

# Yong-Hwan Lee

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

104  
papers

6,893  
citations

36  
h-index

82  
g-index

107  
ext. papers

8,781  
ext. citations

6.6  
avg. IF

5.21  
L-index

| #   | Paper   | IF   | Citations |
|-----|---|------|-----------|
| 104 | Genome-wide profiling of long non-coding RNA of the rice blast fungus <i>Magnaporthe oryzae</i> during infection.. <i>BMC Genomics</i> , <b>2022</b> , 23, 132  | 4.5  | 0         |
| 103 | Alternative splicing diversifies the transcriptome and proteome of the rice blast fungus during host infection.. <i>RNA Biology</i> , <b>2022</b> , 19, 373-385                                       | 4.8  | 1         |
| 102 | ROS homeostasis mediated by MPK4 and SUMM2 determines synergid cell death.. <i>Nature Communications</i> , <b>2022</b> , 13, 1746   | 17.4 | 1         |
| 101 | A rice gene encoding glycosyl hydrolase plays contrasting roles in immunity depending on the type of pathogens. <i>Molecular Plant Pathology</i> , <b>2021</b> ,                                      | 5.7  | 3         |
| 100 | Characterization of the MYB Genes Reveals Insights Into Their Evolutionary Conservation, Structural Diversity, and Functional Roles in .. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 721530 | 5.7  | 1         |
| 99  | Phylogenomic Analysis of a 55.1-kb 19-Gene Dataset Resolves a Monophyletic that Includes the Species Complex. <i>Phytopathology</i> , <b>2021</b> , 111, 1064-1079                                    | 3.8  | 39        |
| 98  | Harnessing Chemical Ecology for Environment-Friendly Crop Protection. <i>Phytopathology</i> , <b>2021</b> , PHYTO01210035RVW  | 12.1 | 1         |
| 97  | The Membrane-Bound Protein, MoAfo1, Is Involved in Sensing Diverse Signals from Different Surfaces in the Rice Blast Fungus. <i>Plant Pathology Journal</i> , <b>2021</b> , 37, 87-98                 | 2.5  | 2         |
| 96  | Draft Genome Sequence of EL000614, a Strain Producing Grammicin, a Potent Nematicidal Compound. <i>Mycobiology</i> , <b>2021</b> , 49, 294-296  | 1.7  |           |
| 95  | Lyso-phosphatidylethanolamine primes the plant immune system and promotes basal resistance against hemibiotrophic pathogens. <i>BMC Biotechnology</i> , <b>2021</b> , 21, 12                          | 3.5  | 6         |
| 94  | Spatiotemporal Assembly of Bacterial and Fungal Communities of Seed-Seedling-Adult in Rice. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 708475   | 5.7  | 3         |
| 93  | Homeobox Transcription Factors Are Required for Fungal Development and the Suppression of Host Defense Mechanisms in the -Pepper Pathosystem. <i>MBio</i> , <b>2021</b> , 12, e0162021                | 7.8  | 5         |
| 92  | Compositional Shift of Bacterial, Archaeal, and Fungal Communities Is Dependent on Trophic Lifestyles in Rice Paddy Soil. <i>Frontiers in Microbiology</i> , <b>2021</b> , 12, 719486                 | 5.7  | 0         |
| 91  | Draft Genome Sequence of JS-1345, an Endophytic Fungus Isolated from Stem Tissue of Korean Fir. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,   | 1.3  | 2         |
| 90  | TGFam-Finder: a novel solution for target-gene family annotation in plants. <i>New Phytologist</i> , <b>2020</b> , 227, 1568-1581   | 9.8  | 5         |
| 89  | Draft Genome Sequence of <i>Alternaria alternata</i> JS-1623, a Fungal Endophyte of <i>Abies koreana</i> . <i>Mycobiology</i> , <b>2020</b> , 48, 240-244   | 1.7  | 1         |
| 88  | Domestication of <i>Oryza</i> species eco-evolutionarily shapes bacterial and fungal communities in rice seed. <i>Microbiome</i> , <b>2020</b> , 8, 20  | 16.6 | 38        |

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| 87 | Draft Genome Sequence of <i>Aspergillus oryzae</i> BP2-1, Isolated from Traditional Malted Rice in South Korea. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,  | 1.3  | 2  |
| 86 | The Rice Microbiome: A Model Platform for Crop Holobiome. <i>Phytobiomes Journal</i> , <b>2020</b> , 4, 5-18   | 4.8  | 23 |
| 85 | Transcriptome Profiling of the Rice Blast Fungus and Its Host During Infection. <i>Molecular Plant-Microbe Interactions</i> , <b>2020</b> , 33, 141-144  | 3.6  | 16 |
| 84 | F-box only and CUE proteins are crucial ubiquitination-associated components for conidiation and pathogenicity in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , <b>2020</b> , 144, 103473                    | 2.9  | 6  |
| 83 | Two nuclear effectors of the rice blast fungus modulate host immunity via transcriptional reprogramming. <i>Nature Communications</i> , <b>2020</b> , 11, 5845   | 17.4 | 15 |
| 82 | Comparative Genomics Platform and Phylogenetic Analysis of Fungal Laccases and Multi-Copper Oxidases. <i>Mycobiology</i> , <b>2020</b> , 48, 373-382   | 1.7  | 2  |
| 81 | Genome-wide functional analysis of phosphatases in the pathogenic fungus <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , <b>2020</b> , 11, 4212  | 17.4 | 7  |
| 80 | Hypoxia: A Double-Edged Sword During Fungal Pathogenesis?. <i>Frontiers in Microbiology</i> , <b>2020</b> , 11, 1920   | 5.7  | 11 |
| 79 | Genome Sequence of <i>Striga asiatica</i> Provides Insight into the Evolution of Plant Parasitism. <i>Current Biology</i> , <b>2019</b> , 29, 3041-3052.e4   | 6.3  | 59 |
| 78 | Genomic comparisons of the laurel wilt pathogen, <i>Raffaelea lauricola</i> , and related tree pathogens highlight an arsenal of pathogenicity related genes. <i>Fungal Genetics and Biology</i> , <b>2019</b> , 125, 84-92                            | 3.9  | 5  |
| 77 | Draft Genome Sequence of JS-1675, an Endophytic Fungus from. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,   | 1.3  | 6  |
| 76 | A novel approach to investigate hypoxic microenvironment during rice colonization by <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , <b>2019</b> , 21, 1151-1169   | 5.2  | 4  |
| 75 | A High-Quality Draft Genome Sequence of <i>Colletotrichum gloeosporioides sensu stricto</i> SMCG1#C, a Causal Agent of Anthracnose on <i>Cunninghamia lanceolata</i> in China. <i>Molecular Plant-Microbe Interactions</i> , <b>2019</b> , 32, 139-141 | 3.6  | 9  |
| 74 | A MYST family histone acetyltransferase, MoSAS3, is required for development and pathogenicity in the rice blast fungus. <i>Molecular Plant Pathology</i> , <b>2019</b> , 20, 1491-1505  | 5.7  | 11 |
| 73 | Evolution of the Genes Encoding Effector Candidates Within Multiple Pathotypes of. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 2575   | 5.7  | 9  |
| 72 | SUMOylation is required for fungal development and pathogenicity in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>Molecular Plant Pathology</i> , <b>2018</b> , 19, 2134-2148   | 5.7  | 11 |
| 71 | Genome wide analysis of the transition to pathogenic lifestyles in <i>Magnaporthales</i> fungi. <i>Scientific Reports</i> , <b>2018</b> , 8, 5862  | 4.9  | 13 |
| 70 | Global DNA Methylation in the Chestnut Blight Fungus and Genome-Wide Changes in DNA Methylation Accompanied with Sectorization. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 103   | 6.2  | 14 |

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|----|---|------|-----|
| 69 | A Small GTPase RHO2 Plays an Important Role in Pre-infection Development in the Rice Blast Pathogen. <i>Plant Pathology Journal</i> , <b>2018</b> , 34, 470-479   | 2.5  | 10  |
| 68 | Characterization of a Heterobasidion irregulare endo-rhamnogalacturonase that mediate growth on pectin. <i>Journal of Phytopathology</i> , <b>2018</b> , 166, 34-43   | 1.8  | 1   |
| 67 | Identification of a Gene Involved in Early Senescence and Defense Response in Rice. <i>Frontiers in Plant Science</i> , <b>2018</b> , 9, 1274   | 6.2  | 14  |
| 66 | Distinct roles of the YPEL gene family in development and pathogenicity in the ascomycete fungus Magnaporthe oryzae. <i>Scientific Reports</i> , <b>2018</b> , 8, 14461   | 4.9  | 7   |
| 65 | Role of the Histone Acetyltransferase Rtt109 in Development and Pathogenicity of the Rice Blast Fungus. <i>Molecular Plant-Microbe Interactions</i> , <b>2018</b> , 31, 1200-1210                                 | 3.6  | 12  |
| 64 | ER retention receptor, MoERR1 is required for fungal development and pathogenicity in the rice blast fungus, Magnaporthe oryzae. <i>Scientific Reports</i> , <b>2017</b> , 7, 1259                                | 4.9  | 9   |
| 63 | Draft Genome Sequence of an Endophytic Fungus, sp. Strain JS-464, Isolated from a Reed Plant,. <i>Genome Announcements</i> , <b>2017</b> , 5,   |      | 7   |
| 62 | New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. <i>Genome Biology</i> , <b>2017</b> , 18, 210                                    | 18.3 | 142 |
| 61 | Genome Sequence of an Endophytic Fungus, JS-169, Which Has Antifungal Activity. <i>Genome Announcements</i> , <b>2017</b> , 5,  |      | 7   |
| 60 | Gapless genome assembly of Colletotrichum higginsianum reveals chromosome structure and association of transposable elements with secondary metabolite gene clusters. <i>BMC Genomics</i> , <b>2017</b> , 18, 667 | 4.5  | 53  |
| 59 | , Encoding a Histone Demethylase Containing JmjC Domain, Is Required for Pathogenic Development of the Rice Blast Fungus,. <i>Plant Pathology Journal</i> , <b>2017</b> , 33, 193-205                             | 2.5  | 7   |
| 58 | Systematic functional analysis of kinases in the fungal pathogen Cryptococcus neoformans. <i>Nature Communications</i> , <b>2016</b> , 7, 12766   | 17.4 | 79  |
| 57 | The complete mitochondrial genome sequence of the ascomycete plant pathogen Colletotrichum acutatum. <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , <b>2016</b> , 27, 4547-4548         | 1.3  | 6   |
| 56 | Kingdom-Wide Analysis of Fungal Small Secreted Proteins (SSPs) Reveals their Potential Role in Host Association. <i>Frontiers in Plant Science</i> , <b>2016</b> , 7, 186   | 6.2  | 96  |
| 55 | Whole genome sequence and genome annotation of Colletotrichum acutatum, causal agent of anthracnose in pepper plants in South Korea. <i>Genomics Data</i> , <b>2016</b> , 8, 45-6                                 |      | 20  |
| 54 | Crystal structure and functional analysis of isocitrate lyases from Magnaporthe oryzae and Fusarium graminearum. <i>Journal of Structural Biology</i> , <b>2016</b> , 194, 395-403                                | 3.4  | 8   |
| 53 | Genome-wide profiling of DNA methylation provides insights into epigenetic regulation of fungal development in a plant pathogenic fungus, Magnaporthe oryzae. <i>Scientific Reports</i> , <b>2015</b> , 5, 8567   | 4.9  | 76  |
| 52 | Potential roles of laccases on virulence of Heterobasidion annosum s.s. <i>Microbial Pathogenesis</i> , <b>2015</b> , 81, 16-21   | 3.8  | 9   |

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|----|--|------|-----|
| 51 | Systematic functional profiling of transcription factor networks in <i>Cryptococcus neoformans</i> . <i>Nature Communications</i> , <b>2015</b> , 6, 6757  | 17.4 | 99  |
| 50 | Systematic characterization of the bZIP transcription factor gene family in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Environmental Microbiology</i> , <b>2015</b> , 17, 1425-43                       | 5.2  | 34  |
| 49 | Systematic characterization of the peroxidase gene family provides new insights into fungal pathogenicity in <i>Magnaporthe oryzae</i> . <i>Scientific Reports</i> , <b>2015</b> , 5, 11831                        | 4.9  | 40  |
| 48 | dbHiMo: a web-based epigenomics platform for histone-modifying enzymes. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2015</b> , 2015, bav052   | 5    | 9   |
| 47 | Role of the MoYAK1 protein kinase gene in <i>Magnaporthe oryzae</i> development and pathogenicity. <i>Environmental Microbiology</i> , <b>2015</b> , 17, 4672-89   | 5.2  | 26  |
| 46 | Genome-Wide Analysis of Hypoxia-Responsive Genes in the Rice Blast Fungus, <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , <b>2015</b> , 10, e0134939  | 3.7  | 16  |
| 45 | Integrative structural annotation of de novo RNA-Seq provides an accurate reference gene set of the enormous genome of the onion ( <i>Allium cepa</i> L.). <i>DNA Research</i> , <b>2015</b> , 22, 19-27           | 4.5  | 47  |
| 44 | Insights on the evolution of mycoparasitism from the genome of <i>Clonostachys rosea</i> . <i>Genome Biology and Evolution</i> , <b>2015</b> , 7, 465-80   | 3.9  | 93  |
| 43 | Secret lifestyles of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , <b>2014</b> , 4, 5135  | 4.9  | 60  |
| 42 | Genome sequence of the hot pepper provides insights into the evolution of pungency in <i>Capsicum</i> species. <i>Nature Genetics</i> , <b>2014</b> , 46, 270-8  | 36.3 | 594 |
| 41 | A quick and accurate screening method for fungal gene-deletion mutants by direct, priority-based, and inverse PCRs. <i>Journal of Microbiological Methods</i> , <b>2014</b> , 105, 39-41                           | 2.8  | 4   |
| 40 | fPoxDB: fungal peroxidase database for comparative genomics. <i>BMC Microbiology</i> , <b>2014</b> , 14, 117   | 4.5  | 37  |
| 39 | Role of MoAND1-mediated nuclear positioning in morphogenesis and pathogenicity in the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , <b>2014</b> , 69, 43-51                  | 3.9  | 15  |
| 38 | Regulation of cellular diacylglycerol through lipid phosphate phosphatases is required for pathogenesis of the rice blast fungus, <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , <b>2014</b> , 9, e100726           | 3.7  | 9   |
| 37 | In silico sequence analysis reveals new characteristics of fungal NADPH oxidase genes. <i>Mycobiology</i> , <b>2014</b> , 42, 241-8  | 1.7  | 1   |
| 36 | Comparative functional analysis of the velvet gene family reveals unique roles in fungal development and pathogenicity in <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , <b>2014</b> , 66, 33-43 | 3.9  | 26  |
| 35 | Roles of Forkhead-box Transcription Factors in Controlling Development, Pathogenicity, and Stress Response in <i>Magnaporthe oryzae</i> . <i>Plant Pathology Journal</i> , <b>2014</b> , 30, 136-50                | 2.5  | 17  |
| 34 | Transcriptome Analysis of Early Responsive Genes in Rice during <i>Magnaporthe oryzae</i> Infection. <i>Plant Pathology Journal</i> , <b>2014</b> , 30, 343-54   | 2.5  | 34  |

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|----|--|------|------|
| 33 | Analysis of in planta Expressed Orphan Genes in the Rice Blast Fungus <i>Magnaporthe oryzae</i> . <i>Plant Pathology Journal</i> , <b>2014</b> , 30, 367-74  | 2.5  | 4    |
| 32 | Histone acetylation in fungal pathogens of plants. <i>Plant Pathology Journal</i> , <b>2014</b> , 30, 1-9  | 2.5  | 43   |
| 31 | Fungal plant cell wall-degrading enzyme database: a platform for comparative and evolutionary genomics in fungi and Oomycetes. <i>BMC Genomics</i> , <b>2013</b> , 14 Suppl 5, S7  | 4.5  | 49   |
| 30 | Two conidiation-related Zn(II)2Cys6 transcription factor genes in the rice blast fungus. <i>Fungal Genetics and Biology</i> , <b>2013</b> , 61, 133-41   | 3.9  | 32   |
| 29 | Global expression profiling of transcription factor genes provides new insights into pathogenicity and stress responses in the rice blast fungus. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003350                              | 7.6  | 43   |
| 28 | CFGP 2.0: a versatile web-based platform for supporting comparative and evolutionary genomics of fungi and Oomycetes. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D714-9   | 20.1 | 40   |
| 27 | <i>Agrobacterium tumefaciens</i> -mediated transformation of the lichen fungus, <i>Umbilicaria muehlenbergii</i> . <i>PLoS ONE</i> , <b>2013</b> , 8, e83896   | 3.7  | 35   |
| 26 | Comparative Analysis of the Korean Population of <i>Magnaporthe oryzae</i> by Multilocus Microsatellite Typing. <i>Plant Pathology Journal</i> , <b>2013</b> , 29, 435-9   | 2.5  | 3    |
| 25 | Lifestyle transitions in plant pathogenic <i>Colletotrichum</i> fungi deciphered by genome and transcriptome analyses. <i>Nature Genetics</i> , <b>2012</b> , 44, 1060-5   | 36.3 | 564  |
| 24 | Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , <b>2012</b> , 194, 1001-1013  | 9.8  | 168  |
| 23 | Gene expression profiling during conidiation in the rice blast pathogen <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , <b>2012</b> , 7, e43202  | 3.7  | 26   |
| 22 | The cell cycle gene <i>MoCDC15</i> regulates hyphal growth, asexual development and plant infection in the rice blast pathogen <i>Magnaporthe oryzae</i> . <i>Fungal Genetics and Biology</i> , <b>2011</b> , 48, 784-92         | 3.9  | 19   |
| 21 | The PEX7-mediated peroxisomal import system is required for fungal development and pathogenicity in <i>Magnaporthe oryzae</i> . <i>PLoS ONE</i> , <b>2011</b> , 6, e28220  | 3.7  | 40   |
| 20 | Cyber infrastructure for <i>Fusarium</i> : three integrated platforms supporting strain identification, phylogenetics, comparative genomics and knowledge sharing. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D640-6      | 20.1 | 56   |
| 19 | Comparative genomics reveals mobile pathogenicity chromosomes in <i>Fusarium</i> . <i>Nature</i> , <b>2010</b> , 464, 367-73   | 50.4 | 1085 |
| 18 | <i>Pseudomonas</i> sp. LSW25R, antagonistic to plant pathogens, promoted plant growth, and reduced blossom-end rot of tomato fruits in a hydroponic system. <i>European Journal of Plant Pathology</i> , <b>2010</b> , 126, 1-11 | 2.1  | 28   |
| 17 | Fungal secretome database: integrated platform for annotation of fungal secretomes. <i>BMC Genomics</i> , <b>2010</b> , 11, 105  | 4.5  | 128  |
| 16 | Rice blast fungus ( <i>Magnaporthe oryzae</i> ) infects <i>Arabidopsis</i> via a mechanism distinct from that required for the infection of rice. <i>Plant Physiology</i> , <b>2009</b> , 149, 474-86                            | 6.6  | 54   |

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|----|---|------|------|
| 15 | Homeobox transcription factors are required for conidiation and appressorium development in the rice blast fungus <i>Magnaporthe oryzae</i> . <i>PLoS Genetics</i> , <b>2009</b> , 5, e1000757                  | 6    | 143  |
| 14 | A novel pathogenicity gene is required in the rice blast fungus to suppress the basal defenses of the host. <i>PLoS Pathogens</i> , <b>2009</b> , 5, e1000401   | 7.6  | 143  |
| 13 | A Quick and Safe Method for Fungal DNA Extraction. <i>Plant Pathology Journal</i> , <b>2009</b> , 25, 108-111   | 2.5  | 121  |
| 12 | Functional analysis of MCNA, a gene encoding a catalytic subunit of calcineurin, in the rice blast fungus <i>magnaporthe oryzae</i> . <i>Journal of Microbiology and Biotechnology</i> , <b>2009</b> , 19, 11-6 | 3.3  | 33   |
| 11 | Fungal cytochrome P450 database. <i>BMC Genomics</i> , <b>2008</b> , 9, 402   | 4.5  | 96   |
| 10 | FTFD: an informatics pipeline supporting phylogenomic analysis of fungal transcription factors. <i>Bioinformatics</i> , <b>2008</b> , 24, 1024-5  | 7.2  | 119  |
| 9  | Phytophthora Database: A Forensic Database Supporting the Identification and Monitoring of Phytophthora. <i>Plant Disease</i> , <b>2008</b> , 92, 966-972   | 1.5  | 51   |
| 8  | Genome-wide analysis of T-DNA integration into the chromosomes of <i>Magnaporthe oryzae</i> . <i>Molecular Microbiology</i> , <b>2007</b> , 66, 371-82  | 4.1  | 69   |
| 7  | Genome-wide analysis of T-DNA integration into the chromosomes of <i>Magnaporthe oryzae</i> . <i>Molecular Microbiology</i> , <b>2007</b> , 66, 826-826   | 4.1  | 3    |
| 6  | GH3-mediated auxin homeostasis links growth regulation with stress adaptation response in <i>Arabidopsis</i> . <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 10036-10046                          | 5.4  | 346  |
| 5  | The genome sequence of the rice blast fungus <i>Magnaporthe grisea</i> . <i>Nature</i> , <b>2005</b> , 434, 980-6   | 50.4 | 1202 |
| 4  | Molecular characterization of a cDNA for a cysteine-rich antifungal protein from <i>Capsicum annuum</i> <b>2004</b> , 47, 375-382   |      | 8    |
| 3  | Use of <i>Colletotrichum graminicola</i> KA001 to Control Barnyard Grass. <i>Plant Disease</i> , <b>2000</b> , 84, 55-59  | 1.5  | 9    |
| 2  | Regulation of cAMP-dependent protein kinase during appressorium formation in <i>Magnaporthe grisea</i> . <i>FEMS Microbiology Letters</i> , <b>1999</b> , 170, 419-423  | 2.9  | 28   |
| 1  | Vegetative Compatibility Groups and Pathogenicity Among Isolates of <i>Fusarium oxysporum</i> f. sp. <i>cucumerinum</i> . <i>Plant Disease</i> , <b>1998</b> , 82, 244-246                                      | 1.5  | 48   |