Res.* **44**:D27-D37.

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Hoy MA, Waterhouse RM, Wu K, Estep AS, **Ioannidis P**, Palmer WJ, Pomerantz AF, Simão FA, Thomas J, Jiggins FM, Murphy TD, Pritham EJ, Robertson HM, Zdobnov EM, Gibbs RA, Richards S (2016). Genome sequencing of the phytoseiid predatory mite *Metaseiulus occidentalis* reveals

completely atomised *Hox* genes and super-dynamic intron evolution.

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McKenna DD, Scully ED, Pauchet Y, Hoover K, Kirsch R, Geib SM, Mitchell RF, Waterhouse RM, Ahn SJ, Arsala D, Benoit JB, Blackmon H, Bledsoe T, Bowsher JH, Busch A, Calla B, Chao H, Childers AK, Childers C, Clarke DJ, Cohen L, Demuth JP, Dinh H, Doddapaneni HV, Dolan A, Duan JJ, Dugan S, Friedrich M, Glastad KM, Goodisman MAD, Haddad S, Han Y, Hughes DST, **Ioannidis P**, Johnston JS, Jones JW, Kuhn LA, Lance DR, Lee CY, Lee SL, Lin H, Lynch JA, Moczek AP, Murali SC, Muzny DM, Nelson DR, Palli SR, Panfilio KA, Pers D, Poelchau MF, Quan H, Qu J, Ray AM, Rinehart JP, Robertson HM, Roehrdanz R, Rosendale AJ, Shin S, Silva C, Torson AC, Vargas Jentzsch IM, Werren JH, Worley KC, Yocom G, Zdobnov EM, Gibbs RA, Richards S (2016). Genome of the Asian longhorned beetle (*Anoplophora glabripennis*), a globally significant invasive species, reveals key functional and evolutionary innovations at the beetle-plant interface. *Genome Biol.* **17**:227.

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Ioannidis P, Simao FA, Waterhouse RM, Manni M, Seppey M, Robertson HM, Misof B, Niehuis O, Zdobnov EM (2017). Genomic features of the damselfly *Calopteryx splendens* representing a sister clade to most insect orders. *Genome Biol Evol.* **9**:415-430.

Waterhouse RM, Seppey M, Simao FA, Manni M, **Ioannidis P**, Klioutshnikov G, Kriventseva EV, Zdobnov E (2018). BUSCO applications from quality assessments to gene prediction and phylogenomics. *Mol Biol Evol.* **35**:543-548.

Kapheim KM, Pan H, Li C, Blatti C, Harpur BA, **Ioannidis P**, Jones BM, Kent CF, Ruzzante L, Sloofman L, Stolle E, Waterhouse RM, Zayed A, Zhang G, Wcislo WT (2019). Draft genome assembly and population genetics of an agricultural pollinator, the solitary alkali bee (Halictidae: *Nomia melanderi*). *G3 (Bethesda)*. **g3**. 200865.2018.

Panfilio KA, Vargas Jentzsch IM, Benoit JB, Erezyilmaz D, Suzuki Y, Colella S, Robertson HM, Poelchau MF, Waterhouse RM, **Ioannidis P**, Weirauch MT, Hughes DST, Murali SC, Werren JH, Jacobs CGC, Duncan EJ, Armisen D, Vreeke BMI, Baa-Puyoulet P, Berger CS, Chang C, Chao H, Chen MM, Chen Y, Childers CP, Chipman AD, Cridge AG, Crumière AJJ, Dearden PK, Didion EM, Dinh H, Dolan A, Dugan-Perez S, Extavour CG, Febvay G, Friedrich M, Ginzburg N, Han Y, Heger P, Horn P, Hsiao Y, Jennings EC, Johnston JS, Jones TE, Jones JW, Khila A, Koelzer S, Kovacova V, Leask M, Lee SL, Lee C, Lovegrove MR, Lu H, Lu Y, Moore PJ, Munoz-Torres MC, Muzny DM, Palli SR, Parisot N, Pick L, Porter M, Qu J, Refki PN, Richter R, Rivera-Pomar R, Rosendale AJ, Roth S, Sachs L, Santos ME, Seibert J, Sghaier E, Shukla JN, Stancliffe RJ, Tidswell O, Traverso L, van der Zee M, Viala S, Worley KC, Zdobnov EM, Gibbs RA, Richards S (2019). Molecular evolutionary trends

and feeding ecology diversification in the Hemiptera, anchored by the milkweed bug genome. *Genom Biol.* **20**:1-26.

Seppey M, Ioannidis P, Emerson BC, Pitteloud C, Robinson-Rechavi M, Roux J, Escalona HE, McKenna DD, Misof B, Shin S, Zhou X, Waterhouse RM, Alvarez N (2019). Genomic signatures accompanying the dietary shift to phytophagy in polyphagan beetles. *Genome Biol.* **20**: 98.

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Συμμετοχές σε συνέδρια

Siozios S, Tsiamis G, **Ioannidis P** and Bourtzis K. Ankyrin repeat-containing genes in *Wolbachia* and their role in host-symbiont interactions. Poster session presented at: Conference of the Greek Society for biochemistry and molecular biology, November 25-27, Larissa, 2004.

Ioannidis P, Reczko M, Kouranov A, Megraw M, Skarlas L, Hatzigeorgiou A (2004). Identifying microRNA genes and their targets *in silico*. Poster session presented at: Conference of the Greek Society for biochemistry and molecular biology, November 25-27, Larissa, 2004.

Ioannidis P, Dunning Hotopp JC, Sapountzis P, Siozios S, Tsiamis G, Bordenstein SR, Baldo L, Werren JH, Bourtzis K. The origin of DNA replication in *Wolbachia* and closely related Rickettsiales. Poster session presented at: Hellenic society for Bioscientists. "Biosciences in the 21st century", 13-15 April, Athens, 2006.

Siozios S, Sapountzis P, **Ioannidis P**, Klasson L, Darby A, Näslund K, Braig HR, Andersson SGE Bourtzis K. Distribution and expression analysis of bacterial ankyrin genes in different *Drosophila-Wolbachia* symbiotic associations. Poster session presented at: Fourth International *Wolbachia* Conference, Paradisus, Puerto Rico, June 24-29, 2006.

Ioannidis P, Dunning Hotopp JC, Sapountzis P, Siozios S, Tsiamis G, Bordenstein SR, Baldo L, Werren JH, Bourtzis K. On the origin of DNA replication of *Wolbachia* and closely related bacteria. Poster session presented at: Fourth International *Wolbachia* Conference, Paradisus, Puerto Rico, June 24-29, 2006.

Ioannidis P, Braig HR, Garrett R, Andersson SGE, Bourtzis K (2008) In silico analysis of *Wolbachia* ankyrin genes. Poster session presented at: Fifth International *Wolbachia* Conference, Kolymbari, Crete, Greece, June 9-16, 2008.

Saridaki A, Sapountzis P, Siozios S, **Ioannidis P**, Boleti H, Bourtzis K. *Wolbachia* ankyrins and their potential role on *Drosophila-Wolbachia* symbiosis. Poster session presented at: FEBS Journal 275: 266.

Ioannidis P, Uroz S, Buee M, Morin E, Martin F (2010). Comparative metagenomics of mineral and organic layers of a forest soil. Poster session presented at: Soil Metagenomics 2010, Braunschweig, Germany, December 8-10, 2010.

Ioannidis P, Johnston KL, Riley DR, Foster JM, Taylor MJ, Dunning Hotopp JC. Lateral gene transfer from endosymbionts to medically important filarial nematodes. Poster session presented at: Seventh Annual NIH Director's Pioneer Award Symposium, Bethesda, MD, USA, September 20, 2011.

Ioannidis P, Lu Y, Kumar N, Creasy T, Ott S, Tallon LJ, Pick L, Dunning Hotopp JC. Transcriptomics of the invasive brown marmorated stink bug (*Halyomorpha halys*). Poster session presented at: Sixth Annual Arthropod Genomics Symposium, Kansas City, MO, USA, May 30 - June 2, 2012.

Ioannidis P, Johnston KL, Riley DR, Kumar N, Olarte KT, Ott S, Tallon LJ, Foster

JM, Taylor MJ, Dunning Hotopp JC. Lateral gene transfer from endosymbionts to the human filarial nematode *Brugia malayi*. Poster session presented at: Seventh International Wolbachia Conference, St Pierre d' Oleron, France, June 7 – 14, 2012.

Ioannidis P, Simao Neto F, Peters RP, Misof B, Niehuis O, Zdobnov EM. Genome sequencing of *Calopteryx splendens* (Odonata) and *Thermobia domestica* (Zygentoma). Poster session presented at: Seventh International Symposium on Molecular Insect Science, Amsterdam, Netherlands, July 13 – 16, 2014.

Ioannidis P. Phylogeny of the hessian fly, *Mayetiola destructor*. Oral presentation at: ALPHY/PhylosIB 2014, Swiss-French meeting on Bioinformatics and Evolutionary Genomics, Geneva, Switzerland, February 4 – 5, 2014.

Ioannidis P. Intron dynamics of the in the predatory mite *Metaseiulus occidentalis* (Acari:Phytoseiidae). Oral presentation at: Department of Genetic Medicine and Development Seminar Series, Geneva, Switzerland, September 23, 2014.

Ioannidis P, Simao Neto F, Niehuis O, Misof B, Zdobnov EM. Genome sequencing of the damselfly *Calopteryx splendens* (Arthropoda:Odonata). Poster session presented at: Ninth Annual Arthropod Genomics Symposium, Manhattan, Kansas, USA, June 17 – 19, 2015.

Ioannidis P. Sequencing the genome of a 'basal' insect: the damselfly *Calopteryx splendens*. Oral presentation at: Department of Genetic Medicine and Development Seminar Series, Geneva, Switzerland, October 6, 2015.

Ioannidis P, Simao F, Waterhouse RM, Manni M, Seppey M, Misof, Niehuis O, Zdobnov EM. The draft genome of the damselfly *Calopteryx splendens* reveals unique features of early-divergent insect lineages. Poster session presented at: SIB Days 2016, Biel/Bienne, June 7 – 8, 2016.

Ioannidis P. Genomic features of the damselfly *Calopteryx splendens*, representing a sister clade to most other insect orders. Oral presentation at: Department of Genetic Medicine and Development Seminar Series, Geneva, Switzerland, October 11, 2016.

Ioannidis P. (2016). Genomic features of the damselfly *Calopteryx splendens*, representing primitively-winged insect clades. Oral presentation at: Hellenic Bioinformatics (HBio) 2016, Thessaloniki, 19-21 November 2016.

Ioannidis P. The genome of *Calopteryx splendens*, a species belonging to an insect clade with very few genomic resources. Oral presentation at: Department of Biochemistry and Biotechnology Seminar Series, Larissa, 22 March 2017.

Ioannidis P. Genome sequencing of the jumping bristletail *Lepismachilis y-signata* (Insecta:Archaeognatha). Poster presentation at: Arthropod Genomics Symposium, Urbana-Champaign, IL, USA, 05-07 June 2018.